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Result
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Maximum
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Perfect
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length: 2000000000
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Match
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2: pir2:*
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4: pir4:*
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  283366 segs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
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                                              RESULT 2
D36005
IIg heavy chain V region (M43) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: D36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Scatus: preliminary
A,Status: preliminary
A,Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: GB:M34024
C;Genetics:
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87; Conservat
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Pred. No. 4.8e-30;
8; Mismatches 20;
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chain	heavy cha	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy ch	heavy	heavy		TICOVY

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Ig heavy chain V region (30p1) - human
C;Species Homo sapiens (man)
C;Decies Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C;Accession: C36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: C36005
A;Status: preiminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: GB:M18513
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
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heavy chain variable gene :
                                                                                         16-Dec-1998
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Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human C;Species: Homo sapiens (man) C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change C;Accession: S48798  
C;Accession: S48798  
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D. submitted to the EMBL Data Library, October 1994  
A;Description: Molecular characterization of natural human anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
S48798
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A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Recession: S48798
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 - <AMH>
A;Cross-references: EMBL:Z46382; NID:g562324; PIDN:CAA86521.1; PID:g1340167
A;Cross-references: EMBL:Z46382; nregion; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;15-98/Domain: immunoglobulin homology <IPM>
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                                R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: H36005
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Matches 85
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Status: preliminary Molecule type: mRNA
                                                                                                                                 Accession: H36005
                                                                                                                                                 g heavy chain V region (M85) - human
;Species: Homo sapiens (man)
;Date: 21-Dec-1990 #sequence_revision
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70.2%;
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Pred. No. 1.2e-29;
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'ig heavy chain V region - C;Species: Homo sapiens (C;Date: 06-Jan-1995 #sequ-C;Accession: $30531 R;Mariette, X.
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A;Title: Restricted utilization of germ-line V(H)3 genes and short d A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31114
A;Status: preliminary; nucleic acid sequence not shown; translation
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
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A;Cross-references: GB:
C;Genetics:
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A; Cross-references: GDB:
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submitted to the EMBL Data A; Reference number: 830520
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Best Local S
Matches 86
                                                                                                                   ;Species: Homo sapiens (man)
;Date: 06-Jan-1995 #sequence_revision
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Pred. No. 1.4e-29;
7; Mismatches 25
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Pred. No. 1.4
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Ig heavy chain - human (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999 C;Accession: S31108
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.: Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse ta;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31108
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A;Title: The human cord blood antibody repertoire. Frequent A;Reference number: $26786; MUID:92111632; PMID:1730251
A;Accession: $26798
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterottetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Cross-references: EMBL:Z18317
A;Cross-references: EMBL:Z18317
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;15-98/Domain: immunoglobulin homology <IVM>
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A; Residues: 1-121 < MOR>
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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A;Status: preliminary
A;Molecule type: mRNA
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Pred. No. 3.8e-29;
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Pred. No. 1.7e-29;
0; Mismatches 22;
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                                                                    Tol, M.J.D.; Vossen, J.M.; Schuurmar
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Ig heavy chain V region - human (fragment)
c;Species: Homo sapiens (man)
c;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_cha
C;Caccession: S31666
C;Accession: S31666
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.;
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin
A; Description: Mechanisms that A; Reference number: S31585 A; Accession: S31666
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A;Molecule type: DNA
A;Residues: 1-114 <FIG>
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A;Title: In vitro assembly of repertoires of antibody chains A,Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46390
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S46390
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A;Note: the nucleotide sequence was submitted G;Superfamily: immunoglobulin V region; immuno C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMY>
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A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
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Best Local S
Matches 84
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Pred. No. 4.9e-29;
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Pred. No. 4.6e-29;
8; Mismatches 21
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                              immunoglobulin diversity operate
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C;Species: Hor
C;Date: 13-Jar
C;Accession: (
R;Olee, T.; In
J. Exp. Med. 1
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S23624
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A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from A;Reference number: 823623; MUID:92156804; PMID:1740665
A;Accession: $23624
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585 A;Accession: S31588
                                                              C;Accession: S31588
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
                                                                                                                                    Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Uul-1999
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A;Molecule type: mRNA
A;Residus: 1-138 <CUI>
A;Residus: 1-138 <CUI>
A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964
A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-143 <OLE>
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 401; DB 2;
Pred. No. 7.6e-29;
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Pred. No. 6.6e-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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A;Accession: S31107
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-119 <RRAA-
A;Cross-references: EMBL:X62955
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Octob
                                                                                                                                                                                                                                                                                                                                                                                                  If heavy chain - human (;Species: Homo sapiens (man) (;Species: Homo sapiens (man) (;Species: Homo sapiens (man) (;Date: 02-Dec-193) #sequence_revision 26-May-1995 #text_change 17-Mar-1999 (;Accession: S31107 (;Accession: S31107 (;Accession: F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain - human (Ran) (Ran) (Species: Homo sagiens (Man) (Species: 19-Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999 (Spate: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999 (Spate: 03-Dec-1993 #sequence_revision 26-May-1995 #sequence_r
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S31110
                                                                                                                                                                                                                                                                   Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third
A;Reference number: S31104; MUID:92111633; PMID:1730252
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S31107
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A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third
A;Reference number: S31104; MUID:92111633; PMID:1730252
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A; Residues: 1-140 < CUI>
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         EMBL Data Library, October 1991
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A;Status; preliminary
A;Molecule type; DNA
A;Molecule type; DNA
A;Residues: 1-114 <FIG>
A;Cross-references: EMBL:Z31687; NID:g509784; PIDN:CAA83492.1; PID:g1335144
A;Cross-references: EMBL:Z31687; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Dates: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Dates: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Dates: 27-Jun-2000
C;Dates: A, Figini M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by A;Reference number: $46390; MUID:94254092; PMID:8196048
A;Accession: $46391
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Search completed: October Job time: 21.9028 secs
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Best Local Similarity 69.4%;
Matches 84; Conservative
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Post-processing: Minimum Match 0%
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## ALIGNMENTS

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Scoring table: Sequence: Run on:

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R HSSP; P01799; INCP.

R GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0003823; F:immune response; NAS.
DR InterPro; IPR007110; Iglike.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
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"Complete amino acid sequence of the alpha 2 heavy cha
"Complete amino acid sequence of the allotype.",
IgA2 immunoglobulin of the A2m (2) allotype.",
Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
-1. MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2,
REGION OF THIS MYELOMA PROTERIN IS ALSO GIVEN.
-1. SIMILARITY: Contains 1 immunoglobulin-like domain.
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10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region BUT.
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Mammalia; Eutheria;
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ain V-III region KOL.
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MEDILINE=83289131; PubMede-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies.
structure of crystallized monoclonal immunoglobulin IgG1
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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GO; GO:0003823; F:antigen binding; NJ
GO; GO:0006955; P:immune response; NJ
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PDB; 2FB4; 12-JUL-89.
PDB; 2IG2; 12-JUL-89.
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                                                                                                      53.5%;
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PYRROLIDONE CARBOXYLIC
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                                                                                           Score 364; DB
Pred. No. 6.5e
L3; Mismatches
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QMDSLRPEDTGVYFC
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omic models of the antigen-binding
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                                                                                                         DB 1;
 -ARDGGHGFCSSASCFGPDYWGQG
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                                                                                                                   Length
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TOVTVSS

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HIMMAN

PU17 HUMAN

PU17 B1;

I 21-JUL-1986 (Rel. 01, Created)
I 21-JUL-1986 (Rel. 01, Last sequence update)
JT 10-0CT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region GAL.
OS Homo sapiens (Human).
OS Elkaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Primates; Catarrhini; Hc
                                                                              SSEPPER
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HV3B_H
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Best Local S
Matches 77
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21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
7 heavy chain V-III region WEA.
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"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";

Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

-i- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.
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PIR; A02046; M3HUWE
HSSP; P01772; 2FB4
C:ex
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InterPro; IPR003596; Ig v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN 1 112 IG-LIKE.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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12256 MW; D88294FB418A07B7
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Pred. No. 7.3e
14; Mismatches
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                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local S
Matches 79
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:000823; F:antigen binding; NAS.
GO; GO:0006955; P:imune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin v region.
DOMAIN
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P01782;
P01782;
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
10-CCT-2003 (Rel. 42, Last annotation update)
7-any chain V-III region DOB.
                                                                                                                                    MEDIINE=80020921; PubMed=114209;
Steiner L.A., Garcia Pardo A., Margolies
"Amino acid sequence of the heavy-chain v
crystallizable human myeloma protein Dob.
Biochemistry 18:4068-4080(1979).
  "The crys
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NON TER
SEQUENCE
                                                                  CRYSTALLIZATION.
MEDLINE=80020920; Pubmed=114208;
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Hilschmann N.;
Submitted (JUN-1975) to
                       Steiner L.A., Lopes A.D.; "The crystallizable human myeloma
                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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116
116 AA;
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Pred. No. 7.5e
8; Mismatches
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Best Local S
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Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSTTE; PS50835; IG LIKE; 1

Immunoglobulin V region.

112
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HSSP; P01772; 2FP4.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0003823; F:antigen binding; NAS.
G0; G0:0003823; P:immune response; NAS.
G0; G0:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007310; Ig-v.
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21-JUL-1986
10-OCT-2003
             Immunoglobulin DOMAIN 1
MOD_RES 1
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                                                                                                                                     SMART; SI
PROSITE;
                                                                                                                                                            GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003825; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemistry 18:4054-4067(1979).
MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE
HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
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                                          '; pS50835; IGV; 1.
lobulin V region; Pyrroi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 01, Created)
(Rel. 01, Last sequence up
(Rel. 42, Last annotation
ain V-III region CAM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13440 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.4%;
                                                Pyrrolidone carboxylic acid.
IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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Pred. No. 4e-29
(2; Mismatches
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RESULT 8
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RESULT 9
HV3C_HUMAN
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01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
r 15-JUL-1999 (Rel. 38, Last annotation updat
g heavy chain V region 5A precursor.
G Carassius auratus (Goldfish).
E Bukaryota, Metazoa; Chordata; Craniata; Ve. Cartinopterygii; Neopterygii; Teleostei; Os Cyprinidae; Carassius.
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Best Local S
Matches 69
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HSSP; P01772; 2FB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=88144476;
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SMART; SM00406; IGv;
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InterPro; IPR007110;
InterPro; IPR003596;
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                                                                                                                                                                             DSVKGRFTISRDNAKNIMYLQMNSLKPEDTAVYYC
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nilarity 61.5%;
Conservative 1
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Pred. No. 5.1e-29;
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COMPLEMENTARITY-DETERMINING-2
FRAMEWORK-3.
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COMPLEMENTARITY-DETERMINING-1.
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Ostariophysi; Cypriniformes;
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P01762;
21-JUL-1986 (Rel. C
21-JUL-1986 (Rel. C
10-OCT-2003 (Rel. 4
Ig heavy chain V-III region TRO.

Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1]
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig_v. Pfam; PF00047: io. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matthyssens G., Rabbitts T.H.;
"Structure and multiplicity of genes for the human imm heavy chain variable region.";
Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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SMART; SM00406; IG:
PROSITE; PS50835;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Iq heavy chain V-III region VH26 precursor.
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NA
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PDB; 1HOU; 23-DEC-99.
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EMBL; M35415; AAA58735.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PS59835; IG LIKE; 1.
obulin V region; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                              QVQLQDSGGGLVQAGGSLRLSCAASGSIFSSDLMGWYRQAPGKEREAVARIT-RGGTTSY
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117 /
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...V-III region TRO.
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12582 MW;
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74.0%;
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Pred. No. 1.7e-28;
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003823; F:antigen binding; NAS.
InterPro; IPR00355; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Pyrrolidone carb
DOMAIN

108
IG-LIKE; 1.
IGNAIN
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P01785;
21_JUL_1986 (Rel. 01, Created)
21_JUL_1986 (Rel. 01, Last sequence update)
10_OCT_2003 (Rel. 42, Last annotation update)
11_Standard V region MOO.
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae;
                                                                        MOL. IMMUNDAL. 16:565-5/0(13/7).
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-112.

MEDLINE=77242268; PubMed=407924;

Wasserman R.L., Capra J.D.;

"Primary structure of the variable regions immunoglobulin heavy chains.";

Biochemistry 16:3160-3168(1977).
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Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
-!- MISCELLAMEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN
                                            PIR; A90403; MHDGMO.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                     MEDLINE=80077682; PubMed=117299;
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MEDLINE=76023781; PubMed=809331;
    InterPro; IPR007110;
                                                                                                                                                                                                                                                             McCumber L.J., Capra J.D.;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 113-117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hilschmann N.;
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                                                                                                                                                                                         complete amino-acid sequence of a canine mu chain.", Immunol. 16:565-570(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116
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122 AA;
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.; 13472 MW;
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Ig-like
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Pred. No. 6.6e-28;
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RESULT 12
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Best Local S
Matches 74
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Best Local S
Matches 76
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DOMAIN 1
MOD_RES 1
NON_TER 121
SEQUENCE 121
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SEQUENCE
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chair V-III region HIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
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PROSITE; PS50835; IG_LIKE;
Immunoglobulin V region.
DOMAIN 1 116
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SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chiu Y.-Y.H., Lopez de Castro J.A., Polja "Amino acid sequence of the VH region of cryoimmunoglobulin IgG Hil.";
Biochemistry 18:553-560(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=79124695; PubMed=420800;
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76; Conserv
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                                                                                    OVOLODSGGGLVOAGGSLRLSCAASGSIFSSDLMGWYROAPGKEREAVARI-TRGGTTSY
          ADSVKGRFTISRDNAKNTMYLQMNSLKPEDTAVYYCNARRSNYDRSWG-DYWGQGTQVTV
                                              QVKLVQAGGGVVQPGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Butheria; Primates; Catarrhini; Hominidae; Homo.
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)047; ig; 1.
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117 AA;
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IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID
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Pred. No. 7e-28;
3; Mismatches
                                                                                                                                               Score 342.5;
Pred. No. 9.
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                                                                                                                              ed. No. 9.2e-28;
Mismatches 31
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on of human myeloma
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Best Local S
Matches 73
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P017765;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
To heavy chain V-III region TIL.
                                                                           HUMAN
                                                                                                                                                                                                                                                                                                      DOMAIN
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Immunoglobulin structure and genetics. Identity between variable regions of a mu and a gamma2 chain.";
J. Biol. Chem. 252:7192-7199(1977).
-i- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
HV3I HUMAN STANDARD; PRT; 119 AA P01770; P01770; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation updat If heavy chain V-III region NIE. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
DCMAIN
1 108
                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A02048; H3HUTL.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang A.-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=78005528; PubMed=409716; Wang A.-C., Wang I.Y., Fudenberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                 30; GO:0005576; C:extracellular; NAS. 30; GO:0003823; F:antigen binding; NAS. 30; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
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                                                                                                                                                                                                                EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYVMSWVRQAPGKGLZWVGA1ZGLSVSZSY
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115 AA;
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12356 MW;
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Pred. No. 1.1
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DISULFID
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SEQUENCE
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P01784;
P1-JUL-1986 (Rel. 01, Created)
P1-JUL-1986 (Rel. 01, Last sequence update)
P1-JUL-1986 (Rel. 42, Last annotation update)
P1-CT-2003 (Rel. 42, Last annotation update)
P1-JUL-1986 (Rel. 42, Last annotation update)
P1-JUL-1986 (Rel. 01, Created)
P1-JUL-1986 (Rel. 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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Ponsting1 H., Hilschmann N.;

"The rule of antibody structure. The primary structure of a monocional IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";

Poppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CANFA
SEQUENCE.
MEDLINE=77242268; PubMed=407924;
                                                                                                               NCBI_TaxID=9615;
                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A91668; G1HUNI.
HSSP; P01772; 2FB4.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADSVKGRFTISRDNAKUTMYLOMNSLKPEDTAVYYCNARRSNYDRSWGDYWGQGTQVTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLVQSGGGVVQPGRSLRLSCAASGFTFSRYTIHWVRQAPGKGLEWVAVMSYBGBBKHY
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119
119 AA;
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13242 MW; C96935A6E55E165B CRC64;
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SMART; SM00406; IGV; 1.
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                                      113
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                                                                                         ADSVKGRFTISRDNAKNTMYLQMNSLKPEDTAVYYCNARRSNYDRSWG-DYWGQGTQVTV 118
                                      SS-
                                                          SS 120
                                                                            ADAVKGRFTISKDNAKDSLYLQMNSLRAEDTAVYYC----APWQFEYWGQGTLVTV 112
                                                                                                                 EVOLVESGGDLVKPGGSLRLSCVASGITFSGYDMQWVRQAPGKGLQKVAYFNDALSAQGY 60
                                                                                                                                     QVQLQDSGGGLVQAGGSLRLSCAASGSIFSSDLMGWYRQAPGKEREAVARITRG-GTTSY 59
                                                                                                                                                                                               114 AA; 12430 MW; B1D4745D2C4E13C4 CRC64;
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                                                                                                                                                       49.9%; Score 339; DB 1; Length 114; llarity 59.8%; Pred. No. 1.9e-27; Conservative 11; Mismatches 28; Indels
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
6: sp_mammal:*
7: sp_mho:*
9: sp_blage:*
10: sp_plage:*
11: sp_virus:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMM	
ARIES	

Query         Query         Description           400.5         58.9         597.4         Q96BB9         Q96bb9 homo sapien           399         58.7         118.4         Q9UL72         Q9172 homo sapien           379.5         55.8         119.1         Q920E7         Q9187         Q9188           379.5         55.8         131.4         Q9UL90         Q9189         homo sapien           376.5         55.4         113.4         Q9UL90         Q9189         homo sapien           373.5         54.9         121.4         Q9UL71         Q9171         Q9171         homo sapien           373.5         54.9         121.4         Q9Y509         Q99509         homo sapien           373.5         54.9         121.4         Q9Y509         Q99509         homo sapien           373.5         54.9         121.4         Q9Y509         Q99509         homo sapien           371.5         54.9         112.4         Q9Y509         Q99509         homo sapien           367.5         54.0         112.4         Q991801         homo sapien           367.5         54.0         49.9         4         Q80184         Q80184         mus musculu	F	, r	1 H	14	13	12	11	10	9	00	7	o	υī	4	w	2	۲	No.	Result
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## ALIGNMENTS

RESULT 1

Db	8.	Дb	γQ	3 0	B 10	SO	뒩	DR	DR.	7 5	ב א א	DR	DR	RI.	R.A	RC	R R	20	8	8	SO	DΕ	ဌ	ΡŢ	25	38	Q96BB9
80 ADSVKGRFTISRDNSRDTLYLOMNSLRAEDTAVYYCAKDPRGYSASGNYTREDYWGQG 137	60 ADSVKGRFTISRDNAKNTMYLQMNSLKPEDTAVYYCNARRSNYDRSWGDYWGQG 113	20 EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYY 79	1 QVQLQDSGGGLVQAGGSLRLSCAASGSIFSSDLWGWYRQAPGKEREAVARIT-RGGTTSY 59	Matches 86; Conservative 11; Mismatches 25; Indels 9; Gaps 3;	Y Match 58.9%; Score 400.5; I	SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;	)290;	PS50835; IG_LIKE;	~-	1047. 10. 5	InterPro: IPR003006; IG_MHC.		.5760; AAH15760.1;	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.	Strausberg R.;		SECUENCE FROM N.A.	NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Chordata;	(Human).	Hypothetical protein.	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	. (TrEMBLrel. 1	01-DEC-2001 (TrEMBLrel. 19, Created)	Q96BB9 PRELIMINARY; PRT; 597 AA.	

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114

TOVTVSSAHHS 124

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QSULT2
ID QSULT2
AC QSULT2
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AC QSULT2
DT 01-MAY-2
DT 01-MAY-2
DT 01-MAY-2
DT 01-MCT-2
DT Myosin-1
DB (Fragmen
OS Homo sap
OC Mammalia
OX NCBI_Tax
RN (1)
Tax
RN (1)
RA Young D.
RA Young D.
RT "Myosin-
RT Clin. "Myosin-
RT Clin. AI
DR EMBL; AI
DR EMBL; AI
DR HSSP; P(
DR InterProperty of the Security
DR FROSITS, STANNON_TER
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Best Local S
Matches 81
                           Atkin J.D., Tape A., Jennings "Definition of the Idiotope o in Mammalian Cells."; Submitted (SEP-2000) to the EEMBL; AFS07937; AAL09421.1; -PIR; C25913; C25913.
                                                                                                                                                                                                                                                                                                                0920E7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Prerin-mimicking anti-idiotope heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q920E7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SPROSITE; PS50835; IG_LIKE; 1.
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EMBL; AF035042; AAD56278.1; -.
PIR; S21205; S21205.
HSSP; P01772; 2FB4.
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Young D.C.;
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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01.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
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                                                                                                                    Jennings I.G., Horaitis O.,
liotope of Pterin-Mimicking
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                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 399; DB 4; Length 118; Pred. No. 2.6e-33; Indels 1; Mismatches 26; Indels
                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Catarrhini; Hominidae;
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RESULT 4
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ID Q9UL8
ID Q9UL
DT 01-V
DT 01-V
DT 01-V
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Best Local S
Matches 81
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Best Local S
Matches 81
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SEQUENCE
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Q9UL88;

01-MAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Myosin-reactive immunoglobulin heavy chain variable
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF035026; AAD56262.1;
PIR; S21205; S21205.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98277139; PubMed=9614934; Wit X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eetus.";
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                                                                                                                                                                                                                                                                                 Similarity
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SWGDYWGQGTQVTVSS
                                                                                                                 SYADSVKGRETISRDNAKNTMYLOMNSLKPEDTAVYYC-----
                                                                                                                                                                                                            QVQLQDSGGGLVQAGGSLRLSCAASGSIFSSDLMGWYRQAPGKEREAVARI----TRGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                 M00406; IGv; 1.
PS50835; IG_LIKE; 1.
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                                                                    DYAAPVKGRLTISRDSSKNTLYLRMNSLKTEDTAVYYCTTGITMIIVVITTSSKRTSF--
                                                                                                                                                               EVOLVESGGGLVKPGGSLRLSCAASGFTFSKAWMSWVRQAPGKGLEWVGRIKSKTDGGTT
                                                                                                                                                                                                                                                                                                                                                   131
131 AA;
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119 AA;
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13025 MW;
                                                                                                                                                                                                                                                                                                                                                   131
14142 MW;
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                                                                                                                                                                                                                                                                                 55.8%; Score 379.5; DB 59.6%; Pred. No. 3e-31;
                           120
                                                                                                                                                                                                                                                        14; Mismatches
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                                                                                                                                                                                                                                                                                                       DB 4;
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RESULT 5

Q9UL90
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DE MYOSIN-
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OS Homo sa
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RM [1]
RM SEQUENC
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RH CIIN. I
DR HESE; A
DR SAART;
DR SAART;
DR SAART;
SG SEQUENC
              RESULT 6
Q8WUK1
ID Q8WU
ID Q8WU
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Best Local S
Matches 83
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC020240; AAH20240.1; -
PIR; PL0120; PL0120.
PIR; S15590; S15590.
InterPro; IPR007110; Ig-like.
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01-MAY-2000
01-MAY-2000
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                      QBWUK1;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIID. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035024; AAD56260.1; -.
HSSP; P01772. 255.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=98277139; PubMed=9614934;

Wu X., Liu B., Van der Merwe P.L.,

Young D.C.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8WUK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                              TISSUE=Tonsil;
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYC-AKDLN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                         Chordata;
Primates;
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Pred. No. 5.1e-31;
8; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local S
Matches 80
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Best Local S
Matches 83
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InterPro; IPR003596; Ig_v.
Pfam; pP00047; ig; 5.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG_LIXE; 5.
PROSITE; PS50835; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67296 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clin. Immunol. Immunopathol. 87:
EMEL; AF035043; AAD56279.1; -.
HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NOW TEED
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Tim B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09UI71;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQÜENCE
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                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                        VSS
                 SSA
                                                                                                                                                                                                                                  EVQLVESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGGSTYY
                                                                                                                                                                                                                                                                                      OVOLODSGGGLVOAGGSLRLSCAASGSIFSSDLMGWYROAPGKEREAVARIT-RGGTTSY
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                                                                                                                            ADSVKGRFTISRDNSKNSLYLOMNSLRAEDTALYYCAKGKVTTIYDRF--DIWGQGTMVT
                                                                                                                                                                              ADSVKGRFTISRDNAKNTMYLOMNSLKPEDTAVYYCNARR--SNYDRSWGDYWGQGTQVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADSVKGRFTISRDNAKVIMYLQMNSLKPEDTAVYYCNARRSNYDRSWG-----DYWGQG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC-----AKDWSEGVETFDIWGQG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.1%;
ilarity 63.4%;
Conservative
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                 121
                                                                     120
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13154 MW; 2F045CCFA5D50736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67296 MW;
                                                                                                                                                                                                                                                                                                                                                                        54.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                     Score 373.5; DB 4;
Pred. No. 1.1e-30;
""amatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60C7F5950671E315 CRC64;
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Q9Y509;
01-NOV-1999
01-NOV-1999
01-OCT-2003
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Q9HCC1;
01-MAR-2001
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SEQUENCE
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"A CD10-positive subset of malignant cells is identifie myeloma using PCR with patient-specific immunoglobulin Leukemia 9:1948-1953(1995).
EMBL; S80860; AAD14339.1; -.
EMBL; P01772; 2FB4.
                                        SEQUENCE FROM N.A.

Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

"An antibody fragment2A3 specific for native lysozyme :Isolaion human synthetic phage display library and characterization.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB049915; BAB16829:1; -.

EMBL; AB049915; PSTA16829:1; -.
                                                                                                                                                                                                                                                                                                                                                           Single chain Fv (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GG; GO:0016489; F:immunoglobulin receptor activity;
GO; GO:0016066; F:cellular defense response (sensu v
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Pfam; PF0047; ig; 1.
SMART; SM00406; IGv; 1.
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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Pred. No. 1.5e
12; Mismatches
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Catarrhini;
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i; Hominidae;
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Vertebrata);
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Q9UL91;
Q9UL91;
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Q9UAY-2000 (TrEMBLrel. 13, Last sequence up
O1-OCT-2003 (TrEMBLrel. 25, Last annotation
Myosin-reactive immunoglobulin heavy chain v
(Fragment).
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Q8N5K4;
Q8N5K4;
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InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
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SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE;
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MEDLINE=98277139; PubMed=9614934;
... v f.in B.. Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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l Similarity 65.8%;
77; Conservative 1
                                                                                                                                                                                                                                                                                                                                                     Similarity
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PS50835; IG_LIKE;
                                                                                                                                                                                     ADSVKGRFTISRDNAKNTMYLQMNSLKPEDTAVYYCNARRSNYDRSWGDYWGQGTQVTVS
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112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    118
118 AA;
                                                                                                                                                                                                                                                                                                                                     Conservative
    (TrEMBLrel.
                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                54.3%; Score 369; DB 4; 67.5%; Pred. No. 3.2e-30; tive 10; Mismatches 25
    22,
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Pred. No. 1.8e
10; Mismatches
    Created
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                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                         D0633949F2AC149D CRC64;
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                                                                                                                                                                                                                                                                                                                                     Indels
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Q99XA

Q99XA

AC Q99XA

AC Q99XA

AC Q99XA

DT 01-UD

DT
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Best Local S
Matches 77
      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003599; Ig
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003096; Ig_V.
Pfam; PF000407; IG; 4.
SMART; SM00409; IG; 4.
SMART; SM00409; IGC1; 2.
SMART; SM00400; IGC1; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00836; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 499 AA; S3376 MW;
                                                                                   InterPro; IPRO07110; Ig-like.
InterPro; IPRO03006; Ig_MGC.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS0035; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chord
Mammalia, Eutheria, Roden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99KA4
Q99KA4;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                           Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004786; AAH04786.1; -
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ
EMBL; BC032249; AAH32249:1; -.
                                                  Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLQDSGGGLVQAGGSLRLSCAASGSIFSSDLMGWYRQAPGKEREAVARIT-RGGTTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOVTVSSA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADSVKGRFTISRDNAKNTMYLQMNSLKPEDTAVYYCNARRSNYDRS-----WGDYWGQG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVŐLVESGGGVVRPGGSLRLSCATSGFTFDDSGASWVRQAPGKGLEWVSSINWNGGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTVTVSSA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADSVKGRFTISRDNAKNSLYLQMNSLRVEDTALYYCARDPTKYCSGGSCLGYYMDVWGKG
                                              ar protein.
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                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53376 MW; 93A5C89582054F32 CRC64;
                                                52554 MW;
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    54.0%;
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17,
25,
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; Pred. No. 2.9e-29;
14; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
      Score 367;
                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                7DC8E96DB333077B
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    BG
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  Length 487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499;
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  RESULT 14
Q9UL9
ID Q9UL9
AC Q9UL9
AC Q9UL9
DT 01-MA
DT 01-OC
DE MYOSI
DE (Frag
OS Homo
OC Eukar
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Homo sapiens (Human)
Eukaryota; Metazoa;
                                         Fragment)
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QBWUJA 13
QBWUJA
ID QBWUJ
AC QBWUJ
AC QBWUJ
DT 01-M2
DT 11-M2
DR EMBLI,
DR Intes
DR 
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JAN-2002) to the EME EMBL, BC021276; AMH21276.1; -

PIR; S21205; S21205.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 4.

SMART; SM00406; IGY; 1.

PROSITE; PS00835; IG_LIKE; 4.

PROSITE; PS00835; IG_MHC; 2.
Q9UL93 PRELIMINARY; PRT; 116 AA.
Q9UL93;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation updat
Myosin-reactive immunoglobulin heavy chain variab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical SEQUENCE 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
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01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                            TVSSA 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADSVXGRFTISRDNAKNTMYLQMNSLKPEDTAVYYC--NARRSNYDRSWG-DYWGQGTQV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
                                                                                                                                                                                                                                                                                                                                                                    TVSSA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al protein.
573 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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(TrEMBLrel. 20, Last sequence update)
(TremBLrel. 25, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62967 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.5%;
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%; Pred. No. 8.1e
11; Mismatches
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2; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FD072344033AC530 CRC64;
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ies 30;
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Chordata;

Craniata;

Vertebrata;

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RESULT 15
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ID Q91Z0
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NON_TER
SEQUENCE
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GG; G0:0005489; F:electron transporter activity; IEA.
GG; G0:0006118; P:electron transport; IEA.
InterPro; IPR000345; CytC heme BS.
InterPro; IPR007110; Ig-1Ike.
InterPro; IPR003006; Ig_MEC.
InterPro; IPR003006; Ig_MEC.
InterPro; IPR003906; Ig_V.
Pfam; PF00047; ig; 3.

SMART; SM00406; IGy; 1.
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PROSSITE; PS50835; IG_LIKE; 1.

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EMBL, AF035021; AAD56257.1; -
PIR; PL0120; PL01
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MEDLINE=98277139; PubMed=9614934;
MM.X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                       Hypothetical SEQUENCE 47
                                                                                                                                              PROSITE; PS00190; CYTOCHROME C; PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC010327; AAH10327.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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nterPro; IPR003596; Ig_v.
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116 AA;
                                                                           473 AA;
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                                                                           51946 MW;
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       52.9%; Score 360;

    Created)
    Last sequence update)
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       DB 11;
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                                                                                                                         ADSVKGRFTISRDNAKNIMYLOMNSLKPEDTAVYYCNARRSNYDRSWGDYWGOGTQVTVS 119
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                                                                                                                                                                                                    Conservative
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1: geneseqp1980s:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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RESULT 1 AAE10551

AAE10551 standard; peptide; 129

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HPL inhibiting VHH fragment, HPL #11 from llama species.

10-DEC-2001 AAE10551;

(first entry)

1t		Query *				
	Score	Match	Length	BB	ID	
_	680	100.0	129	42	AAE10551	Aae10551 HPL inhib
N	501	73.7	129	4	AAE10558	S8 HPL
w	0	73.5	129	4	AAE10553	
4			130	4	AAE10560	0
ហ	493.5		124	4	AAE10562	HGL
თ	490		150	4.	AAE05284	Anti
7	ø	72.1	153	4	AAE05285	
œ	9	٠	153	4.	AAE05282	
9	486.5	71.5	507	7	σ	
10	•		138	u	ABG30619	Abg30619 Immunoglo
11	476.5		149	4	AAE05288	
12	474	69.7	131	4.	AAE10555	5 HPL in
13	467.5	•	119	4	AAB67777	
14	465.5	68.5	119	41	AAB67778	Aab67778 Amino aci
15	ወ		124	Ŋ	AAY28615	Aay28615 Llama ant
16	465		129	4,	AAE10561	
17	O)		118	N	AAY39819	9 Llam
18	463.5		.130	4	AAE10557	HPL
19	459	67.5	129	44.	AAE10564	Aae10564 HGL inhib
20	458.5		125	N	AAY39817	Llar
21	57.	7	111	N	AAY39816	9816 Llama
22	457.5	7	124	4	AAE10563	Aae10563 HGL inhib
23	455	66.9	131	σı	ABG30620	0
24	454.5	σ	124	4.	AAE10566	Aae10566 HGL inhib
25	454.5	66.8	130	4	AAE10556	Aae10556 HPL inhib

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Example 2; Page 9; 37pp; English

45	44	43	42	41	40	39	38	37	36	ω G	υ 4.	ω ω	32	31	30	29	28	27	Δ
435.5	435.5	436.5	437	437.5	440	440.5	442	442	442	442	444.5	444.5	444.5	446	446.5	450	453.5	453.5	404.5
	.4	•	4.	64.3	4.			5	<u>ب</u>	<u>ب</u>	U	65.4	65.4	<u>.</u>	ÿ	σ,	66.7		σ α
121	121	123	133	125	128	121	500	500	114	114	408	200	146	152	130	131	130	119	TOO
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AAB37430	AAY15412	ABR82061	ABG30972	AAY08985	AAE07141	AAY28617	AAB72413	AAB07654	AAY70991	AAY15399	AAY08990	ABB07635	AAY08987	AAE05283	AAE10554	ABG30970	AAE10567	AAB67779	7CC01955
Aab37430	Aay15412	Abr82061	Abg30972	Aay08985	Aae07141	Aay28617	Aab72413	Aab07654	Aay70991	Aay15399	Aay08990	Abb07635	Aay08987	Aae05283	Aae10554	Abg30970	Aae10567	Aab67779	7CC0TabW
Llama hea	Anti-lact	Camel ant	Immunoglo	Llama ant	. Llama ant	'Llama ant	Llama bi-	Llama ant	Llama HC-		llama pro	Anti-E	Llama pro	Anti-pota	HPL inhib	Immunoglo	HGL inhib	Amino aci	HEL TIMITE

## ALIGNMENTS

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New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                             Key
Region
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                                                                                                                                                                 20-FEB-2001; 2001EP-00200703.
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                                                                                                              (UNIL ) UNILEVER NV.
                                                                                         Van De Burg
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/note= "Complementarity determining region 2"
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                                                                                                                                                                                                                                                                                         /label= CDR1
/note= "Complementarity determining region 1"
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Matches 129
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                                                                                                                                                                                                                                                                                                                                                                                  Key
Region
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tric lipase; HGL; cosmetic control; body weight.
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Pred. No. 1.3e-37;
l; Mismatches 20;
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                                                                                                                                                                                                                                                                                                                                          peptide; 124
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75.6%;
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                        "Complementarity
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Pred. No. 1.8e-37;
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                      17-DEC-1999;
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                                                                                                                                                                                                                                                                                                             Heavy chain immunoglobulin; pathogen resistance; metabolism modulator; passive immunisation; heavy chain variable domain; VH; anti-GUS antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSVKGRFTISRDNIKNTMYLQMNSLTPEDTGVYYCAGTGAE-----GHYWGQGTQVTVSS
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                                                                         2000EP-00310997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
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Pred. No. 4.9e-37;
8; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                  attached with myc and his6 tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haard
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin or an active fragment or derivative, or a protein that is functionally equivalent for increasing the pathogen resistance in a plant or to modulate metabolism in a plant. Under some circumstances it may be desirable to retain the antibody product with the plant rather than extracting and isolating the product. In particular, edible selected antigens may be used in a method of passively immunising an animal, preferably human, against the antigen, e.g., pathogenic organisms. The present sequence is an anti-GUS antibody (denoted Clonel8) heavy chain variable domain (VH) attached to peptide linkers, myc and his6 tag. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for modifying a plant to produce an antibody or an active fragment or derivative, or a protein functional equivalent, in a cellular compartment comprises introducing a DNA sequence encoding a heavy chain immunoglobulin, where the DNA is linked to promoters and provided with an additional sequence encoding a peptide capable of targeting heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain immunoglobulin or an active fragment or derivative, or a protein that is immunoglobulin or an active fragment or derivative, or a protein that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
                                                                                                                                Heavy chain immunoglobulin; pathogen resistance; metabolism passive immunisation; heavy chain variable domain; VH; anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                Anti-GUS VH region attached
                                                                                                                                                                                                                     18-SEP-2001
                                                                                                                                                                                                                                                     AAE05285;
                                                                                                                                                                                                                                                                                      AAE05285 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GUS is beta-glucuronidase
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                                                                                                               beta-glucuronidase
                                                                                                                              passive immunisation; heavy
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UNILEVER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 AA;
                                                                                                                                                                                                                                                                                                                                                                         SAHHSEDPSS
                                                                                                                                                                                                                                                                                                                                                                                                         SAHHSEDPSS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADSVKGRFTISRDNAKNTMYLOMNSLKPEDTAVYYCNARRSNYDRSWGDYWGQGTQVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADSVKGRFAVSRDYAENTVYLOMNSLKPEDTAVYYCNTRA--
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                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                    protein;
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75.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 490; DB 4;
Pred. No. 1.3e-36;
8; Mismatches 14
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                                                                                                                                                                                      됬
                                                                                                                                                                                  retention signal, myc and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                   olism modulator;
anti-GUS antibody;
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114 119 63 59

EP1118669-A2 Unidentified

08-DEC-2000;

2000EP-00310997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method for modifying a plant to produce an antibody or an active fragment or derivative, or a protein functional equivalent, in a cellular compartment comprises introducing a DNA sequence encoding a heavy chain immunoglobulin, where the DNA is liked to promoters and provided with an additional sequence encoding a peptide capable of targeting heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain that is immunoglobulin or an active fragment or derivative, or a protein that is immunoglobulin or an active fragment or derivative, or a protein that is functionally equivalent for increasing the pathogen resistance in a plant or to modulate metabolism in a plant. Under some circumstances it may be desirable to retain the antibody product with the plant rather than extracting and isolating the product. In particular, edible selected antigens may be used in a method of passively immunising an animal, preferably human, against the antigen, e.g., pathogenic organisms. The preferably human, against the antigen, e.g., pathogenic organisms. The preferable domain (VH) attached with endoplasmic reticulum (ER) retention variable domain (VH) attached with endoplasmic reticulum (ER) retention beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 153
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 Solanum tuberosum Unidentified.
                                              Potato; heavy chain immunoglobulin; pathogen resistance, metabolism modulator; passive immunisation; heavy chain VH; anti-potato SBZII; starch branching enzyme; SBE A.
                                                                                                                       Anti-potato SBEII antibody VH region attached with myc and his6
                                                                                                                                                          18-SEP-2001
                                                                                                                                                                                                                           AAE05282 standard; protein; 153
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                                                                                                                                                                                                                                                                                                                   115
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98; Conservative
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                                                                                                                                                                                                                                                                                                                   SAHHSEDPSS
                                                                                                                                                                                                                                                                                                                                                 SAHHSEDPSS 129
                                                                                                                                                                                                                                                                                                                                                                                      ADSVKGRFAVSRDYAENTVYLOMNSLKPEDTAVYYCNTRA-----
                                                                                                                                                                                                                                                                                                                                                                                                                        ADSVKGRFTISRDNAKNTMYLOMNSLKPEDTAVYYCNARRSNYDRSWGDYWGOGTQVTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVKLQQSGGGLVQAGGPLRLSCAASGRTFSNYAVGWFRQAPGKEREFVAAISRDGGRTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                        (first entry)
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75.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 490; DB 4;
Pred. No. 1.3e-36;
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                                                                    variable domain
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RESULT 9
ABR82065
ID ABR8
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AC ABR8
AC ABR8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin or an active fragment or derivative, or a protein that is functionally equivalent for increasing the pathogen resistance in a plant or to modulate metabolism in a plant. Under some circumstances it may be desirable to retain the antibody product with the plant rather than extracting and isolating the product. In particular, edible selected antigens may be used in a method of passively immunising an animal, preferably human, against the antigen, e.g., pathogenic organisms. The present sequence is an anti-potato SBEII antibody heavy chain variable domain (vH) attached to peptide linkers, myc and his6 tag. The potato SBEII is a starch branching enzyme also designated SBE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for modifying a plant to produce an antibody or an active fragment or derivative, or a protein functional equivalent, in a cellular compartment comprises introducing a DNA sequence encoding a heavy chain immunoglobulin, where the DNA is linked to promoters and provided with an additional sequence encoding a peptide capable of targeting heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
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                                                                 23-SEP-2003
                                                                                                   ABR82065;
                                                                                                                                 ABR82065 standard; protein; 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric.
                               Immunoconjugate cAb-CEA5-beta-lactamase amino acid SEQ ID NO:14.
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                                                                                                                                                                                                                                                                                                                                                                                                                     97;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                  AHHSEDPSS 129
                                                                                                                                                                                                                                                                                                                  DSVKGRFTISRDNAKNIMYLOMNSLKPEDTAVYYCNARRSNYDRSWGDYWGQGTQVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                OVOLODSGGGLVOAGGSLRLSCAASGSIFSSDLMGWYROAPGKEREAVARITRGGTTSYA
                                                                                                                                                                                                                  AHHSEDPSS
                                                                                                                                                                                                                                                                                  DSVKGRFTISRDNAKNTVYLQMDSLKPEDTAVYYCAAKGRGLQAM--QYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                   QVQLQQSGGGLVQAGGSLRLSCVASESSFSNNHMGWYRRAPGNQRELVATISPGGSTHYV
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                               (first
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                                                                                                                                                                                                                  127
                                                               entry.
                                                                                                                                                                                                                                                                                                                                                                                                                                 72.1%;
75.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 490; DB
Pred. No. 1.3e
9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
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CEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Teh
 anti-CEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 153
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Camel; antibody; carcinoembryonic

antigen;

antibody;

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RESULT 10
ABG30619
ID ABG30
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Best Local
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Lama glama.
Synthetic.
                                                                                                                                                                                                                                                                                                                                       The present invention describes an immunoconjugate devoid of a light chain. The immunoconjugate binds to a tumour antigen that contains at least one variable domain of heavy chain antibody having an anti-tumour agent attached. Also described is the use of the immunoconjugate for the manufacture of a medicament to treat tumours expressing a tumour marker that is recognised by the immunoconjugate. The immunoconjugate has cytostatic activity and can be used as a tumour growth inhibitor. It can be used for the manufacture of a medicament to treat tumours expressing a tumour marker that is recognised by the immunoconjugate. The present sequence represents a cemel anti-carcinoembryonic antigen (CEA) antibody WH region designated chb-CEA5 and beta-lactamase immunoconjugate, from
                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JAN-2002; 2002EP-00075048.
09-JUL-2002; 2002EP-00077734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta-lactamase; :
tumour; cAb-CEA5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 31-33; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New immunoconjugate useful for the manufacture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ACF06073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                              present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003-569408/53
                                                                             121
                                                                                                        118 VSSAHHSEDPSS
                                                                                                                                    61
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                                                                                                                                                                                        1-4
                                                                                                                                                                                                          1 QVQLQDSGGGLVQAGGSLRLSCAASGSIFSSDLMGWYRQAPGKEREAVARITR-GGTTSY
                                                                                                                                                                                                                                               98;
                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                     507
                                                                             VSSAHHSEDPSS
                                                                                                                                                             ADSVKGRFTISRDNAKNTMYLOMNSLKPEDTAVYYCNAR--RSNYDRSWGDYWGOGTOVT 117
                                                                                                                                                                                        QVQLVESGGSVQAGGSLRLSCAASGDTYGSYWMGWFRQAPGKEREGVAAINRGGGYTVY
                                                                                                                                    ADSVKGRFTISRDTAKNTVYLQMNSLRPDDTADYYCAASGVLGGLHEDWFNYWGQGTQVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cortez-Retamozo V,
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                     ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
140. .50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoconjugate; cytostatic; tumour growth inhibitor;
5-beta-lactamase; VH region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= 6xHis_tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= cAb-CEA5_VH_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label= beta-lactamase
                                                                                                                                                                                                                                                          71.5%;
74.2%;
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                                                                                                        129
                                                                             132
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                                                                                                                                                                                                                                             Score 486.5; DB 7
Pred. No. 1.1e-35;
7; Mismatches 24
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ABG30619 standard;

protein; 138

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QVQLQDSGGGLVQAGGSLRLSCAASGSIFSSDLMGWYRQAPGKEREAVARIT-RGGTTSY

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Condition of a cell or tissue in the extract or sample to be proteins in a cell or tissue in the extract or sample to be groteins in a sample, comparing the distribution of proteins in different cell types, and identification of proteins that may be of importance in determining the altered properties of cells in disease, aging or other conditions. Using a heavy-chain variable domain derived from an cell immunoglobulin that is naturally devoid of light chains (VHH) in (I) comparitively/resolution in the order of 10-100 times, and detection of central translationally modified proteins. The invention also describes a method (II) that enables the simultaneous processing of large numbers of target antigens in a controlled way. The incorporated phage-ELISA central central complete automation of the technology, based on computer-made decisions on the values of the phage-ELISA for contitions can be tested, varying amounts of imput-phages can be used central canditions can be tested, varying amounts of input-phages can be used conditions. In (II), due to the fact that many different concluse, enabling the generation of large numbers of attitude the simultaneously in order to decrease the enrichment of sticky phage-central candies. Micro-panning is an effective tool for selecting both naive, synthetic and immune libraries on large numbers of different target time frames needed for the generation of large panels of antibodies in short time frames needed for the generation of large panels of antibodies in short cantilogy (VHH)
                Query Match
Best Local
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel protein array useful for detecting the presence of individual proteins in sample, comprises heavy-chain variable domain antibodies antibody fragments obtainable from Camelidae.
                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-DEC-2001; 2001WO-EP014471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heavy chain variable domain; antibody; immunoglobulin; sticky phage-antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain variable domain antibodies or antibody fragments, obtain Camelidae. The method is useful for removing abundant protein extract or sample which do not provide useful information on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 3; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-583487/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     De Haard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNIL ) UNILEVER NV.
(UNIL ) UNILEVER PLC.
(UNIL ) HINDUSTAN LEVER LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200248193-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin G specifc heavy chain variable domain antibody #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNILEVER
UNILEVER
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JJW,
                                                                       138 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       describes a protein array (I)
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                71.2%;
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Score 484.5; l
Pred. No. 3.6e
8; Mismatches
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micro-panning;
                    .6e-36;
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y fragments, obtainable from
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                                                   DNA sequence encoding a heavy chain immunoglobulin, where the DNA is linked to promoters and provided with an additional sequence encoding a peptide capable of targetting heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain immunoglobulin or an active fragment or derivative, or a protein that is functionally equivalent for increasing the pathogen resistance in a plant or to modulate metabolism in a plant. Under some circumstances it may be desirable to retain the antibody product with the plant rather than extracting and isolating the product. In particular, edible selected antigens may be used in a method of passively immunising an animal, preferably human, against the antigen, e.g., pathogenic organisms. The present sequence is an anti-potato SBEII antibody (denoted Clone68) heavy chain variable domain (VH) attached to peptide linkers, myc and his6 tag. The potato SBEII is a starch branching enzyme also designated SBE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for modifying a produce an antibody or an active fragment or derivative, or functional equivalent, in a cellular compartment comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 13; Fig 28; 81pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a plant to
or a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        introducing
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Query Match

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Score 476.5;

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Length

Sequence 149

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ARESULT 12
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #15 from
                                                                                                                                                                                                                                                                                                   New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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Best Local :
                                                                                               The present sequence represents the heavy chain variable region of an antibody isolated from llama, which was immunised with Malassezia furfur M. furfur has been implicated in dandruff formation. The heavy chain variable region is conjugated to an active agent, and used to produce a composition for topical application, e.g. to the scalp. The topical composition, e.g. hair care products such as shampoos and conditioners, skin care lotions, shower gels, etc., is useful for targeting an active agent to a site at which M. furfur is present for the treatment and prevention of dandruff. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition for use in targeting active agent, especially antimicrobial agent to scalp for treating, preventing dandruff, has active agent conjugated to antibody capable of binding specifically to Malassezia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van Der Vaart JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.7%;
72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region;
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88
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  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         llama; Malassezia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 474; DB 4;
Pred. No. 3.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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  467.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
  멂
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  4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         furfur; dandruff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 131;
Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                   furfur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115
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RESULT 14
AAB67778
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                                                                                                 Matches
                                                                                                               Best
                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                              The present sequence represents the heavy chain variable region of an antibody isolated from llama, which was immunised with Malassezia furfur M. furfur has been implicated in dandruff formation. The heavy chain variable region is conjugated to an active agent, and used to produce a composition for topical application, e.g. to the scalp. The topical composition, e.g. hair care products such as shampoos and conditioners, skin care lotions, shower gels, etc., is useful for targeting an active agent to a site at which M. furfur is present for the treatment and prevention of dandruff. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                        Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                    Composition for use in targeting active agent, especially antimicrobial agent to scalp for treating, preventing dandruff, has active agent conjugated to antibody capable of binding specifically to Malassezia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNIL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB67778;
                                                                                                                                                                                                                                                                                                                             Claim 13; Page 9; 50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-257877/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frenken LGJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-2000; 2000WO-EP008380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200119871-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lama glama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hair care
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a llama heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-SEP-2003
11-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB67778 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1999;
                                                                                                               Local
                61
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                                                                                                 l Similarity
94; Conser
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UNILEVER NV.
HINDUSTAN LEVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
DSVKGRETISRDNAKNIMYLQMNSLKÞEDTAVYYCNARRSNYDRSWGDYWGQGTQVTVSS
                                           QVQLQESGGGLVQAGGSLRLSCQASGNIFRINDMGWYRQAPGTRRELVAAITSGGSTKYA
                                                                   QVQLQDSGGGLVQAGGSLRLSCAASGSIFSSDLMGWYRQAPGKEREAVARITRGGTTSYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSVKGRFTISRDNAKNTVYLOMNSLKPEDTAVYYCAAEDRHRIGTVG-YWGQGTQVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSVKGRFTISRDNAKNIMYLOMNSLKPEDTAVYYCNARRSNYDRSWGDYWGQGTQVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OVOLQESGGGLVQAGGSLRLSCQASGNIFRINDMGWYRQAPGTQRELVAAITTGGSTKYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLQDSGGGLVQAGGSLRLSCAASGSIFSSDLMGWYRQAPGKEREAVARITRGGTTSYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variable region; llama; Malassezia furfur; dandruff;
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Der
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99EP-00307356
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                                                                                                             68.5%;
78.3%;
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                                                                                                               Score 465.5; DB 4
Pred. No. 1.6e-34;
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8; Mismatches
                                                                                                 Mismatches
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ches 17;
                                                                                                                             DB 4;
                                                                                                   18;
                                                                                                                             Length 119;
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61

DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCAAEDRHRVGTVG-YWGQGTQVTVSS 119

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Qy 1 QVQLQDSGGGLVQAGGSLRLSCAASGSIFSSDLMGWYRQAPGKEREAVARITRGGTTSYA 60
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RESULT 15
AAY28615
ID AAY28
XX AAY28
XX 17-OC
DT 17-OC
XX 17-OC
XX Lama
XX Heavy
KW Heavy
KW Heavy
KW Enthin
XX PHEN.
XX Lama
XX Lama
XX Lama
XX Regic
FT Regic
FT Regic
                                                               Query Match
Best Local S
Matches 93
                                                                                      The present sequence is an isolated anti-Di acid heavy chain variable (HC -V) fragment, nDl. This antibody fragment is specific to antigen, Dicarboxylic linoleic acid (Di acid). Antibodies specific to target antigen can be produced by cloning the cDNA encoding the antibody fragment derived from immunoglobulins naturally devoid of light chains from non-immunised source, with sequences encoding one or more of heavy chain constant domains and expressing the product in pHEN.5 vector. This method avoids the need for the donor previously to have been immunised with the target antigen and is also preferable to hybridoma technology, or cloning from B cells and spleen cells where a new library is needed for each antigen. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                          (HIND-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heavy chain variable fragment; HC-V; anti-Di acid; nD1; antigen; cloning; antibody fragment; dicarboxylic linoleic acid; Di acid; llama; donor; immunoglobulin; non-immunieed source; constant domain; light chain; pHEN.5 vector; immunised; hybridoma technology; B cell; spleen cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY28615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-2003
26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY28615 standard; protein; 124
                                                               Sequence 124 AA;
                                                                                                                                                                                                                                                                                                               Preparing antibodies derived from a non-immunized source, useful for providing specificity for target antigens.
                                                                                                                                                                                                                                                                                                                                                                                            Frenken LGJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9937681-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lama glama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Llama anti-Di Acid heavy chain variable fragment-nD1.
                                                                                                                                                                                                                                                                                  Example 5; Fig 8; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-479034/40.
                                                                                                                                                                                                                                                                                                                                                                                                                          UNILEVER PLC.
UNILEVER NV.
HINDUSTAN LEVER LTD.
                Similarity
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                            Van Der Logt CPE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98EP-00300525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-EP000481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
27. .35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= CDR2
note= "Complementarity-determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Complementarity-determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= CDR1
note= "Complementarity-determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .113
                68.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDR3
10;
Score 465; DB 2; Length 124; Pred. No. 1.9e-34; O; Mismatches 17; Indels
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   4;
   Gaps
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Qy 117 TVSS 120 |||| Db 121 TVSS 124

Search completed: October 5, 2004, 08:00:09 Job time: 100.144 secs

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                    388
384.5
384.5
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## ALIGNMENTS

RESULT 1 831107 Ig heavy chain -

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M.J.D.; Vossen, J.M.; Schuurman. short diverse third compleme

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RESULT 2
S31588
II heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-19
C;Accession: S31588
R;Cuisinter, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity of A;Reference number: S31585
A;Reference number: S31585
A;Reference preliminary
A,Accession: S31589
A;Status: preliminary
A,Accession: France mRRAA
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens
C.Schuuz
R.Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuuz
R.Raaphorst, F.M.; Timmers, B.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuuz
R.; Timmunol. 22, 247-251, 1992
R.; Feference number: S31104; MUID:9211633; PMID:1730252
R.; Accession: S31107
R.; Accession: S31107
R.; Accession: S31107
R.; Molecule type: mRNA
R.; Residues: 1-19 <- RAA-
R.; Residues: 1-19 <- RAA-
R.; Cross-references: EMBL:X62955
R.; Cross-references: Homonoglobulin homology
C.; Keywords: heterotetramer; immunoglobulin
R.; EMBL:X62955
R.; Cross-references: Homonoglobulin homology
C.; Keywords: heterotetramer; immunoglobulin
R.; EMBL:X62955
R.; Cross-references: Homonoglobulin homology
R.; Cross-references: Homonoglobul
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
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A; Restruct.
A; Cross-references: EMBL:X62956
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C: Kerwords: heterotetramer; immunoglobulin
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R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, P.M.; Timmers, E.; 1992
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
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                                                                                         submitted to the EMBL Data Library, Octobe A; Description: Molecular characterization A; Reference number: S48797
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A;Molecule type: mRNA
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Matches 81
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;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.; Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.; Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.; Mahmoudi, M.; Cottober 1994
                   ;Molecule type: mRNA
;Residues: 1-120 <MAH>
                                                                                       Reference number:
                                                                                                                                                                 y heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) -
; Decies: Homo sapiens (man)
;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
;Accession: S48798
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;15-98/Domain:
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Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
Cross-references: EMBL:Z46382; NID:g562324; PIDN:CAA86521.1;
                                                     Status: preliminary
                                                                           Accession: S48798
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in: immunoglobulin homology
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68.0%;
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Pred. No. 1.6e-26;
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Ig heavy chain precursor - human (frac
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision
C;Accession: S05271; S04602
R;Kishimoto, T.
submitted to the EMBL Data Library, Ma;Reference number: S05270
A;Reference number: S05270
Ig variable region (VDJ) (clone T20-11) - human (fragment) C;Species: Homo sapiens (man) C;Date: 16-Feb-1996 #sequence revision 16-Feb-1996 #text_c:C;Accession: I37780; S25474 R;Demalson, C:; Chastagner, P:; Theze, J:; Zouali, M. Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-144 < XIS2>
A;Cross-references: EMBL:X14584
A;Cross-references: EMBL:X14584
C;Superfanily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keymondin: signal sequence #status predicted <SIG>F;1-19/Domain: signal sequence #status prefixed-text ig heavy chain (fragment) #status prefixed-text ig heavy chain (fragment) #status prefixed-text immunoglobulin homology <INM>
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                                                                                                                                 RESULT
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A;Title: Nucleotide sequences of the cDNAs encoding the V-regions A;Reference number: S04601; MUID:89296497; PMID:2500644
A;Accession: S04602
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A; Residues: 1-160 <KIS1>
A; Cross-references: EMBL: X14584
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Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996;

Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996;
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Pred. No. 1.8e-26;
9; Mismatches 27;
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Pred. No. 4.9e-26;
0; Mismatches 28
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                                                                      16-Feb-1996 #text_change
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A;Residues: i-147 <RES>
A;Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579 C;Superfamily: immunoglobulin V region; immunoglobulin homology F;28-111/Domain: immunoglobulin homology <IMM>
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence
C;Accession: S31114
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A;Molecule type: mRNA
A;Residues: 1-147 <RES>
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A;Map position: 14932.33-14932.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Accession: I55673
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-121 < RE
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J. Exp. M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Species: Homo sapiens (man)
;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
;Accession: I55673
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Exp. Med. 178, 1903-1911, 1993
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!ences: GB:M87268; NID:g186197;
                                                                                                                                                                                                                                                                                                                                    QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQ-DGGSTNY
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                                                                                                                                                        SS
                                                                                                                                                                                                                                                           ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYCNADVRPYRTSRYLEVWGQGTLVTV
                                                                                                                                                                                                                                                                                                      EVQLLESGGGLVQPGGSLRLSCTASGFTFSTYGMSWVRQAPGKGLEWVSAISGSGGSTYY
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                                                                                                                                                                                              SS 121
                                                                                                                                                                                                                                                                                                                                                                                55.2%;
ilarity 66.4%;
Conservative
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                       #sequence_revision
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Pred. No. 7.4e
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Score 378; DB 2;
Pred. No. 6.6e-26;
9; Mismatches 30
                       26-May-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIDN:AAC37536.1;
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hes 31;
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R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31114
A;Status: preliminary; nucleic acid sequence not shown; tran
A;Nolecule type: mRNA
A;Residues: 1-123 <RAA>
A;Cross-references: EMBL:X62963
A;Cross-references: EMBL:X62963
A;Note: the nucleotide sequence was submitted to the EMBL Da
C;Keywords: heteroretramer; immunoglobulin
C;Keywords: heteroretramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-138 <CUR
A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; P:C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S3166
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
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S31666
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                                                                                                   ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYCNADVRPYRTSRYLEVWGQGTLVTV 119
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                                                                                  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKARTGY---WYFDLWGRGTLVTV
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                                                                                                                                                                                                                                             55.2%; Score 378; DB 2; 65.6%; Pred. No. 7.6e-26; tive 10; Mismatches 28
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Pred. No. 6.7e-26;
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RESULT 10
D36005
Ig heavy chain V region (M43) C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence\_re
C;Accession: D36005

revision

21-Dec-1990

#text\_change

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Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20
C;Accession: S26798
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Bur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage A;Reference number: S26786; MUID:92111832; PMID:1730251
A;Accession: S26798
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A; Residues: 1-121 < MOR>
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                  RESULT 12
C36005
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roc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
"Title: Preferential utilization of conserved immunoglobulin heavy
"Reference number: A36005; MUID:90349571; PMID:2117273
"Accession: D36005
                                                                                                                                                                                                                                                                                                                                                                         ;Cross-references: EMBL:X61015; NID:g32795; PIDN:CAA43349.1; PID:g1335126; Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin ketwortstamer; immunoglobulin; immunoglobulin homology <IMM>
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;Cross-references: GDB:
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;Molecule type: mRNA
;Residues: 1-119 <SCH>
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Best Local :
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15-98/Domain:
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                heavy chain V
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                  human
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Pred. No. 9.7e-26;
0; Mismatches 29
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A;Residues: 1-119 <SCH>
A;Residues: 1-119 <SCH>
A;Cross references: GB:MB513
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IVM>
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C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C;Accession: C36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene & R;Reference number: A36005; MUID:90349571; PMID:2117273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eur. J. Immunol. 22, 241-245, 1992
A,Title: The human cord blood antibody repertoire. Frequent usage
A,Reference number: S26786; MUID:92111632; PMID:1730251
A,Accession: S26794
A,Status: preliminary
RESULT 14
$31110
Ig heavy chain - human
C;Species: Homo sapiens
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C;Superfamily: immunoglobulin vegion; immunoglobulin homology
C;Kupwords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Pred. No. 1.2e-25;
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA A;Residues; 1-116 < RRAA A;Residues; 1-116 < RRAA A;Residues; 1-116 < RRAA A;Ross-references: EMBL:X62958 A;Cross-references: EMBL:X62958 C;Superfamily: immunoglobulin vegion; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology C;Keywords: immunoglobulin homology C;Keywords: immunoglobulin homology < RMM>
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R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992.
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, June 1993
A; Description: Human antibody fragments specific for human blood group antigens from a A; Reference number: S38488
A; Accession: S38489
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2.$species: Homo sapiens (man)
2.Patte: 06-dan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38489
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;Molecule type: DNA
;Residues: 1-127 <MAR>
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Best Local Similarity 63.6
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                    Query Match 54.3%; Score 372; DB 2; I Best Local Similarity 62.5%; Pred. No. 2.3e-25; Matches 80; Conservative 10; Mismatches 28;
   120
                                                        112 GOGTLVTV 119
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2; Mismatches 27
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1 QVQLQESGGLVQAGGSLRL.....WGQGTLVTVSSEPKTPKPQP
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ID HV3F_HUMAN
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ID HV3F_HUMAN
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region BUT.
OC Homo sapiens (Human)
OC Homo sapiens (Human)
OC Mammalia; Eutheria; Primates; Catarrhini; Hominion NCBI_TaxID=9606;
RN [1]
RR SEQUENCE.
RR MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR InterPro; IPRO01596; IG_U.
DR SO, GO:0003823; F:antigen binding; NAS.
DR InterPro; IPRO01596; IG_U.
DR SO, GO:00046; IGY; 1.
DR SMART; SM00406; IGY; 1.
DR FROSITE; PS50835; IG_LIKE; 1.

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Torano A., Putnam F.W.;
Torano A., Putnam F.W.;
"Complete amino acid sequence of the alpha 2 heavy cha
IgA2 immunoglobulin of the A2m (2) allotype.";
Proc. Natl. Acad. Sci. U.S.A. 75:966-963(1978).
-1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2)
REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.0%; Score 363; DB 1; larity 61.2%; Pred. No. 4.6e-28; Conservative 16; Mismatches 25;
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HV22 MOUSE
HV25 MOUSE
HV21 MOUSE
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HV25 MOUSE
HV55 MOUSE
HV18 MOUSE
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P18791
P01791
P01804
P01790
P01769
P01769
P18524
P18524
P18527
P01797
P01797
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ALLOTYPE,

Offi a

human

Result No.

Score

Query Match

Length

DB

352.5 339.5 339.5 339.5 331.5 328.5

HV3G HUMAN
HV3H HUMAN
HV3H HUMAN
HV3E MOUSE
HV4E MOUSE

6,

Gaps

120 114

0.9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Minimum DB Maximum DB

seq length:
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20000000000

Scoring table: Sequence: Title: Perfect score:

BLOSUM62 Gapop 10.0 ,

Gapext

0.5

141681 segs, 52070155 residues

Run

9

October 5,

OM protein -

protein search, using sw model

Copyright

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SOFTTT WARREST TO THE COLUMN T
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Best Local S
Matches 73
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007/110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; P850835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                          HV31 HUMAN
P01770;
21-JUL-1986
21-JUL-1986
10-OCT-2003
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MOD_RES
NON_TER
SEQUENCE
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P01768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location of a possible JH segment.";

Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).

PROC. NATLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THI-
PATIENT WITH MACROCLOBULINEMIA:

-!- SIMILARITY: Contains 1 immunoglobulin-like domain
                     MEDLINE=77070269; PubMed=826475; Ponstingl H., Hilschmann N.; Ponstingl H., Hilschmann N.; "The primary structure of a "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
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Matazoa: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
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"Amino acid sequence of the variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=81013859; PubMed=6774332;
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                                                                                                                                                                                                                                                Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin
                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region NIE.
                                                                                                                                                                                                                        _TaxID=9606;
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bulin V region; Pyrrolidone carboxylic acid.

1 112 IG-LIKE.

1 12 PYRROLIDONE CARBOXYLIC ACID.
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122 AA;
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(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
ain V-II, region CAM.
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Pred. No. 5.1e
13; Mismatches
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RESULT
HV3N_H
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P01775;
21-JUL-1986
21-JUL-1986
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Pyrrolidone carboxylic acid.

DOMAIN

1 112

IG-LIKE.
                                                                                                                                                                     MEDLINE=75046755; PubMed=4139708; Capra J.D., Kehoe J.M.; Capra J.D., Kehoe J.M.; Capra J.D., Kehoe J.M.; the "Structure of antibodies with shared idiotypy: the of the heavy chain variable regions of two immunoglanti-gamma globulins."; Proc. Natl. Acad. Sci. U.S. A. 71:4032-4036(1974).
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
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                          PIR; A02058; M3HULY.
HSSP; P01772; 2FB4.
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HSSP; P01772; 2FB4.
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Mammalia; Eutheria;
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                                                                                          -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM GLOBULIN ACTIVITY.
-!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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GO:0005576; C:extracellular;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01, Last sequence up 42, Last annotation III region LAY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.7%;
60.7%;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYRROLIDONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C96935A6E55E165B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
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.7e-26;
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                                                                                                                                                                                 ANTI-GAMMA
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RESULT 5
HV3K_HUMAN
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Best Local S
Matches 69
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P01772;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up)
10-OCT-2003 (Rel. 42, Last annotation
10-OCT-2003 (Rel. 42, Last annotation)
                    DISULFID
DISULFID
STRAND
STRAND
                                                                                                                                 GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; id: 1
SMART.
                                                                                                                                                                                       PDB; 2FB4; 12-UUL-89.
PDB; 2IG2; 12-UUL-89.
GO; GO:0005576; C:extracellular; N:GO; GO:0003823; F:antigen binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                   and 1
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, AND DISULFIDE BONDS.

MEDLINE=83289131; PubMed=6884994;

MEDLINE=83289131; PubMed=6884994;

Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;

Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;

"Three-dimensional structure determination of antibodies.

structure of crystallized monoclonal immunoglobulin IgG1 if
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
NON TER
                                                                             90
                                                                                                                  PROSITE;
                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                           Marquart M., Deisenhofer J., Huber R., Palm W.; "Crystallographic refinement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment
                                                                                                                                                                                                                                                                                                          MEDLINE=81072295; PubMed=7441755;
Marquart M., Deisenhofer J., Huber R., I
"Crystallographic refinement and atomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GO; GO:0006955; P:immune response;
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                        DOMAIN
                                                                                                   Immunoglobulin
                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                              A02055;
                                                                                                                                                                                                                                                                                   .0-A resolution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69;
                                                                           PS50835; IG LIKE; : lobulin V region; 3D-
                                                                                                                                                                                                                                                                      Biol. 141:369-391(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQLLESGGGLVQPGGSLRLSCAASGFTFSASAMSWVRQAPGKGLEWVAWKYENGNDKHYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVA-TIQDGGSTNYA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSVNGRFTISRNDSKNTLYLOMNGLOAZVSAIYYCARDAGPYVSPTFFAHWGOGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSVKGRFTISRDNTLNTVYLOMNDLKPEDTAVYYCNADVRPYRTSRYLEVWGQGTLVT
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119
119 AA;
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50.5%;
                                                                                                3D-structure; Pyrrolidone carboxylic
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                                                                       IG-LIKE.
PYRROLIDONE CARBOXYLIC
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RESULT 6
HV05_CARAU
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Best Local
                               InterPic,
InterPic,
InterPro; IPkoc,
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IG LIKE; 1
TOOSITE; PS50835; IG LIKE; 1
                                                                                                          [1]
SEQUENCE FROM N.A.
MEDLINE-88144476; PubMed=3125551;
Wilson M.R., Middleton D., Warr G.W.;
"Immunoglobulin heavy chain variable:
"family relationships of two genes
                                                                                                                                                                                                         HV05 CARAU
P19181;
01-NOV-1990
01-NOV-1990
15-JUL-1999
DOMAIN
DOMAIN
DOMAIN
                               SIGNAL
CHAIN
                                                                       HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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STRAND
HELIX
STRAND
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STRAND
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cyprinidae; Carassius.
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HELIX
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TURN
                                                                                                  Proc. Natl. Acad.
                                                                                                         fish.";
                                                                                                                                                                                           Carassius auratus (Goldfish)
                                                                                                                                                                                                    Ig heavy chain
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TURN ,
STRAND
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                                                                                                                                                                                                                                                                                                                                                  QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQDGGS-TNY
                                                                                                                                                                                                                                                                                            EVWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                        ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYCNAD------
                                                                                                                                                                                                                                                                                                                                         QVQLVESGGGVVQPGRSLRLSCSSSGFIFSSYAMYWVRQAPGKGLEWVAIIWDDGSDQHY
                                                                                                                                                                                                         (Rel. 16, Created)
(Rel. 16, Last sec
(Rel. 38, Last and
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113
120
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                                                                                                 Sci. U.S.A.
116
49
684
848
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                                                                                                                                                                                                                                                                                                                                                                             49.3%;
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                                                                                                                                                                                                                                                                                            121
                                            Signal
                                                                                                                                                                                                 sequence update)
annotation update)
precursor.
                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                     Score 337.5; 1
Pred. No. 1.4e
13; Mismatches
        IG HEAVY CHAIN V REGION 5A. FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2
                                                                                                  85:1566-1570(1988).
                                                                                                                                                                                                                                                                                                                                                                                                     E4D71B52B16F8776 CRC64;
                                                                                                               iable region
genes and a
                                                                                                                                                                                                                                        116
                                                                                                                                                                           Vertebrata; Euteleostomi;
Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                        A
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                                                                                                               gene evolution: pseudogene in a
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RESULT 7

HV3B H

HV3B H

AC P01763

DT 21-JUL

DT 10-OCT

DE 15 homo s

OC EWARTY

OC NCBLT

RN MEDLIN

RA GOIL

RT GANIA

CC -1- MI

CC -1- MI

CC -1- SI

DR HSSP;

DR HSSP;
DR GO; GC

DR GO; GC

DR GO; GC

DR GO; GC

DR Ffam;
DR Ffam;
DR Ffam;
DR Pfam;
DR SEQUEI
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Best Local S
Matches 67
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Best Local S
Matches 72
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DISULFID
NON TER
SEQUENCE
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21-JUL-1986
21-JUL-1986
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region WBA.
Homo sapiens (Human).
Bukarvora Meranan Chandal
                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                               "Amino acid sequence of the Fv region of a human monoclonal IGM (protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33.";

Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

-i- MISCELLANECUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
MEDLINE=83273707; PubMed=6410398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                        WALDENSTROM'S MACROGLOBULINEMIA.
-!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
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                                                                                                        μ
                                                                                                                                                                     Similarity
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          SS
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                                                                           ADSVKGRFTISRDNTLNTVYLOMNDLKPEDTAVYYCNADVRPYRTSRYLEVMGQGTLVTV
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Pred. No. 1.5e-25;
                                                                                                                                                                    Score 335.5;
Pred. No. 2e
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BY SIMILARIT
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HV3U_HUMAN
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Best Local Similarity
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HUMAN
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Stricture of antibodies with shared idiotypy: the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=75046755; PubMed=4139708; Capra J.D., Kehoe J.M.;
                                                                                                                                                                                                                                                                                                              HV3U_HUMAN STANDARD; PRT; 1

P01782;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence up

10-OCT-2003 (Rel. 42, Last annotation

Ig heavy chain V-III region DOB.
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Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
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MEDLINE=80020921; PubMed=114209;
Steiner L.A., Garcia Pardo A., Margolies M.N.;
"Amino acid sequence of the heavy-chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A02057; M3HUPM.
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                                                            SEQUENCE.
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119 AA;
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12953 MW; 2E018AF4DCEB2610 CRC64;
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N -> D (PROBABLY DUE T
DURING ISOLATION).

/FTId=VAR_003966.
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Pred. No. 2.6e
16; Mismatches
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RESULT 10
HV3C_HUMAN
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Best Local
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HV3C HUMAN
P01764;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                             MEDLINE-81101090; PubMed=6450418;
Matthyssens G., Rabbitts T.H.;
Matthyssens G., Rabbitts T.H.;
"Structure and multiplicity of genes for the human immulary chain variable region.";
Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Steiner L.A., Lopes A.D.;
"The crystallizable human myeloma protein Dob has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Biochemistry 18:4068-4080(1979).
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SIMILARITY: Contains 1 immunoglobulin-like domain
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HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
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Best Local S
Matches 67
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR00796; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
                               Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region.

DOMAIN 1 108

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InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang A.-C., Wang I.Y., Fudenberg H.H.;
"Immunoglobulin structure and genetics. Identity between variable
regions of a mu and a gamma chain.";
J. Biol. Chem. 252:7192-7199(1977).
-i- MISCELLANBOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
OF IGM AND IGGZ ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
GAMMODATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P01765;
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region TIL.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J00236; AAA53516.1;
EMBL; M35415; AAA58735.1;
PIR; A02047; H3HU26.
PDB; 1HOU; 23-DEC-99.
   SEQUENCE
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; P01772; 2FB4.
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117 AA;
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117
115
12356 MW; 4DCC67D179F62326 CRC64;
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Pred. No. 9.6e
7; Mismatches
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                                                                          IG-LIKE
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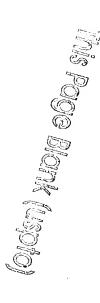
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RESULT 12
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P01785;
21-JUL-1986
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
1g heavy chain V region MOO.
Canis familiaris (Dog).
                                                                                                                                                                                                           Immunoglobulin V region.
DOMAIN
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MEDLINE=77242268; PubMed=407924;
Wasserman R.L., Capra J.D.;
"Primary structure of the variable
                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                           MOL. Immunol. 16:565-5/0/13/7/.
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN
                                                                                                                                                                                                                                                                                                                                             McCumber L.J., Capra J.D.;
"The complete amino-acid sequence of
Mol. Immunol. 16:565-570(1979).
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 113-117.
MEDLINE=80077682; PubMed=117299;
                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulin heavy chains.";
Biochemistry 16:3160-3168(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                 PIR; A90403; MHDGMO.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                        interPro; IPR007110;
interPro; IPR003596;
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117
                     121
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                                                                                                                 ۳,
                                                                                                                                         72;
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S 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYC-NADVRPYRTSRYLEVWGQGTLVT
                     S 121
                                                                  DSVKGRFTISRDNTLNTVYLOMNDLKPEDTAVYYCNADVRPYRTSRYLEVWGQGTLVTVS
                                                                                                                 QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQDGGSTNYA
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                                             DAVKGRESISRDNAKNTLYLØMEDLRVEDTAVYYC-ATEGDIEIPRY---FGQGTIVTVS
                                                                                            EVKLVESGGDLVKPGGSLRLSCVASGFTFSSNGMSWVRQDPGEGLQWVADISSSGQTYYA
                                                                                                                                                                                        117 AA;
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                                                                                                                                          Conservative
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; 12703 MW;
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Ig_v.
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                                                                                                                                                     47.9%;
                                                                                                                                          11;
                                                                                                                                                   Score 328; DB 1;
Pred. No. 1.1e-24;
                                                                                                                                                                                                                IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Canis.
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RESULT 13
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RESULT 14
HV3T_HUMAN
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P01784;
21-JUL-1986
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NON_TER
SEQUENCE
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"primary structure of the variable
immunoglobulin heavy chains.";
Biochemistry 16:3160-3168(1977).
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI — TaxID=9615;
                                                                 MEDIINE-75059123; PubMed=4803843;
Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
"The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu
(macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu
(mype), subgroup H III. Architecture of the complete IgM-molecule.";
hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
                                                                                                                                                                                                                                                                                                                                                                              PRT; 1901781; PRT; 1901781; PRT; 1901781; PO1781; PO1781; PO1781; PO1781; PRT; 121-JUL-1986 (Rel. 01, Last sequence up 10-OCT-2003 (Rel. 42, Last annotation Ig heavy chain V-III region GAL.
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SMART; SM00406; IGv;
PROSITE; PS50835; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986
10-OCT-2003
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A02067; AVDGGM.
HSSP; P01772; 2FB4.
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                        REVISION TO 28-33.
                                                                                                                                                                                                                                 SEQUENCE.
                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110;
InterPro; IPR003596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 SS 114
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(Rel. 01, Last seq
(Rel. 42, Last ann
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9_LIKE; 1.
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Ig_v.
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on update)
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02049; M3HUBW.
HSSP; P01772; 2FB4.
GO; GC:0005576; C:extracellular; NAS.
GO; GC:0005576; C:extracellular; NAS.
GO; GC:0005923; F:antigen binding; NAS.
GO; GC:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
PROMAIN; SMO406; IGv; 1.
SMART; SM0406; IGv; 1.
PROSITE; PS50815; IG LIKE; 1.
Immunoglobulin V region.
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GO; GO:0003523; F:antigen binding; NAS.
GO; GO:0003525; P:immune response; NAS.
InterPro; IPR0077110; Ig-1ike.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
DOMAIN
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SEQUENCE
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AA; 12730 MW; 2C67CA9AAA
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Capra J.D., Hopper J.E.;
Capra J.D., Hopper J.E.;
"Comparative studies on monotypic IgM lambda and IgG kappa from an individual patient. III. The complete amino acid sequence of the vergion of the IgM paraporotein.";
Iregion of the IgM paraporotein.";
Immunochemistry 13:995-999(1976).
-!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR, A02064; MAHUGL.
HSSP; P01772; 2FB4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 ADSVKGRETISRDNTLNTVYLOMNDLKPEDTAVYYCNADVRFYRTSRYLEVWGQGTLVTV 119
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72; Conservative
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12730 MW; 2C67CA9AAAAA1282 CRC64;
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59.0%;
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Pred. No. 1.8e-
11; Mismatches
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les 32; Indels
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                                                                                    1 QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQDGGSTNYA 60
                                                                                                                               Similarity
DSVKGRFTISRNDSKNTLYLNMNSLRAEDTÄVYYCARSPVSLVDGWLYYYYGSVWGQGTL 120
             DSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYCNAD----VRPYRTSRYLEVWGQGTL 116
                                                     EVQLVESGGGLVQPGGSLRLSCAASGFTFSYYNNNWVRQVTGKGLEWVSAIGTAGDQYYA
                                                                                                                                                                         120 AA; 13227 MW;
                                                                                                                Conservative
                                                                                                                            47.4%; Score 325; DB 1; 58.3%; Pred. No. 2.1e-24;
                                                                                                                10; Mismatches
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                                                                                                                                          DB 1; Length 120
                                                                                                                36;
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Search completed: October 5, 2004, 08:01:54 Job time: 12.6358 secs



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Title:
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 Score
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Match
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_funan:*
5: sp_invertebrate:*
6: sp_mammal:*
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Gapop 10.0 , Gapext 0.5
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685
1 QVQLQESGGGLVQAGGSLRL.....WGQGTLVTVSSEPKTPKPQP 130
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Q8n5k4 homo
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Q8n19 homo
Q9u171 homo
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mus mus	mus	homo sap	homo sap	homo	mus	homo	Q8vcx7 mus musculu	e mus mus	homo sap	2 mus	.92 homo	homo	mk4 mus	)w4 oryct	Q9n0w6 oryctolagus	8vea0 mus	OMOT	mus	homo	aums	Q8n4y9 homo sapien	Q91z05 mus musculu	Brw	OMO	mus	Omo	Q9hcc1 homo sapien	iomo sap

## ALIGNMENTS

RESULT 1

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80 ADSVKGRFTISRDNSRDTLYLQMNSLRAEDTAVYYCAKDPRGYSASGNYTREDYWGQGTL 139	60 ADSVKGRFTISRDNTLNTVYLQMVDLKPEDTAVYYCNADVRPYRTS-RYLEVMGQGTL 116	20 EVQLLESGGGLVQFGGSLRLSCAASGFSFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYY 79	1 QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQ-DGGSTNY 59	9; Mismatche	Y Match  10cal Cimilarity 66 4%: Bred NO 2 26-2	SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;	Hypothetical protein.		E; PS50835	; SM00406;	0047; ig; 5		IPR003006;	InterPro; IPR007110; Ig-like.	15760; AAH15760.1;	Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.	Strausberg R.;	TISSUE=B-cell;	SEQUENCE FROM N.A.	[1]	D=9606;	<pre>Sutheria; Primates; Catarrhini; Hominidae;</pre>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Hypothetical protein.	(TrEMBLrel. 25, Last annotation	(TrEMBLrel. 19,	01-DEC-2001 (TrEMBLrel. 19, Created)	Q96BB9;	096BB9 PRELIMINARY; PRT; 597 AA.	Bo

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VIVSS

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RESULT Q99KA4
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Best Local :
                                                                                                                                                                                Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Cha
Mammalia; Eutherii; Roo
NCBI_TaxID=10090;
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Q9UL72;
01-MAY-2000
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01-CCT-2003
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update
Myosin-reactive immunoglobulin heavy chain variab
(Fragment).
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                     Strausberg R.;
Submitted (MAR-2001) to the
EMBL; BC004786; AAH04786.1;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Mammalia; Eutheria;
                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVOLVESGGGLVOPGGSLRLSCAASGFTVSSNYMWVROAPGKGLESVSVTYSGGSSYYA
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118 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Primates;
                                                                                                                                                                                                                               Chordata;
Rodentia;
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Last sequence update)
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                                                         EMBL/GenBank/DDBJ databases
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Pred. No. 1.
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                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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chain variable
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                                                                                                                                                                                                                                  Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
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Best Local :
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Best Local (
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 4.

SYART; SM00409; IG; 4.

SYART; SM00409; IG; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 499 AA; 53376 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-
InterPro; IPR003006; Ig-
InterPro; IPR003596; Ig-
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8N5K4;
01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003599; InterPro; IPR007110; InterPro; IPR003597; InterPro; IPR003006; InterPro; IPR003006; InterPro; IPR003596; INTERPRO; INTERPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein SEQUENCE 487 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JUN-2002)
EMBL; BC032249; AAH32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG_LIKE; PROSITE; PS00290; IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8N5K4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                         . Similarity 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                           QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQ-DGGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYCNADV--RPYRTSRYLEVWGQGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTFGKERDVVATIQDGGS-TNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVOLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVATISDGGSYTYY
    TLVTVSS-EPKTPKPQP
                                                                        ADSVKGRETISRDNTLNTVYLQWNDLKPEDTAVYYCNADVRPYRT-----SRYLEVWGQG
                                                                                                                          EVOLVESGGGVVRPGGSLRLSCATSGETFDDSGASWVRQAPGKGLEWVSSINWNGGSTNY
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                                           ADSVKGRFTISRDNAKNSLYLOMNSLRVEDTALYYCARDPTKYCSGGSCLGYYMDVWGKG
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(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH32249.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig.
Ig-like.
Ig_cl.
Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52554 MW;
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Ig_MHC.
Ig_v.
                                                                                                                                                                                                                               54.1%;
57.7%;
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Pred. No. 1.8e-28;
                                                                                                                                                                                                                             Score 370.5;
Pred. No. 3.8
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                                                                                                                                                                                                                                                                                          93A5C89582054F32 CRC64;
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                                                                                                                                                                                                                               .8e-28;
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on update)
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                                                                                                                                                                                                                                                   DB 4;
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                                                                                                                                                                                                                                                     499;
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Best Local S
Matches 79
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Ol-MAR-2002 (TrEMBLrel. 25, Las
Ol-OCT-2003 (TrEMBLrel. 25, Las
Hypothetical protein.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata; C
Mammalia; Eutheria; Primates; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF035024; AAD56260.1; --
HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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01-MAY-2000
01-MAY-2000
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MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
Van der Merwe P.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                        Q8WUK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06Tn60
EMBL; BC020240; AAH20240.1;
PIR; PL0120; PL0120.
PIR; S15590; S15590.
                                 Strausberg R.;
Submitted (DEC-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                         TISSUE=Tonsil;
                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Fragment)
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79; Conser
                                                                                                                                                                                                                                                             SS
                                                                                                                                                                                                                                                                                                                                  ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYCNADVRPYRTSRYLEVWGQGTLVTV
                                                                                                                                                                                                                                                                                                                                                                               QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQ-DGGSTNY
                                                                                                                                                                                                                                                                                   SS 121
                                                                                                                                                                                                                                                                                                           ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKD
                                                                                                                                                                                                                                                                                                                                                       EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYY
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113 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    113
12437 MW; ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               53.7%;
                                   the
                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                            Created)
                                    EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     Score 368; DB 4;
Pred. No. 9.8e-29;
9; Mismatches 24
                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kalis N.N.,
                                                                                                                                                                                                    613
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                                                                                                                                                   update)
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RESULT 7
2011/1
ID 2011/1
AC 2011
AC 2
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                                                                                                                                                                                         Query Match
Best Local S
Matches 76
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Best Local S
Matches 78
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Q9UL71;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                      InterPro; IPRO07110; Ig-like.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMCSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 5.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 5.

PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035043; AAD56279.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu X., Liu B., Van Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 613 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 5.
                                                                                                                                                                                                                                                                                      SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Myosin-reactive autoantibodies in rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P01772;
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61
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                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDWSEGVETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQ-DGGSTNY
     ADŚVKGRFTIŚRDNSKNSLYLOMNSLRAEDTALYYC---AKGKVTTIYDRFDIWGQGTMV
                                      ADSVKGRETISRDNTLNTVYLQMNDLKPEDTAVYYCNADVRPYRTSRY--LEVWGQGTLV 117
                                                                                                EVOLVESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGGSTYY
                                                                                                                                           QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQ-DGGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYCNAD----VRPYRTSRYLEVWGQGT 115
                                                                                                                                                                                                                                                                                      121
121 AA;
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                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                      13154 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67296 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.5%;
                                                                                                                                                                                                               52.1%;
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                                                                                                                                                                                           15;
                                                                                                                                                                                      Score 357; DB
Pred. No. 1.3e-
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 359.5; DB
Pred. No. 6e-27;
1; Mismatches
                                                                                                                                                                                                                                                                                      2F045CCFA5D50736 CRC64;
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                                                                                                                                                                                                                  .3e-27;
                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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                                                                                                                                                                                                                                      Length 121;
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                                                                                                                                                                                           Indels
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Best Local :
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SEQUENCE
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submitted (JUI-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010798; AAH10798.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003056; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Creat 01-DEC-2001 (TrEMBLrel. 19, Last 01-OCT-2003 (TrEMBLrel. 25, Last Hypothetical protein (Fragment). Mus musculus (Mouse).
                                                                                         InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                           Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC010324; AAH10324.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 4. —
SMART; SM00406; IGV; 1. .
PROSITE; PS0935; IG_MHC; 2.
PROSITE; PS00290; IG_MHC; 2.
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Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91Z07
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                   PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
Mus musculus (Mouse).
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01-OCT-2003
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77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSVKGRFTISRDNTLNTVYLOMNDLKPEDTAVYYCNADVRPYRTSRYLEVWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQDGG-STNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSMKGRFTISRDNAQNTVLLQMTSLNSEDTAVYYCTRG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKLVESGGGLVKPGGSLRLSCAASGFIFSNSYMSWVRQTPEKRLEWVATISNSGYATHYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480 AA; 51936 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
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Rodentia;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 353; DB 11;
Pred. No. 1.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20B9234EEF2B41ED CRC64;
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RESULT 11
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Q9UL88
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 78; Conserv
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Best Local Similarity
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SEQUENCE
Q9Y509
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
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MEDLINE=98277139; PubMed=9614934;
MEX., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 486 AA; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clin. Immunol. Immunopathol. 87:184-192(1998) EMBL; AF035026; AAD56262.1; -.
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HSSP; P01810; 2FBJ.
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interPro; IPR003596;
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                                                                                                                                                                                                                                                           58 NYADSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYCNADV------RPYRTSRYL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYCNADVRP----YRTSRYLEVWGQGT
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                                                                                                                                                                                                                                                                                                                                         EVHLVESGGGLVKPGGSLKLSCVVSGFSFTSYDMSWVRQTPERRLEWVAAITSGGNTYYP
                                                                                                                                                                EVWGQGTLVTVSS 121
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                                                                                                                   EYWGQGTLVTVSS
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                                                                                                                                                                                                                                                                                                                EVOLVESGGGLVKPGGSLRLSCAASGFTFSKAMMSWVRQAPGKGLEWVGRIKSKTDGGTT
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131 AA;
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  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                             50.9%; Suc. No. 58.6%; Pred. No. 50.1; Mismatches
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14142 MW;
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Primates;
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Ig_v.
                                                                                                                      131
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Pred. No. 3.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 349; DB 4
Pred. No. 9e-27;
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     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4FEF835125DA870B CRC64;
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Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
A Lichtenstein A.K., Berenson J.R.;
I "A CDIO-positive subset of malignant cells is identified in mul
myeloma using PCR with patient-specific immunoglobulin gene pri
Leukemia 9:1948-1953(1995).
Leukemia 9:1948-1953(1995).
REMBL; S80860; AAD14339.1; -.
REMBL; S80860; AAD14339.1; -.
REMBL; S80860; ACD14339.1; -.
REMBL; GO:0016066; P:cellular to plasma membrane; NAS.
RGO; GO:0016066; P:cellular defense response (sensu Vertebrata);
RGO; GO:0016066; P:cellular defense response (sensu Vertebrata);
RINTERPRO; IPR003710; Ig-like.
RINTERPRO; IPR003596; Ig-V.
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Best Local (
                                                                                          Atkin J.D., Tape A., Jennings "Definition of the Idiotope of in Mammalian Cells.", Submitted (SEP-2000) to the ELEMBL, AF307937, AAL09421.1; - PIR; C25913; C25913.
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_IIKE; 1.
                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
MCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pterin-mimicking anti-idiotope heavy chain variable
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                       InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQDGGSTN-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYCNADVRPYRTSRY----LEVWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVHLVESGGGVVQPGKSLRLSCEASGFTFSTYGMSWVRQAPGKGLDWVALISYDGSTQYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVTVSSASTKGPSVFP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVTVSS-EPKTPKPQP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGSVKGRFTISRDNSKNTLYLOMTSLRVEDTAVYYCAKDGNYFDSVGYYYAGIDYWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
     IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15768 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.9%;
                                                                                                                                                                                          Jennings I.G., Horaitis O.,
liotope of Pterin-Mimicking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12,
25,
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Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9;
                                                                                                                                                 EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 349; DB 4
Pred. No. 1e-26;
9; Mismatches
                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8489FCAAA7BC925C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 147
                                                                                                                                                                                             Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata); NAS
                                                                                                                                                                                                                                                                                                                     Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J.C.,
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G
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RESULT 14
Q8WU38
ID Q8WU38;
AC Q8WU38;
DT 01-MAR-2002
DT 01-MAR-2002
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ID Q91WP
ID Q91WP
ID Q91WP
DT 01-DE
DT 11-OC
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OS Mus m
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                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MIC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 4.
SMART; SM00476; IGV; I.
PROSITE; PS50835; IG_LIKS; 4.
PROSITE; PS00290; IG_MIC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC013656; AAH13656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q91WP5;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                               Hypothetical
SEQUENCE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    091WP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
133
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                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115
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                                                                                       08
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                                                                                                                                                                                                                          <u>سر</u>
                                                                                                                                                                                                                                                                        73;
                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                           QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATI-QDGGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADSVKGRFTISRDNTLNTVYLQMNDLKFEDTAVYYCNADVRFYRTSRY---LEVWGQGTL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQDGGS-TNY
                                         SSEP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIVSA 119
SSEP 136
                                                                                       SDTMXGRFTISRDNAKSTLYLQMSSLRSEDTAFYYC-
                                                                                                                                ADSVKGRFTISRDNTLNTVYLOMNDLKPEDTAVYYCNADVRPYRTSRYLEVWGQGTLVTV 119
                                                                                                                                                                            EVQLVESGGLVKPGGSLKVSCAASGLTFSNYAMSWVRQSPEKRLEWVAAINSNGGNTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119
119 AA;
                                                                                                                                                                                                                                                                                                                                                               al protein.
479 AA; 5
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                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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13025 MW;
                                                                                                                                                                                                                                                                                                                                                                 51603 MW;
                                                                                                                                                                                                                                                                                             58.9%;
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Last
                                                                                                                                                                                                                                                                        Score 348; DB
Pred. No. 6e-2
L7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F6E904044381CA7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                    ECB2D0877748584F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         479
                                                                                                                                                                                                                                                                                                6e-26;
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.9e-27;
                                                                                                                                                                                                                                                                                                                 DB 11;
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                                                                                                                                                                                                                                                                        26;
                                                                                         ---VR----GGYFDVWGAGTAVTV
                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ARHGDYDVGFAYWGQGTL
                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                         132
                                                                                                                                                                                                                              59
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PRELIMINARY; (TrEMBLrel. (TrEMBLrel.

20,

Created) Last sequ

sequence update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UL91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 78
                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IG; 1.
PR0SITE; PS50835; IG_LIKE; 1.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UL91;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021276; AAH21276.1; -.
PIR; S21205; S21205.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                  Clin. Immunol Immunopathol. 87:184-192(1998)

EMBL; AF035023; AAD56259.1; -.

PIR; S21205; S21205.

HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEX., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00230; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                          Wu X., Liu
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 573 AA; 62967 MW;
                              NON_TER
                                                                                                                                                                                                                                                                                                                                             fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Tonsil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fragment)
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HPL inhib
HGL inhib
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RESULT 1 AAE10552

AAE10552 standard; peptide; 130

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HPL inhibiting VHH fragment, HPL #12 from llama species

10-DEC-2001 AAE10552;

(first entry)

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AAE10560	ABR62884	ABG30617	AAY39817	AAE10562	AAY39816	AAY28615	ABG30972	AAB67779	ABR62885	AAY41173	AAY41165	AAE05282	AAB67777	AAB67778	AAY41167	ABG30618	AAY41172	ABR62880	ABR62878
Aae10560 HGL inhib	Abr62884 Llama ant	0	Aay39817 Llama ant	Aae10562 HGL inhib	Llam	ហ	Abg30972 Immunoglo	Aab67779 Amino aci	Abr62885 Llama ant	w		2 Anti-p	Aab67777 Amino aci	Aab67778 Amino aci	7	Abg30618 Immunoglo	N	Abr62880 Llama ant	Abr62878 Llama ant

## ALIGNMENTS

## WPI; Key Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight. Bezemer S, 14-MAR-2000; 2000EP-00200930 20-FEB-2001; 2001EP-00200703. 19-SEP-2001. EP1134231-A1 Region Region Region (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC. Lama sp. 2001-572718/65. Van De Burg /label= CDR2 /note= "Complementarity determining region 98...110 /label= CDR1 /note= "Complementarity determining region 1" 50..64 /label= CDR3 /note= "Complementarity determining region Location/Qualifiers 3 De Haard JJW, Tareilus

485.5 487.5 479.5 470.5 470.5 470.5 470.5 450.5 450.5 450.5 450.5 450.5

AAE05287 ABR62881

Aae10564 Abe10565 Abe10583 Aae10591 Aay39819 Abe62882 Aae05286 Aae05286

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Example 2; Page 9; 37pp; English

Aae10561 Aae05288 Aae10567

Aae1 Aae1

Aae05283 Aae10563 Abg30620

Aae1

Aae10556

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RESULT 2
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Matches 130;
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   New antibody or its fragments for inhibiting human dietary enzymes,
                                                    Bezemer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; peptide; 130
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note= "Complementarity
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                                                                                                                                                                                                                                                                                                                             CDR3
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Pred.
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1. No. 1.5e-49;
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RESULT 4
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Best Local Simi
Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #30 from plana (camelid) species
                                                                                                                                                                                                                                                                                                                       Region
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                                                                                  19-SEP-2001.
                                                                                                                                                                                                                                          Region
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                         20-FEB-2001; 2001EP-00200703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Llama antibody; camelid; anorectic; heavy chain variable domain; human dietary enzyme inhibitor; medicament; human pancreatic lip;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     food; human
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gastric lipase; HGL; cosmetic
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/label= CDR2
/note= "Complementarity do"
111
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93.1%;
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Pred. No. 5.4e-48;
3; Mismatches 6
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                                                                                                                                                                                                                                                              determining
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control; body weight.
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Best Local Sim
Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #15 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                        Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                Region
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                                                                                                                                                                                                                                           HPL inhibiting VHH fragment, HPL #18 from llama species.
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                                                                                                                                                                                                                                                                                                 AAE10556;
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                                                                                                                                                                                                                                                                                                                        standard;
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                                                                         /note= "Complementarity determining
50     64
/label= CDR2
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                                                                                                              /label= CDR1
                                                            note=
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Pred. No. 1.4e-38;
1; Mismatches 17
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                                                           determining
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                                                                                                                                                                                                      lipase; HPL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE10557 standard; peptide;
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dietary e
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                                                                                                                                                                                                                                       cy enzyme inhibitor; n
gastric lipase; HGL;
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                                                                                                                                                                                                                                                                camelid; anorectic; heavy chain variable domain; VHH;
nzyme inhibitor; medicament; human pancreatic lipase;
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/note= "Complementarity
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    /note= "Complementarity
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                                'label= CDR2
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No. 1.1e-37;
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                                                                                                                    HPL inhibiting VHH
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                                        Lama
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human dietary e:
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                                                            ody; camelid; anorectic; heavy chain variable domain; VHH; ry enzyme inhibitor; medicament; human pancreatic lipase; gastric lipase; HGL; cosmetic control. hadv ....i
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/label= CDR3
/note= "Complementarity determining region
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 Location/Qualifiers 31. .35
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Pred. No. 6.9e-37;
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                                                                                                                       from llama species
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Potato; heavy chain immunoglobulin; pathogen resistance; metabolism modulator; passive immunisation; heavy chain VH; anti-potato SBEII; starch branching enzyme; SBE A.
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                                                    Anti-potato SBEII (Clone46) VH region attached with myc and his6 tag.
                                                                                 18-SEP-2001
                                                                                                           AAE05283;
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                                                                                                                                                                                                                                                                               DSVKGRFTISRDNTLNTVYLOMNDLKPEDTAVYYCNADVRPYRTSRYLEVWGQGTLVTVS
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Pred. No. 8.3e-36;
B; Mismatches 21
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                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for modifying a plant to comproduce an antibody or an active fragment or derivative, or a protein functional equivalent, in a cellular compartment comprises introducing a CC DNA sequence encoding a heavy chain immunoglobulin, where the DNA is compartment. The method is used for producing a heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain inmunoglobulin or an active fragment or derivative, or a protein that is functionally equivalent for increasing the pathogen resistance in a plant cor to modulate metabolism in a plant. Under some circumstances it may be desirable to retain the antibody product with the plant rather than correcting and isolating the product with the plant rather than correcting and isolating the product. In particular, edible selected antigens may be used in a method of passively immunising an animal, preferably human, against the antigen, e.g., pathogenic organisms. The preferably human, against the antigen, e.g., pathogenic organisms. The present sequence is an anti-potato SBEII antibody (denoted Clone46) heavy chain variable domain (VH) attached to peptide linkers, myc and his6 tag.

The potato SBEII is a starch branching enzyme also designated SBE A
                                                                                                                                                                                                                                                                                                                                                                                     Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frenken LGJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNIL )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1118669-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Solanum tuberosum. Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-2000; 2000EP-00310997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                          117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-427157/46.
DB; AAD10054.
                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQDGGSTNYA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNILEVER PLC.
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                     VTVSSEPKTPKPQP 130
                                                                                                                                                                           VIVSSEPKIPKPQP
                                                                                                                                                                                                                                              DSVKGRFTISRDNAKNTVYLQMSSLKPEDTAVYYCAAGNLLVKRPY-
                                                                                                                                                                                                                                                                               DSVKGRFTISRDWTLNTVYLQMNDLKPEDTAVYYCNAD----VRPYRTSRYLEVWGQGTL 116
                                                                                                                                                                                                                                                                                                                 OVOLOESGGGLVOAGGSLRLSCVASGNTFSIIAMAWYROAPGKOREVVASINSIGSTNYA
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van Der
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99EP-00310188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    72.6%;
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                                                                                                                                                                           126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPE,
                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                   Score 497; DB 4
Pred. No. 2e-35;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jobling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SA,
                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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10-DEC-2001 AAE10563;

(first

AAE10563

standard;

peptide;

124

Å

112

HGL inhibiting

ΉH

fragment, HGL #9

from llama

species

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RESULT 10
ABG30620
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                                                                                                                                                                                                                                Query Match
Best Local S
Matches 96
                                                                                                                                                                                                                                                                                                       The patent discloses antibodies or their tragments comprising a weavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #9 from liama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human
food;
 ABG30620 standard; protein; 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1134231-A1
                                                                                                                                                                                                                                                                                     Sequence 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 13; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy chain variable domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-572718/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bezemer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAR-2000; 2000EP-00200930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-2001; 2001EP-00200703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-SEP-2001
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                                                                   115
                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody; camelid;
dietary enzyme inhi
human gastric lipas
                                                                                                                        61
                                                                                                                                                 61
                                                                                                                                                                                                                                  96;
                                                                                                                                                                                                      Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNILEVER NV.
                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                               QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQDGGSTNYA
                                                                                             SEPKTPKPQP 130
                                                                                                                                                    DSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYCNADVRPYRTSRYLEVWGQGTLVTVS
                                                                                                                                                                            QVQLQESGGGLVQAGGSLRLSCAASGSIGSLYVMSWYRQAPGKQREPVAALMGSGSTTYA
                                                                     SEPKTPKPQP 124
                                                                                                                        DSVKGRFTISRDNIKNTMYLQMNSLKPEDTGVYYCAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ody; camelid; anorectic; heavy chain variable domain; VHH;
ry enzyme inhibitor; medicament; human pancreatic lipase; HPL;
gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Van De Burg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= CDR2
/note= "Complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .104
                                                                                                                                                                                                                                             71.5%;
73.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Haard
                                                                                                                                                                                                                                Score 490; DB
Pred. No. 6.5e
6; Mismatches
                                                                                                                                                                                                                                  6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               determining
                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tareilus
                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                          Length 124;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region 3"
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                                                                                                                          -TGAEGHYWGQGTQVTVS
                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                    120
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QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQDGGSTNYA

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The invention describes a protein array (I) comprising a number of heavy-chain variable domain antibodies or antibody fragments, obtainable from CC camelidae. The method is useful for removing abundant proteins from an CC extract or sample which do not provide useful information on the CC condition of a cell or tissue in the extract or sample to be CC investigated. (I) is useful for detecting the presence of individual CC proteins in a sample, comparing the distribution of proteins in different CC cell types, and identification of proteins that may be of importance in CC determining the altered properties of cells in disease, aging or other CC conditions. Using a heavy-chain variable domain derived from an CC immunoglobulin that is naturally devoid of light chains (VHH) in (I) Provides a number of advantages, such as an improvement of CC sensitivity/resolution in the order of 10-100 times, and describes a method (II) that enables the simultaneous processing of large numbers of CC target antigens in a controlled way. The invention also describes a generates on-line information about the success or failure of a certain panning condition. This feature combined with the microtiter plate format CC allows the complete automation of the technology, based on computer-made decisions on the values of the phage-EIISA for continuation of a limited number of selections. In (II), due to the fact that many different conditions can be tested, varying amounts of input-phages can be used synthetic and immune libraries on large numbers of different target time frames needed for the generation of large panels of antibodies in short time frames needed for the generation of large panels of antibodies in short can be tested, and immune of large panels of antibodies in short time frames needed for the generation of large panels of antibodies in short can be completed and immune panels of large panels of antibodies in short time frames needed for the generation of large panels of antibodies in short and the panels of the panels of anti
  Matches
                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel protein array useful for detecting the presence of individual proteins in sample, comprises heavy-chain variable domain antibodies antibody fragments obtainable from Camelidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heavy chain variable domain; antibody; immunoglobulin; sticky phage-antibody; proteomic; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-583487/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-DEC-2000; 2000EP-00311142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-DEC-2001; 2001WO-EP014471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200248193-A2
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                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 3; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNIL ) UNILEVER PLC. (UNIL ) HINDUSTAN LEVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin G
  . Similarity
95; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNILEVER NV.
UNILEVER PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JJW,
                                                                              131 AA;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hermans P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specifo
                70.9%;
72.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heavy chain variable domain antibody #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Landa I,
  10;
  Score 485.5; DB 5;
Pred. No. 1.7e-34;
0; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Verrips CT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein array;
micro-panning;
      Indels
                                      Length
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immune
      1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VHH;
library;
      Gaps
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Matches

95

Conservative

6

Indels

73.1%;

Best Local Similarity

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                                                                                                                              New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                    WPI; 2001-572718/65
                                                                                                                                                                                     Bezemer
                                                                                                                                                                                                      (UNIL )
                                                                                                                                                                                                                                                 20-FEB-2001;
                                                                                                                                                                                                                                                                                    EP1134231-A1
                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                14-MAR-2000; 2000EP-00200930
                                                                                                                                                                                                                                                                   19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                     Lama sp
                                                                                                                                                                                                                                                                                                                                                                                                                        food;
                                                                                                                                                                                                                                                                                                                                                                                                                                numan
                                                                                                                                                                                                                                                                                                                                                                                                                                          Llama
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGL inhibiting VHH fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                     antibody; camelid; anorectic; heavy chain variable domain; VHH; dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                    Š
                                                                                                                                                                                                      UNILEVER NV.
                                                                                                                         chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; peptide; 124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEPKTPKPOP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEPKTPKPQP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSVKGRFTISRDNAKNTVYLOMNSLKPEDTGVYYCNAETVRATTGRFITDLWGQGTTVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSVKGRFTISRDNTLNTVYLOMNDLKPEDTAVYYCNADVRPYRTSRYL-EVWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLQESGGGLVQPGGSLRLSCAASKSIFGFGAVGWHRQAPGKQRELVARITYDSGTNYA
                                                                                                                                                                                   Van De Burg
                                                                                                                                                                                                                                                 2001EP-00200703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                        /label= CDR1
/note= "Complementarity
                                                                                                                                                                                                                                                                                                                                'label= CDR2
'note= "Complementarity
                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                               label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                        .104
                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                    "Complementarity determining
                                                                                                                                                                                   ž
                                                                                                                                                                                                                                                                                                               CDR3
                                                                                                                                                                                    De
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGL
                                                                                                                                                                                     Haard
                                                                                                                                                                                                                                                                                                                                                                                                                                                         #15
                                                                                                                                                                                   JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         from
                                                                                                                                                                                                                                                                                                                              determining
                                                                                                                                                                                                                                                                                                                                                       determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                       llama species
                                                                                                                                                                                    Tareilus
                                                                                                                                                                                                                                                                                                    region
                                                                                                                                                                                                                                                                                                                                                        region
                                                                                                                                                                                                                                                                                                                               region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
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Query Match

70.8%;

Score

485;

В

4.

Length 124;

Sequence

124

AA;

resent peptide sequence (camelid) species

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #15 from

Example 4; Page 14; 37pp; English

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RESULT 12

AABIO558

ID AABIO568

ID AABIO568

AC AABIO

AC AABIO

XX Llama

KW Llama

KW Hood,

XX Key

FT Regio

F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human distary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human distary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #22 from
                                                                                                                                                                                                                                                                                                    New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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         The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes.
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ARESULT 14
AABO5288
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XX AABO5
XX 18-SB
DT 18-SB
XX Potat
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Best Local S
Matches 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 129 AA;
                                                                                                                                                                                                                              Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabblism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potato; heavy chain immunogion metabolism modulator; passive VH; anti-potato SBEII; starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-2001
  The present invention relates to a method for modifying a plant to produce an antibody or an active fragment or derivative, or a protein functional equivalent, in a cellular compartment comprises introducing DNA sequence encoding a heavy chain immunoglobulin, where the DNA is linked to promoters and provided with an additional sequence encoding a peptide capable of targeting heavy chain immunoglobulin to a cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Solanum tuberosum. Unidentified.
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                                                                                                                                                                                Example 13; Fig 28; 81pp; English
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UNILEVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heavy chain immunoglobulin; pathogen resistance; ism modulator; passive immunisation; heavy chain i-potato SBEII; starch branching enzyme; SBE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Pred. No. 2.2e-
10; Mismatches
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ARESULT 15
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ID AARE10
AXX AARE10
AXX i0-DE
AXX I10-DE
XX ILLama
KW LLama
KW Hood;
XX Lama
XX Regio
FT Rull
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Example 4; Page 14; 37pp; English.

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HFL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #16 from llama (camelid) species

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## ALIGNMENTS

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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: H36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: H36005
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SS5536
Ig heavy chain V region pe20 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S5536
R;Boettger, V:, Boettger, A:, Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using utations in the variable region genes.
A;Reference number: S5538 MUID:95239763; PMID:7536850
A;Accession: S5536
                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residuse: 1-121 - 45CH>
A;Cross-references: GB:M34032
C;Genetics:
  A;Gene
A;Cros
A;Map
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
Gene: GDB:IGH@; IGHDY1
;Cross-references: GDB:118731; O;Map position: 14q32.33-14q32.33
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                              OMIM:146910
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Pred. No. 7.4e
11; Mismatches
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nes 27;
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Eur. J. Immunol. 22, 247-251, 1992
A,Title: Restricted utilization of germ-line V(H)3 genes and short c
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31114
A;Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain - human (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999 C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999 C;Accession: S31114 R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Eur. J. Immunol. 22, 247-251, 1992
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                                                    A, Title: Comprehensive epitope analysis of utations in the variable region genes. A, Reference number: 855528; MUID:95239763, A; Accession: $55537
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A,NOte: the nucleotide sequence was submitted to the EMBL Data Library, C,Superfamily: immunoglobulin V region; immunoglobulin homology C,Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-123 < RAA>
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <BOI
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                                                                                                                                                                 Ig heavy chain V region pe21 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
C;Accession: 855537
                                                                                                                               R;Boettger, V.; Boettger, A
J. Mol. Biol. 247, 932-946,
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Best Local S
Matches 82
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Best Local S
Matches 83
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83; Conserv
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28; MUID:95239763; PMID:7536850
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67.5%;
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Pred. No. 2.1e
l1; Mismatches
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Pred. No. 1.
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hes 26;
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C;Species:
C;Date: 13-
C;Accession
R;Mortari,
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                                                                                         A;Reference number: A36005;
A;Accession: A36006
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <SCH>
                                                                                                                                                                       ig heavy chain V region (M26) - human C;Species: Homo sapiens (man) C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 C;Accession: A36006 R;Schroeder Jr., H.W.; Wang, J.Y. Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990 A;Title: Preferential utilization of conserved imm A;Reference number: A36005; MUID:90349571; PMID:21
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Eur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage
A;Reference number: 826786; MUID:92111632; PMID:1730251
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A;Molecule type: mRNA
A;Residues: 1-121 <MOR>
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A;Cross-references: GDB:118731;
A;Map position: 14q32.33-14q32.
                                     A; Gene: GDB: IGH@; IGHDY1
                                                         C;Geneti
                                                                           A; Cross-references: GB:M34023
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Best Local S
Matches 81
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;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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                       OMIM: 146910
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Pred. No. 3.1e
8; Mismatches
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gene

119;

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: GB:M1
C;Superfamily: immunoglob
C;Keywords: heterotetrame
F;15-98/Domain: immunoglo
                                                                                                                            Ig heavy chain V region (30p1) - human
()Species: Homo sapiens (man)
()C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-A
()Accession: C36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: C36005
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R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol,
Bur. J. Immunol. 22, 247-251, 1992

A;Title: Restricted utilization of germ-line V(H)3 genes
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31110
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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                   ;Superfamily: immunoglobulin;Keywords: heterotetramer; in
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;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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                                                         Cross-references: GB:M18513
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81; Conservative
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lin homology
                 V region; immunoglobulin homology mmunoglobulin
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Pred. No. 3.2e-27;
0; Mismatches 26
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Pred. No. 3.1
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A;Reference number: S48797
A;Accession: S48798
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <mAH-
A;Cross-references: EMBL:Z46382; NID:g562324; PIDN:CAA86521.1; PID:g1340167
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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S48798
                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-121 <RES>
A;Cross-references: GB:M87268; NID:g186197; PIDN:AA
                                                                                                                                                                                                      R;Knight, G.B.; Agnello, V.; Bonagura, V.; Barnes J. Exp. Med. 178, 1903-1911, 1993
A;Title: Human rheumatoid factor cross-idiotypes. tinct from the 17.109 and G6 XIds.
                                                                                                                                                                                                                                                                                     Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jull-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I55673
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R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - C;Species: Homo sapiens (man) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
                                                        A;Cross-references:
C;Genetics:
                                                                                                                                                               A;Reference number: A;Accession: I55673
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A;Cross-references: GDB:120086; OMIM:147020
A;Map position: 14q32.33-14q32.33
                                         A;Gene: GDB:IGHM
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                                                                                                                                                                                  I55673; MUID:94065558; PMID:8245772
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67.8%;
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                                                                              NID:g186197; PIDN:AAC37536.1;
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Pred. No. 3.7e
7; Mismatches
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Pred. No. 4.1e-27;
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                                                                                                                                                                                                                                                                 V.; Barnes, J.L.; Panka,
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C;Species: N...
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R;Boettger, V; Boettger, A; Lanc,
R;Boettger: 247, 932-946, 1995
J. Mol. Biol. 247, 932-946, 1995
Title: Comprehensive epitope ana
Title: 555528; MUID:
A;Cross-references: EMBL:X62960
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-100/Domain: immunoglobulin homology <TMM>
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A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
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A,Reference number: S55528; MUID:95239763; PMID:7536850
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;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.;
ur. J. Immunol. 22, 247-251, 1992
ur. J. Immunol. 22, 247-251, 1992
;Title: Restricted utilization of germ-line V(H)3 genes and shore the second of the second secon
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                                                                                                                                                                              Status: preliminary; nucleic acid sequence; Molecule type: mRNA; Residues: 1-117 <RAA>
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Species: Mus musculus (house mouse)
Date: 27-0ct-1995 #sequence_revision 03-Nov-1995 #text_change
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Pred. No. 4.6e-27;
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Pred. No. 6.8e-27;
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A;Status: preliminary; nucleic acid sequenc
A;Molecule type: mRNA
A;Residues: 1-114 <RAA>
A;Cross-references: EMBL:X62972
A;Cross-references: EMBL:X62972
A;Note: the nucleotide sequence was submitte
C;Superfamily: immunoglobulin V region; imm
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IM
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CJSpecies: Homo sapiens (man)
CJDate: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
CJAccession: S31120
RJRaaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.
Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse the properties of the proper
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R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.;
Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse thir A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31108
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C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31108
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: immunoglobulin V region; immunoglobulin homology
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Pred. No. 8.1e-27;
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Pred. No. 8.2e-27;
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                                                              mitted to the EMBL Data Library, immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                   M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
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A;Gross-references: GDB:118731; OMIM:146910
A;Map position: 114432.33-14432.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: D36005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (M43) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: D36005
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D36005
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A;Molecule type: mRNA
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Best Local Similarity
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ol-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 heavy chain V region 5A precursor.
Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
Cyprinidae; Carassius.
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MEDLINE=88144476; PubMed=3125551;

Wilson M.R., Middleton D., Warr G.W.;

"Immunoglobulin heavy chain variable region gene evolution:
and family relationships of two genes and a pseudogene in a
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InterPro; IPR003596; Ig_v.
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TE; PS50835; IG_LIKE; toglobulin V region; Si
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0005955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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SEQUENCE (MYELOMA PROTEIN TRO).
MEDLINE=76023781; PubMed=809331;
Kratzin H., Altevogt P., Ruban E.,
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
1g heavy chain V-III region TRO.
Homo sapiens (Human)
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21-JUL-1986 (Rel. 01, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
10 heavy chain V-III region BUT.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structure of the complete IgA-molecule.";
Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
-i- MISCELLANBOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN
MEDILINE=78137069; PubMed=416441;
Torano A., Putnam F.W.;
"Complete amino acid sequence of the alpha 2 heavy chain IgA2 immunoglobulin of the AZm (2) allotype.";
Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
-!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, AZM(2) AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Immunoglobulin V region; Pyrr
DOMAIN_ 1 108
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HSSP; P01772; 2FB4.
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                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                  P01767;
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II. The amino acid sequence of the H-chain,
                                                                          SEQUENCE
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                                                                                                              Primates;
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57.4%;
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IG-LIKE
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Pred. No. 1
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                                                                                                              Catarrhini; Hominidae; Homo
                                                                                                                           Craniata; Vertebrata; Euteleostomi;
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   A2M(2) ALLOTYPE,
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ubgroup III;
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-!- SIMILARITY: Conta
PIR; A02050; A2HUBU.
HSSP; P01789; 1MCP.
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21-JUL-1986
21-JUL-1986
10-OCT-2003
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_HV3T_F
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
Immunoglobulin V region.
                                                                                                                                                                                                 HSSP; P01772; 2FB4.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region GAL.
Homo sapiens (Human)
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NON TER
SEQÜENCE
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Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
"The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
type), subgroup H III. Architecture of the complete IgM-molecule.";
type-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
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                                                                                                                                                            Pfam; PF00047; ig; 1
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                      Hilschmann N.;
Submitted (JUN-1975) to
-!- MISCELLANEOUS: THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                               SEQUENCE
                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                   PIR; A02064; M3HUGL.
                                                                                                                                                                                                                                                                                                                                                                    MACROGLOBULIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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InterPro; IPR003596; Ig_v.
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                                                                                                               PS50835; IG_LIKE;
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115 AA;
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Pred. No. 1.4
Score 341;
                                                                                           IG-LIKE.
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                                               2C67CA9AAAAA1282 CRC64;
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Length 116;
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RESULT 6

RESULT 6

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Matches 74; Conserv
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PDB; 2152; 12-UUL-89.

PDB; 2162; 12-UUL-89.

G0; G0:0005576; C:extracellular; NAS.

G0; G0:0005323; F:antigen binding; NAS.

G0; G0:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig-like.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; P$50835; IG-LIKE; 1.
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DOMAIN 1
MOD_RES 1
DISULFID 22
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STRAND
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J. Mol. Biol. 141:369-391(1980).
-!- SIMILARITY: Contains 1 immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marquart M., Deisenhofer J., Huber R., Palm W., "Crystallographic refinement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; "Three-dimensional structure determination of antibodies. structure of crystallized monoclonal immunoglobulin IgG1 Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, AND DISULFIDE BONDS.
MEDLINE=83289131; PubMed=6884994;
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                                                                                                                                                                                                                                                                                                                                                   3D-structure; Pyrrolidone carboxylic IG-LIKE.
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Query Match
Best Local S
Matches 71
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Best Local Similarity
Matches 74; Conserv
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DISULFID
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SEQUENCE
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HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003823; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig v.
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STRAND
                                                                                                                                                                              Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic DOMAIN 1 112 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE (MYELOMA PROTEIN BUR).

MEDILINE-79151016; PubMed=107164;

Putnam F.W., Liu Y.-S.V., Low T.L.K.;

Putnam Y.W., Liu Y.-S.V., Low T.L.K.;

Igal protease, digestion, Fab and Fc fragments, and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TURN
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid sequence of the alpha 1 heavy chain.
J. Biol. Chem. 254:2865-2874(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V-III
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986
10-OCT-2003
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  1 Similarity 71; Conser
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(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
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    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       Contains 1 immunoglobulin-like domain.
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                 49.7%;
                                                                                12981 MW;
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  Score 337.5; I
Pred. No. 1.4e.
.4; Mismatches
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Pred. No. 8.
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                                                                                12A709A75344D024 CRC64;
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.4e-26;
                     .4e-25;
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                                        DB 1;
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                                                                                                                        Query Match
Best Local
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SMART; SM00406; IGv; 1.
PROSITE; PS0835; IG_LIKE;
Immunoglobulin V region; SIGNAL
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CHAIN 20 117
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P01764;

21-JUL-1986

21-JUL-1986

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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure and multiplicity of genes for the hum heavy chain variable region.";
Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V-III region VH26 precursor.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Primates; Catarrhini; H
                                                                                                                                                                                                                                                                                   GO; GÓ:0005576; Ć:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=81101090; PubMed=6450418;
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J00236; AAA53516.1; -.
EMBL; M35415; AAA58735.1; -.
                                                                                                                                                                                                                                                                                                                                                            PDB; 1HOU; 23-DEC-99.
Genew; HGNC:5545; IGHV@.
                                                                                                                                                                                                                                                                                                                                                                                        PIR; A02047;

    -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

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                                                                               1 QVQLQESGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRIT-AGGSTNY
                                                                                                           68;
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                                                                                                                        Similarity
                   ADSAKGRFTISKDNAKNTVYLOMNSLKPEDTAVYYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADSAKGRFTISKDNAKUTVYLQMNSLKPEDTAVYYCNALITRWDKSVNDYWGQGTQVTVS
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GDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC
                                                    EVOLLESGEGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                117
117 AA;
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(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                          H3HU26
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                                                                                                                                                                             117
>117
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                                                                                                                                                                                                                                                 IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                 12582 MW; E826733F1A3CB0F1 CRC64;
                                                                                                                        49.3%;
                                                                                                                                                                                                                                  Signal; 3D-structure
                                                                                                                        Score 334.5; DB 1
Pred. No. 2.6e-25;
                                                                                                                                                                                            IG HEAVY CHAIN V-III REGION VH26. IG-LIKE.
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                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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L outstation -
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RESULT 9 HV35\_MOUSE

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Best Local S
Matches 68
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Bernard O., Gough N.M.;

Bernard O., Gough N.M.;

"Nucleotide sequence of immunoglobulin heavy chain joining segments between translocated VH and mu constant regions genes.";

Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).

-!- MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE CREGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE CORDERSPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.
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NON TER
SEQÜENCE
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Immunoglobulin V region.
NON TER
                                                                                                SEQUENCE OF 1-112.

MEDLINE-77242268; PubMed=407924;

Wasserman R.L., Capra J.D.;

"Primary structure of the variable immunoglobulin heavy chains.";

Biochemistry 16:3160-3168(1977).
MEDLINE=80077682; PubMed=117299; MCCUmber L.J., Capra J.D.; WCCumber L.J., Capra J.D.; WThe complete amino-acid sequence of Mol. Immunol. 16:565-570(1979).
                                                                                                                                                                                       NCBI_TaxID=9615;
                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Ig heavy chain V region MOO.
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                     CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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P01804;
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V-III
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region HPC76 (Fragment).
                                                                                                                                                                                                                                                                                                          P01785;
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                                                                      SEQUENCE OF 113-117.
                                                                                                                                                                                                                                                                                                                      CANFA
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111
111 AA;
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larity 58.1%;
Conservative 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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  FROM A MYELOMA PROTEIN.
                              chain.";
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; Murinae; Mus
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RESULT 11
HV39 MOUSE
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Best Local S
Matches 70
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunglobulin V region.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1
Immunoglobulin V region.
DOMAIN
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NON TER
SEQUENCE
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21-JUL-1986
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complementarity-determining regions.";
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979)
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Cr
21-JUL-1986 (Rel. 01, La
10-OCT-2003 (Rel. 42, La
Ig heavy chain V region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rao D.N., Rudikoff S., Krutzsch H., Potter M. "Structural evidence for independent joining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THAT BINDS GALACTAN.
-!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=79223895; PubMed=111245;
Rao D.N., Rudikoff S., Krutzsch H.,
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InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISSP; P01810; 2FBJ.
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QVQLQESGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRITAGGSTNYA
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                                                                                        EVKLLESGGGLVQPGGSL-LSCAASGFDFSRYWMSWARQAPGKGQEWIGEINPGSSTINY 59
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117 AA;
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                                                                                                                                                                                                                                                                        13105 MW;
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                                                                                                                                                                             49.1%; Score 333.5; DB 1
59.0%; Pred. No. 3.2e-25;
tive 13; Mismatches 32
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Pred. No. 3.2e
14; Mismatches
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; Murinae; Mus
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proteins
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RESULT 12
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RESULT 13
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P01784;
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21-JUL-1986
10-OCT-2003
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NON TER
SEQUENCE
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HSSP, P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=80020921; PubMed=114209;
Steiner L.A., Garcia Pardo A., Margolies M.N.;
"Amino acid sequence of the heavy-chain variable region of the
crystallizable human myeloma protein Dob.";
Biochemistry 18:4068-4080(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 18:4054-4067(1979).
-!- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN
HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
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SMART; SM00406; IGV; 1.
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HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steiner L.A., Lopes A.D.; "The crystallizable human myeloma protein Dob has a hinge-region
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE; 1
Immunoglobulin V region.
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(Rel. 42, Last annotation
ain V-III region DOB.
                       (Rel. 01, Created)
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Pred. No. 3.
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HV3B
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Best Local
                                                                                 Goni F., Frangione B.;
Indian monoclonal IgM
"Amino acid sequence of the Fv region of a human monoclonal IgM
"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3.4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

-i- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
-i- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A PATIENT WITH
                                                                                                                                                                                                                                                                                                    21-JUL-1986
21-JUL-1986
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                HV3B_HUMAN
P01763;
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SEQUENCE
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10-OCT-2003 (Rel. 42, Last annotation
Ig heavy chain V region GOM.
Canis familiaris (Dog).
HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS
                                                                                                                                                                                                                                                                          Ig heavy chain V-III region WEA. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                               HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
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InterPro; IPR003596; Ig_v.
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HSSP; P01772; 2FB4.
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MEDLINE=77242268; PubMed=407924;
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 16:3160-3168(1977).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wasserman R.L., Capra J.D.;
"Primary structure of the variable regions of two
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                                         PIR; A02046; M3HUWE.
                                                                                                                                                                                      MEDLINE=83273707; PubMed=6410398;
                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin heavy chains."
                                                       -!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                      AGAINST 3,4-PYRUVYLATED GALACTOSE AND WALDENSTROM'S MACROGLOBULINEMIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      114 S
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114
114 AA;
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(Rel. 01, Last sequence up
(Rel. 42, Last annotation
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12430 MW;
                                                                                                                                                                                                                                             Chordata; Craniata; Ve
Primates; Catarrhini;
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Pred. No. 6.8e-25;
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                                                                                                                                                                                                                                                              Vertebrata; Euteleostomi;
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Canis.
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RESULT 15
HV37_MOUSE
ID HV37_MOUSE
AC P01807;
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                                                                                                                                                                                                                                                           COMPLEMENTATITY-determining regions.";

Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).

CHOOS NATL. Acad. Sci. U.S.A. 76:2890-2894 (1979).

CHAIN SCELLANGOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN THAT BINDS GALACTAN.

CHAIN LARITY: Contains 1 immunoglobulin-like domain.

PIR; A02077; AVMS44.

RE HSSP; P01810; 2FBU.

RE HSSP; P01810; 2FBU.

RE InterPro; IPR007110; Ig-like.

RE InterPro; IPR003596; Ig-v.

RE FAGRIT; SM00406; IGV; 1.

RE SMART; SM00406; IGV; 1.
                                                                                 Matches
                                                                                                              Query Match
Best Local
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NON TER
SEQUENCE
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NON_TER
SEQUENCE
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-79223895; PubMed=111245;
Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins its potential role in generating diversity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region X44.
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                                                                                                                  Similarity
QVQLQESGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRITAGGST-NY
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119 AA;
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                                                                                    Conservative
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12256 MW; D88294FB418A07B7 CRC64;
                                                                                                                                                                                                      119
13246 MW; BC34FC8F31CD41B3 CRC64;
                                                                              48.6%; Score 330; DB 1; Length 119; 57.4%; Pred. No. 7.1e-25; tive 16; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYRROLIDONE CARBOXYLIC ACID
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EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 60

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Qy 60 ADSAKGRFTISKDNAKNTVYLQMNSLKPEDTAVYYCNALITRWDKSVNDYWGQGTQVTVS 119
Db. 61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYC-ARLHYYGYAA--YWGQGTLVTVS 117
Qy 120 SE 121
Db 118 AE 119
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Search completed: October 5, 2004, 08:01:54
Job time: 11.5463 secs

THE PAGE BATH (MISSO)

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Score
                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    of hits satisfying chosen parameters:
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679
                                                                                                                                               Match
                                                                                                                                                                                                                           110:
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*
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                                                                                                                                                       Query
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QVQLQESGGGLVQAGGSLRL.....WGQGTQVTVSSEPKTPKPQP 129
                                                                                                                                                                                                                                                                                  sp_organelle:*
sp_phage:*
sp_plant:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
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sp_invertebrate:*
                                                                                                                                              Length
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118
597
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Q8N5K4
Q9UL91
Q920E7
Q99EA4
Q91Z07
Q91Z07
Q9HCC1
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Q9HCC1
Q9HCC1
Q9HCC1
Q9HCC1
                                                                          Q8WUK1
Q9UL90
Q9UL71
                                                                                                    Q9UL72
Q96BB9
Q9UL88
Q9UXE1
                                                                                                                                                                        SUMMARIES
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                                                                                                    Q96bb9 homo
Q9u188 homo
Q91xe1 mus
                                                          Q8n5k4
Q9u191
             155460
                                                                                          Q8wuk1
                        Q920e7 mus 1
Q99ka4 mus 1
Q91z05 mus 1
Q91z07 mus 1
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Q8VDC9	Q924P9	Q924R6	Q924Q3	Q924R1	Q924Q9	Q9N0W4	Q99NG4	Q9N0W6	Q8K172	Q9UIL92	Q924R0	Q8VCX7	Q9UL73	Q91X92	Q7TMK4	Q8VEA0	Q9UL84	Q9ULB6	Q8N4Y9	Q8NCL6	Q8R3V9	Q80ZI7	Q7Z5W1	Q9R1A4	Q9QYF0	Q9Y509	Q9UL93	Q96K68
Q8vdc9 mus musculu	Q924p9 mus musculu	Q924r6 mus musculu	Q924q3 mus musculu	Q924rl mus musculu	9 mus	Q9n0w4 oryctolagus	Q99ng4 mus musculu	Q9n0w6 oryctolagus	Bnw	Q9ul92 homo sapien	mus	mus	Q9ul73 homo sapien	mus	mus	mus	homo	homo	homo	OMO	ยกต	Q80zi7 mus musculu	omo	Bru	o mus	Q9y509 homo sapien	homo	Q96k68 homo sapien

# ALIGNMENTS

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RESULT 1
Q9UL72
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                                                                                                                                Query Match
Best Local Similarity
Matches 80; Conserv
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Q9UL72;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig v.
Pfam; PF00447; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035042; AAD56278.1; -
FIR; S21205; S21205.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=98277139; PubMed=9614934;

Mu X. Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            etus.";
1 QVQLQBSGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRITAGGSTNYA 60
                                                                                                                                                                                                                                                                                                    118 118
118 AA; 12872 MW;
                                                                                                                       57.6%; Score 391; DB 4; Length 118; ilarity 66.7%; Pred. No. 1.4e-32; Conservative 12; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                         B4D1A5944B2D5CCA CRC64;
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Q8wu38 homo

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11;

Gaps

120 109 60

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RESULT
Q9UL88
ID Q9UL89
AC Q9UA
AC Q9
AC Q
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Q96B9

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RP SEQU

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Best Local S
Matches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; i9; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pi
                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TYEMMBLrel. 13, Created)
01-MAY-2000 (TYEMMBLrel. 13, Last sequence update)
01-CCT-2003 (TYEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical SEQUENCE 59
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01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q96BB9;
                      "Myosin-reactive autoantibodies fetus."; Clin. Immunol. Immunopathol. 87:
                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                             Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UL88;
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                                                                                                                                                                                                                                                                                                    Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRIT-AGGSTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIVSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADSVKGRFTISRDNSRDTLYLQMNSLRAEDTAVYYCAKDPRGYSASGNYTREDYWGQGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADSAKGRETISKDNAKNITVYLOMNSIKPEDTAVYYCNALITRWDKSVN----DYWGQGTQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAFYYCAR--DRFGEFLFDYWGQGTLVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                 ; Chordata;
; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Primates;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 378.5; :
Pred. No. 2.4e
L1; Mismatches
                        87:184-192(1998)
                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                    in rheumatic
                                                                                                                Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    597
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                                                                       carditis
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Best Local
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG LIKE; 4.
PROSITE; PS50835; IG MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation updat
01-CCT-2003 (TrEMBLrel. 25, Last annotation updat
Hypothetical protein (Fragment).
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrat
Mammalia; Eutheria; Rodentia; Sciurognathi; Murid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUL
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF035026; AAD!
PIR; S21205; S21205
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC010798; AAH10798.1; -.
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InterPro; IPR003596;
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                                                                                                                     DSMKGRFTISRDNAQNTVLLQMTSLNSEDTAVYYC---
                                                                                                                                              DSAKGRFTISKDNAKNTVYLOMNSLKPEDTAVYYCNALITRWDKSVNDYWGQGTQVTVSS
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131 AA;
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14142 MW;
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Ig_v.
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                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                         Score 368.5; DB 1
Pred. No. 1.9e-29;
9; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                      20B9234EEF2B41ED CRC64;
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les 27;
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480; <u>ن</u>

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RESULT 5
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Best Local S
Matches 79
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, BC020240, AAH20240.1; -.
PIR; PL0120; PL0120.
PIR; S15590; S15590.
RINGETPO; IPR003006; Ig_MHC.
RINGETPO; IPR003596; Ig_W.
RINGETPO; IPR003596; Ig_V.
REARLY, SM00406; IGV; I.
SMART; SM00406; IGV; I.
REASSITE; PS00835; IG_LIKE; S.
RPROSITE; PS00835; IG_LIKE; S.
RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UL90 PRELIMINARY; PRT; 113 AA.
Q9UL90; Q9UL90;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8WUK1;
                            EMBL; AF035024; AAD56260.1; -. HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                               "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fragment).
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                                                                                                          lin. Immunol. Immunopathol. 87:184-192(1998)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 362; DB 4; Length 613; Pred. No. 1.3e-28; 7; Mismatches 31; Indels
                                                                                                                                                                                                                                                             Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo.
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RESULT 7
Q9UL-
1D U-9UL
AC Q9UL-
AC Q9UL-
DT 01-M
DT 01-M
DT 01-M
DT 01-M
OC MAMMA
OC HUMAN
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Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 79
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Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON TER 1 1 11
NON TER 13 113
SEQUENCE 113 AA; 12437 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UL71;
01-MAY-2000
01-MAY-2000
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG_LIKE; 1.
NON_TER 1 1
NON_TER 121 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=98277139; PubMed=9614934;

Wu X., Liu B., Van der Merwe P.L.,

Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF035043; AAD56279.1; HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UL71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig~like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Myosin-reactive autoantibodies in rheumatic carditis and normal
119
                                               118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 S 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 ADSAKGRPTISKDNAKNTVYLQMNSLKPEDTAVYYCNALITRWDKSVNDYWGQGTQVTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRITAGGSTN-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mmunol. Immunopathol.
                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                               VSS 120
                                                                                                                                                                                                                          QVQLQESGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRITA-GGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S 113
VSS 121
                                                                                              ADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGKVTTIYDRF--DIWGQGTMVT 118
                                                                                                                                           ADSAKGRFTISKUNAKNTVYLQMNSLKPEDTAVYYC--NALITRWDKSVNDYWGQGTQVT 117
                                                                                                                                                                                           EVŐLVESGGGVVÓPGGSLRLFCAASGFTFDGYAMHWVRÓAPGKGLEWVSLISGDGGSTYY
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                                                                                                                                                                                                                                                                                                                                                                                              121
121 AA;
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              121
13154 MW;
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12437 MW;
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                                                                                                                                                                                                                                                                                       52.9%; Score 359.5; DB 4; 62.6%; Pred. No. 2.6e-29; tive 12; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 361.5; 1
Pred. No. 1.5e.
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                              2F045CCFA5D50736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kalis N.N.,
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                                                                                                                                                                                                                                                                                                                                         DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
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                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region
                                                                                                                                                                                                                                                                                                                                              121;
                                                                                                                                                                                                                                                                                            5
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                                                                                                                                                                                                                                                                                            Gaps
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RESULT 8
Q8N5K4
ID Q8N5 K4
ID Q8N5 K4
ID Q8N5 G1-(
DT 01-(
DT 
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Q9UL91
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PRESENTA ARREST OCCUPANTO 
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases:
EMBL BC032249; AAH32249.1; -.
R Interpro; IPR003599; Ig.
R Interpro; IPR003599; Ig.
R Interpro; IPR003506; Ig.—MHC.
R Interpro; IPR003506; Ig.—MHC.
R Interpro; IPR003506; Ig.—MHC.
R Interpro; IPR003506; Ig.—WHC.
R Interpro; IPR003506; Ig.—WHC.
R Interpro; IPR003506; Ig.—WHC.
R INTERPOORT; IRR003506; Ig.—WHC.
R SMART; SM00409; IG.; 4.
SMART; SM00409; IG.; 1.
SMART; SM00407; IGC1; 2.
SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00209; IG.—MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 79
                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8N5K4;
01-OCT-2002
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation updat
Myosin-reactive immunoglobulin heavy chain variab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UL91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                 "Myosin-reactive
                                                                                                                                                                                                  Young D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                             . Immunol. Immunopathol. 87:184-192(1998); AF035023; AAD56259.1; -. $21205; $21205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140
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79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQLVESGGGVVRPGGSLRLSCATSGFTFDDSGASWVRQAPGKGLEWVSSINWNGGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTVTVSSASPTSPKVFP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADSVKGRFTISRDNAKNSLYLQMNSLRVEDTALYYCARDPTKYCSGGSCLGYYMDVWGKG
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499 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Primates;
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Primates;
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57.7%;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 359; DB
Pred. No. 2e-2
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                        rheumatic
                                                                                                                                                                                                                                              Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain variable
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                                                                                                                                                                            carditis
                                                                                                                                                                                                                                              Berney S.M.,
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RESULT 10
Q920E7
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Best Local S
Matches 77
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pterin-minicking anti-idiotope heavy chain variable
(Fragment).
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InterPro; IPR003596; 1
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Atkin J.D., Iape A., Jennings I.G., Horaltis V., Curcus
"Definition of the Idiotope of Pterin-Mimicking Antibodi
in Mammalian Cells.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01772; 2FB4
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InterPro; IPR003596;
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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79; Conserv
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                                                                                        PDSVKGRFTISRDNAKUTLYLQMSSLKSEDTAMYYC---ARHGDYDVGFAYWGQGTLVTV
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SA 119
                                                                                                                        ADSAKGRFTISKDNAKNTVYLQMNSLKÞEDTAVYYCNALITRWDKSVN-DYWGQGTGVTV
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                                                                                                                                                                                                                                                                                Conservative
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Ig_v.
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Ig_v.
                                                                                                                                                                                                                                                                                                    52.1%;
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liotope of Pterin-Mimicking Antibodies E
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Pred. No. 5
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Pred. No. 1.1e-28;
1; Mismatches 29;
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Sciurognathi; Muridae; Murinae; Mus
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5.9e-29;
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RESULT 12
Q91Z05
ID Q91Z0
AC Q91Z0
DT 01-DE
DT 01-OC
DE HYPOT
GN AU044
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MAS m
OC Eukar
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Best Local S
Matches 76
          Submitted (JUL-2001) to the EMBL/GenBank/DDBJ datable EMBL; BC010327; AAH10327.1; -.

MGD; MG1:2144967; AU044919.

GO; GO:0005489; F:electron transporter activity; IE; GO; GO:0006118; F:electron transport; IEA.

Interpro; IPR003145; CytC heme_BS.

Interpro; IPR003110; Ig-1Ike.

Interpro; IPR003106; Ig_MHC.

Interpro; IPR003596; Ig_WHC.

Interpro; IPR003596; Ig_WHC.

Interpro; IPR003596; Ig_WHC.
                                                                                                                                                                                                                                                                           Q91Z05;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                           Strausberg R.;
Submitted (JUL
                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC004786; AAH04786.1; -
HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Underpro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (MAR-2001) to the
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                                                                                                                                                                                                                                                          Hypothetical AU044919.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              Q91Z05
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PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS50290; IG MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 4.
SMART; SM00406; IGv;
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                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGTQVTVSSE 121
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487 AA; 52554 MW;
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                                                                                                                                                                                                                                                                      protein'.
                                                                                                                                                                                                                 Chordata;
Rodentia;
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Last annotation update)
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Pred. No. 7.9e-28;
4; Mismatches 26;
                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                              PRT;
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RESULT

Q1Z07

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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 486 AA; 52682 MW;
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Q91Z07;
01-DEC-2001
01-DEC-2001
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Mus musculus (Mouse).
Eukaryota, Metazoa; Chemamalia; Eutheria; Ro
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PROSITE; PS50835; IG LIKE; 4-
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 473 AA; 51946 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JUL-2001) to the
SMBL, BC010324; AAH10324.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003
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                                                                                                                                                                                                                                                                                              DSAKGRFTISKDNAKUTVYLOMNSLKPEDTAVYYC---NALITRWDKSVNDYWGQGTQVT 117
                                                                                                                                                                                                                                                                                                                                                                                                       QVQLQESGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRITAGGSTNYA 60
                                                                                                                                                                                  VSSE
                                                                                                                                                                                                                           VSSE 121
                                                                                                                                                                                                                                                                                                                                                            EVHLVESGGGLVKPGGSLKLSCVVSGFSFTSYDMSWVRQTPERRLEWVAAITSGGNTYYP
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52682 MW;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 348.5; DB 1
Pred. No. 2.3e-27;
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Q9HCC1; Q9HCC1; 01-MAR-2001 01-MAR-2001

(TrEMBLrel. (TrEMBLrel. PRELIMINARY;

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sequence update)

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RESULT 15
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INTERPRO; IPR007110; Ig-like.
INTERPRO; IPR003596; Ig-v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_wHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv. 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS508290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.; "An antibody fragment2A3 specific for native lysozyme: Isolaion from human synthetic phage display library and characterization."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB049915; BAB16829.1; -.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC021276; AAH21276.1; -.
PIR; S21205; S21205.
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                                                                                                                                                                                       Hypothetical protein. SEQUENCE 573 AA; 6
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. Homo sapiens (Human).
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01-OCT-2003
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                                                                                                                 Similarity
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     EVOLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
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112 AA;
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                                                                                               Conservative
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Last annotation updat
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                                                                                          Score 345.5; DB 4
Pred. No. 5.9e-27;
9; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 347; DB 4;
Pred. No. 4.6e-28;
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114

Search completed: October 5, 2004, 08:13:45 Job time : 69.2824 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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        $32 $507.55 $18.32 $507.55 $507.55 $500.55 $500.55 $500.55 $500.55 $500.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $600.55 $60
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HPL inhib
HGL inhib
Llama ant
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Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.

HPL inhibiting VHH fragment,

HPL #13 from llama species

# ALIGNMENTS

AAE10553 standard; peptide; 129

8

AAE10553;

10-DEC-2001

(first entry)

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RASULT 1
RABIO553
ID AD553
ID AD553
ID AD553
ID AD6553
I
                                                           New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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/note= "Complementarity determining region
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Example 2; Page 9; 37pp; English

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Best Local S
Matches 129
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                                                                                                                                                                                                                                                                                                                                                                Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
          New antibody or its fragments
                               WPI; 2001-572718/65
                                                                                                                                       20-FEB-2001; 2001EP-00200703
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                                                       Bezemer S,
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                                                                                                                 14-MAR-2000; 2000EP-00200930
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                                                       Van De Burg
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Pred. No. 4.6e-52;
          for inhibiting
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                                                         Tareilus
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Pred. No. 1.4e-39;
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Matches 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                Solanum tuberosum.
Unidentified.
                                                                                                                                                                                                       metabolism modulator; passive immunisation; heav VH; anti-potato SBEII; starch branching enzyme;
                                                                                                                                                                                                                                                             Anti-potato SBEII (Clone46) VH region attached with myc
                                                                                                                                                                                                                                                                                                                                             AAE05283 standard;
                                                                  08-DEC-2000;
                                                                                              25-JUL-2001.
                                                                                                                        EP1118669-A2
                                                                                                                                                                                                                                   Potato;
                                                                                                                                                                                                                                                                                                                   AAE05283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
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                                          17-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                   heavy chain immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLQESGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRITAGGSTNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYYCNALIRRKFTSEYNEYWGQGTQVTVS
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                                                                    2000EP-00310997
                                                                                                                                                                                                                                                                                       (first entry)
                                          99EP-00310188
                                                                                                                                                                                                                                                                                                                                             protein; 152
                                                                                                                                                                                                                                                                                                                                                                                                                 130
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78.5%;
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Pred. No. 5.9e
6; Mismatches
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nes 21;
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                                                                                                                                                                                                                       heavy
                                                                                                                                                                                                                                   resistance;
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SBE A.
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                                                                                                                                                                                                                     variable
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(HGL)
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(UNIL ) UNILEVER PLC

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for modifying a plant to CC produce an antibody or an active fragment or derivative, or a protein CC functional equivalent, in a cellular compartment comprises introducing a CC DNA sequence encoding a heavy chain immunoglobulin, where the DNA is CC linked to promoters and provided with an additional sequence encoding a compartment. The method is used for producing a heavy chain to a cellular CC compartment. The method is used for producing a heavy chain to a cellular CC immunoglobulin or an active fragment or derivative, or a protein that is CC immunoglobulin or an active fragment or derivative, or a protein that is CC immunoglobulin or an aplant for increasing the pathogen resistance in a plant CC or to modulate metabolism in a plant. Under some circumstances it may be CC desirable to retain the antibody product with the plant rather than CC extracting and isolating the product. In particular, edible selected CC antigens may be used in a method of passively immunising an animal, preferably human, against the antigen, e.g., pathogenic organisms. The CC present sequence is an anti-potato SBEII antibody (denoted Clone46) heavy chain variable domain (VH) attached to peptide linkers, myc and his6 tag. The potato SBEII is a starch branching enzyme also designated SBE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
                                                   Region
                                                                                                                                                                                  Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                          10-DEC-2001
                                                                                                                                                                                                                                                                                                                             AAE10557;
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                                                                                                                                                                                                                                                                                                                                                            standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQESGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRITAGGSTNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSSEPKTPKPQP 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSAKGRETISKDNAKNTVYLOMNSLKPEDTAVYYC---NALITRWDKSVNDYWGOGTOVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLQESGGGLVQAGGSLRLSCVASGNTFSIIAMAWYRQAPGKQREVVASINSIGSTNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSVKGRFTISRDNAKNTVYLOMSSLKPEDTAVYYCAAGNLLVKR-----PYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                  Location/Qualifiers
                                /label= CDR2
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                  "Complementarity
                                                                 "Complementarity
                                                                                     CDR1
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Pred.
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                determining
                                                                 determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; DB 4;
5.5e-37;
nes 16;
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                  region
                                                               region
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RESULT 7
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human baings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #19 from llama (camelid) species
Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                            Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                  HPL inhibiting
                                                                                                                                                                       AAE10552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 130 AA;
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                                                                                                                                                                                                  AAE10552 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2000; 2000EP-00200930
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                                       ds,
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                                                                                                                                                                                                                                                                    SEPKTPKPQP 130
                                                                                                                                                                                                                                                                                              SEPKTPKPQP 129
                                                                                                                                                                                                                                                                                                                       DSVKGRFTISRDNDKNTEYLOMNIKPEDTAVYYCNAQVRVRFSSDYTNYWGQGTQVTVS
                                                                                                                                                                                                                                                                                                                                               DSAKGRFTISKDNAKNIVYLOMNSLKPEDTAVYYCNALI-TRWDKSVNDYWGQGTQVTVS
                                                                                                                                                                                                                                                                                                                                                                            QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASITATGPPNYT
                                                                                                                                                                                                                                                                                                                                                                                                    OVOLOESGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRITAGGSTNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 10; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                               (first entry)
                                                                                                                    VHH fragment,
Location/Qualifiers 31...35
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/note= "Complementarity determining region
                                                                                                                                                                                                  peptide; 130
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74.6%;
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Pred. No. 8.2e-37;
                                                                                                                     HPL #12 from
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                                                                                                                     llama
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                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                     species
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RESULT 8
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Matches 100;
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Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                    AAE10551
                                                             10-DEC-2001
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 9; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bezemer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1134231-A1
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UNILEVER PLC
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                                                                                                   standard;
                                                                                                                                                                                                                                            QVQLQESGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRITAGGSTNYA
                                                                                                                                                    SEPKTPKPQP
                                                                                                                                                                       SEPKTPKPOP 129
                                                                                                                                                                                         DSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYCNADVRPYRTSRYLEVWGQGTLVTVS
                                                                                                                                                                                                             DSAKGRFTISKDNAKNTVYLOMNSLKPEDTAVYYCNALITRWDKS-VNDYWGQGTQVTVS
                                                                                                                                                                                                                                 QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGKERDVVATIQDGGSTNYA
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                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001EP-00200703
                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
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                                                                                                   peptide;
                                         fragment,
                                                                                                                                                     130
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                                                                                                                                                                                                                                                                                 73.7%;
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                                                                                                                                                                                                                                                                       Score 500.5; DB 4;
Pred. No. 2.3e-36;
8; Mismatches 21;
                                          HPL #11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haard JJW,
                                         from llama species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tareilus
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                           130;
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HPL;

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RESULT 9
AAE05288
ID AAEC
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AC AAEC
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AC AAEC
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AC AAEC
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AC AAEC
XX
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #11 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                      18-SEP-2001
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 129
                                                          AAE05288;
                                                                                              AAE05288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1134231-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 9; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GNIL )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                   96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNILEVER
UNILEVER
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                            standard;
                                                                                                                                                                                        AHHSEDP 127
                                                                                                                                                                                                                          EPKTPKP 127
                                                                                                                                                                                                                                                                DSVKGRFTISRDNAKNIMYLQMNSLKPEDTAVYYCNARRSNYDRSWGDYWGQGTQVTVSS
                                                                                                                                                                                                                                                                                                  DSAKGRFTISKUNAKNTVYLQMNSLKPEDTAVYYCNALITRWDKSVNDYWGQGTQVTVSS
                                                                                                                                                                                                                                                                                                                                     QVQLQDSGGGLVQAGGSLRLSCAASGSIFSSDLMGWYRQAPGKEREAVARITRGGTTSYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van De Burg M,
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA,
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                      (first
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/note= "Complementarity determining region
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                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                     73.6%;
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                                                                                              149
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 500; DB
Pred. No. 2.5e
11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 129;
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Anti-potato SBEII (Clone68)

VH region attached with myc

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                                                                                                                                                                                                                                                                                                                                                                                             CT The present invention relates to a method for modifying a plant to produce an antibody or an active fragment or derivative, or a protein CC functional equivalent, in a cellular compartment comprises introducing a CC DNA sequence encoding a heavy chain immunoglobulin, where the DNA is CC piptide capable of targeting heavy chain immunoglobulin to a cellular CC compartment. The method is used for producing a heavy chain to a cellular CC compartment. The method is used for producing a heavy chain to a cellular CC immunoglobulin or an active fragment or derivative, or a protein that is CC immunoglobulin or an active fragment or derivative, or a protein that is CC immunoglobulin or an active fragment or derivative, or a protein that is CC desirable to retain the antibody product with the plant rather than CC desirable to retain the antibody product with the plant rather than CC extracting and isolating the product. In particular, edible selected CC present may be used in a method of passively immunising an animal, correspond to the product of passively immunising an animal, against the antigen, e.g., pathogenic organisms. The CC present sequence is an anti-potato SBEII antibody (denoted Clone68) heavy C chain variable domain (VH) attached to peptide linkers, myc and his6 tag. The potato SBEII is a starch branching enzyme also designated SBE A
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                                      RESULT 10
                      ABG30620
                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying a plant to produce an antibody useful for increasing pathogen resistence or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potato; heavy chain immunoglobulin; pathogen resistance; metabolism modulator; passive immunisation; heavy chain VH; anti-potato SBEII; starch branching enzyme; SBE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Solanum tuberosum 
Unidentified.
     ABG30620 standard;
                                                                                                                                                                                                                                                                                                                                                                   Sequence 149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Frenken LGJ, Van Der Logt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-2000; 2000EP-00310997.
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                                                                                           115
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                                                                                                                                                                                                                                                                                                   97;
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                                                                                                                                                                                                                                                         QVQLQESGGGLVQAGGSIRLSCAASGTILSIIYMDWYRQTPGKQRELVGRITAGGSTNYA 60
                                                                                                                                                                                            DSAKGRFTISKDNAKNTVYLOMNSLKPEDTAVYYCNALITRWDKSVNDYWGQGTQVTVSS
                                                                                                                                                                                                                               QVQLQESGGGLVQAGGSLRLSCAASGSIFRRPHMGWFRQAFGQERELVALISAGGRTWYA
                                                                                           EPKTPKPQP
                                                                                                                       EPKTPKPQP 129
                                                                                                                                                             DSVKGRFTISRDNAKNTLYLOMNSLKPEDTAVYYCTA-
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 28; 81pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NV.
   protein; 131
                                                                                                                                                                                                                                                                                                                  73.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPE,
                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                                                                                                                                                  Score 496; DB 4;
Pred. No. 6.5e-36
                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jobling
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                                                                                                                                                                                                                                                                                                     15;
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                                                                                                                                                                                                                                                                                                                                  Length 149
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                               -GGSYWGQGTQVTVAS
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                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                120
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OVOLOESGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRITAGGSTNYA

Matches

Similarity

Conservative

6

Indels

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Gaps

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The invention describes a protein array (I) comprising a number of heavy-cc chain variable domain antibodies or antibody fragments, obtainable from CC camelidae. The method is useful for removing abundant proteins from an CC extract or sample which do not provide useful information on the CC condition of a cell or tissue in the extract or sample to be condition of a cell or tissue in the extract or sample to be condition in a sample, comparing the distribution of proteins in different CC cill types, and identification of proteins that may be of importance in CC determining the altered properties of cells in disease, aging or other conditions. Using a heavy-chain variable domain derived from an CC immunoglobulin that is naturally devoid of light chains (VHH) in (I) cprovides a number of advantages, such as an improvement of consistivity/resolution in the order of 10-100 times, and detection of consistivity/resolution in the order of 10-100 times, and detection of consistivity/resolution in the order of 10-100 times, and describes a method (II) that enables the simultaneous processing of large numbers of target antigens in a controlled way. The incorporated phage ELISA companing condition. This feature combined with the microtiter plate format allows the complete automation of the technology, based on computer-made decisions on the values of the phage-ELISA for continuation of a limited conditions can be tested, varying amounts of input-phages can be used conditions on the values of the phage-ELISA for continuation of a limited condition and immunoglobulin (IgC) heavy chain variable domain variable domain in frames naeded for the generation of large panels of antibodies in short time frames naeded for the generation of large panels of antibodies in short continuation of antibodies in short continuation of antibodies in short time frames naeded for the generation of large panels of antibodies in short continuation of antibodies in short continuation of antibodies in short continuation of antibodies in short contin
                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel protein array useful for detecting the presence of individual proteins in sample, comprises heavy-chain variable domain antibodies antibody fragments obtainable from Camelidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteomic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heavy chain variable domain; antibody; immunoglobulin; sticky phage-antibody;
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                                                                               Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 3; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-583487/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UNIL ) UNILEVER PLC.
(UNIL ) HINDUSTAN LEVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mmunoglobulin
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                                                                                                                            (HHV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G specifc heavy chain variable domain antibody #3
                  72.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Landa I,
Score 494; DB 5;
Pred. No. 8.5e-36;
6; Mismatches 25;
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micro-panning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aging; VHH; immune library;
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δ 문

61 4

DSAKGRFTISKDNAKNTVYLOMNSLKPEDTAVYYCNALITR--WDKSVNDYWGQGTQVTV 118 QVQLQESGGGLVQPGGSLRLSCAASKSIFGFGAVGWHRQAPGKQRELVARITYDSGTNYA

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RESULT 11
AAB10561
ID AAB10
XX AAB10561
AC AAB10
XX AAB10
AC AAB10
XX LIAM
KW Human
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KW Human
KW Human
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XX LAm
XX ET Reg
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                                        chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #4 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                             New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                     Example 4; Page 13; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bezemer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNIL )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-2001;
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note= "Complementarity determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= CDR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
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Query Match

72

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Score

493;

DB

4;

Length

The present peptide

sequence is HPL inhibiting VHH

fragment,

HPL

#14 from

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HFL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human brings.

Sequence

129

B

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RESULT 12
AAE10554
ID AAE10
XX AAE10
AX AAE10
XX ILlama
KW LLlama
KW Human
KW Food,
XX FFT Regic
FT Re
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97; Conserv
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ry enzyme inhibitor; medicament; human-pancreatic lipase; gastric lipase; HGL; cosmetic control; body weight.
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                 The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes.
                                                                                                                                                                        New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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                                                                                                             Example 4; Page 13; 37pp; English.
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Pred. No. 1.1e-35;
9; Mismatches 21
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RESULT 14
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        New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprisheavy chain variable domain derived from immunoglobulin naturally dof light chains.
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                                                                                                                                             14-MAR-2000; 2000EP-00200930
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Example 4; Page 13; 37pp; English.

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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HFL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #10 from llama (camelid) species
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 130
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99; Conservative
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6; Mismatches 19;
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EPKTPKPQP 129 EPKTPKPQP 129

121 121 61 61

AAE10567 standard; peptide; 130 AA

Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.

HGL inhibiting VHH fragment, HGL #16 from llama species

10-DEC-2001 (first entry)

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NSVKGRFTISRENAKNTVYLQMNSLKPEDTAVYYCKGRGGLTQYSEHDYWGQGTQVTVSS

Matches

97; Н

Conservative

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Score 489; DB 4; Pred. No. 2.3e-35; 5; Mismatches 26

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Gaps

Length 129; Indels

Best Local Query Match

Similarity

72.0%; 75.2%;

Sequence 129 AA;

Search completed: October Job time: 98.1435 secs

THE POWE BILLY (USE)

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	GenCore Copyright (c) 1993	ore version 5.1.6 993 - 2004 Compugen Ltd.	
OM protein - prote	ein search, using	y sw model	
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Title: US Perfect score: 68 Sequence: 1	3-09-805-290A-21 33 QVQLQESGGGLVQAGGS	LRLwgQgtlvTvss	врктркеде 130
Scoring table: BI Ga	BLOSUM62 Gapop 10.0 , Gapext	ct 0.5	
Searched: 28	83366 seqs, 96191	.526 residues	
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Minimum DB seg len Maximum DB seg len	19th: 0 19th: 2000000000		
Post-processing: W	Minimum Match 0% Maximum Match 100 Listing first 45	)% summaries	
Database : P 1: 2: 3: 4:	IR 78:*  pir1:*  pir2:*  pir3:*		
Pred. No. is score greate and is deriv	s the number of rer than or equal ved by analysis o	esults predicted by chance to the score of the result lof the total score distribut	to have a being printed, tion.
Result Que	ry ch Length DB	D D	ecripti
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371	138 2 138 2		heavy chain V
2 W C	3.9 121 2		heavy chain -
(A)	3.9 160 2	,	heavy chain
0 366.5 5 5	3.7 151 2 3.5 147 2		heavy chain
365	3.4 119 2		heavy chain
365 5	3.4 119 2		heavy chain
55 A	3.1 125 2		heavy chain V heavy chain V
362.5	3.1 116 2		heavy chain -
8 362.5 5	3.1 124 2 3.0 120 2		heavy chain V heavy chain V
362 362 55	3.0 122 2 3.0 127 2		
361.5	2.9 114 2		heavy chain V
3 361.5 5 3 361 5	2.9   140   2 $2.9   140   2$		heavy chain
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5 359	2.6 119 2		heavy chain
8 358.5 5	2.6 127 2 2.5 128 2		g heavy chain V r
פתנ	2.4 135 2		heavy chain

4. UJ	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
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#### ALIGNMENTS

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Ig heavy chain V r
                           Ig heavy chain V region - human (fragment)
()Species: Homo sapiens (man)
()Species: Homo sapiens (man)
()Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
()Accession: S31588
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the {
A;Reference number: S31585
A;Reference number: S31585
A;Accession: S31588
A;Status: preliminary
A;Molecule type: manA
A;Residues: 1-140 <CUI>
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S31107

Ig heavy chain - human

C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C.Accession: S31107
R.Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,
Eur. J. Immunol. 22, 247-251, 1992
Bur. J. Immunol. 22, 247-251, 1992
A.Fitle: Restricted utilization of germ-line V(H)3 genes and short diverse third compleme
A.Fitle: Restricted number: S31107
A.Accession: S31107
A.Accession: S31107
A.Accession: S31107
A.Accession: S31107
A.Accession: S31107
A.Accession: Taxary; nucleic acid sequence not shown; translation not shown
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A,Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-119 < RAA>
A;Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
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358

135 N

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C;Superfamily: 10
C;Keywords: hete:
F;15-98/Domain:
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C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31108
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31108
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C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                          submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human
A;Reference number: $48797
A;Accession: %40797
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A;Molecule type: mRNA
A;Residues: 1-120 <MAH>
A;Cross-references: EMB
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A; Residues: 1-119 < RAA>
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C;Species: Homo sapiens (man)
C;Sate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_
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Best Local S
Matches 80
                                                                      ;Accession: S48798
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                                                     Status: preliminary
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 EMBL: Z46382; NID: g562324; PIDN: CAA86521.1;
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Pred. No. 3.5e-26;
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Pred. No. 3.6e-26;
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   PID:g1340167
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Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
C;Accession: S31666
C;Accession: S31666
C;Accession: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonn
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S31666
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-121 (-MOR>
A;Cross-references: EMBL:X61015; NID:g32795; PIDN:CAA43349.1; PID:g1335126
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                    R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W. Eur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage A;Reference number: S26786; MUID:92111632; PMID:1730251
A;Accession: S26798
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Pred. No. 9.
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RiRaaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31114
A;Status: preliminary; nucleic acid sequence not shown; t A;Molecule type: mRNA
                                                                                   C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31114
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.I.
Eur. J. Immunol. 22, 247-251, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:120086; OMIM:147020
A;Map position: 14g32.33-14g32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology
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F;15-98/Domain: immunoglobu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .Molecule type: mRNA
,Residues: 1-121 <RES>
,Cross-references: GB:M87268; NID:g186197; PIDN:AAC37536.1; PID:g186198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;15-98/Domain: immunoglobulin homology <IMM>
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Exp. Med. 178, 1903-1911, 1993
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Pred. No. 1.5e-25;
9; Mismatches 31
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Pred. No. 1.5e-25;
1; Mismatches 29
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                                                                                                        Tol, M.J.D.; Vossen, J.M.;
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A;Residues: 1-123 <RAA>
A;Cross references: EMBL:X62963
A;Cross references: EMBL:X62963
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-144 <KIS2>
A;Cross-references: EMBL:X14584
A;Cross-references: EMBL:MI4584
C;Superfamily: immunoglobulin v region; immunoglobulin
C;Keywords: heterotetramer; imm
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Nucleic Acids Res. 17, 4385, 1989
A;Title: Nucleotide sequences of the cDNAs
A;Reference number: S04601; MUID:89296497;
A;Accession: S04602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain precursor - human (fragment)
(;Species: Homo sapiens (man)
(;C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996
(;Accession: $05271; $04602
R;Kishimoto, T.
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A; Residues: 1-160 <KIS1>
A; Cross-references: EMBL: X14584
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VIVSS
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                                                                                                                                    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAVVRGVISYYYYGMDVWGQGTT 139
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Pred. No. 2.1e-25;
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Ig heavy chain precursor V region (clone HN.14) - C;Species: Homo sapiens (man) C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993

31-Dec-1993 #text\_change 17-Mar-1999

RESULT A60943

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Ig variable region (VDJ) (clone T20-11) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence revision 16-Feb-1996 #text_change 23-0
C;Accession: I37780; S25474
R;Demaison, C; Chastagner, P.; Theze, J.; Zouali, M.
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali
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A;Residues: 1-36, 'M', 38-62, 'AR', 67-151 <DE2>
A;Rote: this sequence has been corrected in reference A60943
A;Note: this sequence has been corrected in munoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IVM>
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A;Residues: 1-151 (-DES)
A;Residues: 1, Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat
T.Neuroimmunol. 26, 35-41, 1990
J.Neuroimmunol. 26, 35-41, 1990
J.Title: Molecular cloning of a human immunoglobulin heavy chain variable (V-H)
A;Reference number: A48165, MUID:90094677; PMID:1688442
A;Accession: A48165
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R;Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A.; J. Neuroimmunol. 30, 245, 1990
A;Title: Molecular cloning of a human immunoglobulin heavy chain variable (V-H) region waterence number: A60943; MUID:91036050; PMID:1699976
A;Accession: A60943
A;Status: not compared with conceptual translation
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A; Residues: 1-147 < RES>
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Best Local Similarity

Matches 79; Conserv
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                                                                                                                                                                                     ADSVKGRFTISRDNILNTVYLQMNSLKÞEDTAVYHCNAÐVRÞYRTSRY--LELWGQGTLV
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Pred. No. 2.6e-25;
0; Mismatches 32
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Ig heavy chain V region (M43) - human
C;Species: Homo sapiens (man)
C;Ante: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
C;Antes: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
C;Ancession: D36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin he.
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: D36005
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: GB:M18513
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMNS
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C36005
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-119 < SCH>
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                                                                                                                                                                                                                                 Similarity
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- S
                                             ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTÄVYYC---AKKDWNDNWFDPWGQGTLVTV
                                                                             ADSVKGRFTISRDNILNTVYLQMNSLKPEDTAVYHCNADVRPYRTSRYLELMGQGTLVTV
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63.9%;
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8; Mismatches
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0; Mismatches
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Pred. No. 2.8e-25;
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B

118

SS 119

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Ig heavy chain V region - human
()Species: Homo sapiens (man)
()C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
()Accession: $26794
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Bur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family. Reference number: $26786; MUID:92111632; PMID:1730251
A;Accession: $26794
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, October 1992
A;Reference number: $30520
A;Accession: $30531
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-125 <MARA
A;Residues: 1-125 <MARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Mariette, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region - human
C.Species: Homo sapiens (man)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C.Accession: S30531
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A;Molecule type: mRNA
A;Residues: 1-123 <MOR>
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                                            116 LVTVSS 121
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                                                                                                                                                                                                                                            1 QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQDGGST-NY 59
                                                                                                                                                                                                                                                                                              79; Conservative
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LVTVSS 125
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Search completed: October 5, 2004, 08:17:14 Job time: 21.0648 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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683
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                    SwissProt_42:*
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                              HV3F HUMAN
HV3I HUMAN
HV3I HUMAN
HV3K HUMAN
HV3K HUMAN
HV3B MOUSE
HV40 MOUSE
HV53_MOUSE
HV55_MOUSE
HV24_MOUSE
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Compugen Ltd
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SEQUENCE 115 I
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Result No.

Score

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Minimum Maximum

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Scoring table: Sequence: Perfect score: Title: OM protein

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Database :

	P01795
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	P01787
	P01790
	P01804
	P01791
	P01809
	P01794
	P01796
	P01808
	P01792
	P01769

# ALIGNMENTS

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PIR; A02050; A2HUBU.

HSSP; P01799; 1MCP.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
IGLIKE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=78137069; PubMed=416441;
Torano A., Putnam F.W.;
Torano A., Putnam F.W.;
"Complete amino acid sequence of the alpha 2 heavy chain of a human IgA2 immunoglobulin of the A2m (2) allotype.";
Proc. Natl. Acad. Sci. U.S.A. 75.966-969(1978).
-!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HV3F HUMAN STANDARD; PRT; 115 AA.
P01767;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region BUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                          61 DSVKGRPTISRDNILNTVYLQMNSLKPEDTAVYHCNADVRPYRTSRYLELWGCGTLVTVS 120
                                                                                                                                      Similarity 61.2
74; Conservative
                                                                                                         EVQLVETGGGLIQPGGSLRLSCAASGFTVSBHSMSWVRQAPGKALZWVSAIYRGGTTYYA
DSVKGRFTISRDDSRBTVYLQMBSLRAEDTAVYYCARDLAAAR----
                                                                                                                                                                                                                                                                                                                        1 111 IG-LIKE.
115 115
115 AA; 12379 NW; 208876A7DF52DCF4 CRC64;
                                                                                                                                                                                                               52.1%; Score 356; DE 61.2%; Pred. No. 6.2e Live 15; Mismatches
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RESULT 3
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InterPro; IPKU.
InterPro; IPRU03596,
InterPro; IPRU03596,
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; PS50835; IG LIKE; 1
SMO406; IGV; 1.
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21-JUL-1986
21-JUL-1986
10-OCT-2003
             Ponsting1 H., Hilschmann N.;
"The rule of antibody structure. The primary structu monoclonal IgG1 immunoglobulin (myeloma protein Nie) chymotryptic peptides of the H-chain, alignment of t peptides and discussion of the complete structure.";
                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
1g heavy chain V-III region NIE.
Homo sapiens (Human)
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Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).

-:- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PATIENT WITH MACROGLOBULINEMIA.

-:- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR; A02051; M3HUAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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Mammalia; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lehman D.W., Putnam F.W.;
"Amino acid sequence of the variable location of a possible JH segment.";
                                                                                                                          MEDLINE=77070269; PubMed=826475
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                      NCBI_TaxID=9606;
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Eutheria;
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122 AA;
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01, Last sequence update)
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Primates;
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RESULT 4
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21-JUL-1986 (Rel. 01, Last sequence up
10-OCT-2003 (Rel. 42, Last amoutation
Ig heavy chain V-III region KOL.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HV3K_HUMAN
P01772;
                                                                                                                                                                     SEQUENCE, AND DISULFIDE BONDS.

MEDLINE=83289131; PubMed=6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;

"Three-dimensional structure determination of antibodies.

structure of crystallized monoclonal immunoglobulin IgG1

thoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A91668; GHUNI.

HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003823; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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Mammalia; Eutheria;
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MEDLINE-81072295; PubMed=7441755;
Marquart M., Deisenhofer J., Huber R., Palm W.;
"Crystallographic refinement and atomic models of thimmunoglobulin molecule Kol and its antigen-binding and 1.0-A resolution.";
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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SMART; SM00406; IGv;
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119
                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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PYRROLIDONE CARBOXYLIC ACID
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RESULT 5
HV05 CARAU STANDARD; PRT; 116 AA.

ID HV05 CARAU STANDARD; PRT; 116 AA.

AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-UUL-1999 (Rel. 38, Last annotation update)
DE 19 heavy chain V region 5A precursor.

OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyr
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Matches 75
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-!- SIMILARITY: Contains 1 immunog
PIR; A02055; GHUWL.
PDB; 2FB4; 12-JUL-89.
PDB; 2IG2; 12-JUL-89.
GO; GO:0005576; C:extracellular; N
GO; GO:0003823; F:antigen binding;
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Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; P850835; IG_LIKE; 1.

PROSITE; P850835; IG_LIKE; 1.

Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic Immunoglobulin V region; 3D-structure; Pyrrolidone Carboxylic ACID.
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PDB; 2IG2; 12-UII-89.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                              QVQLVESGGGVVQPGRSLRLSCSSSGFIFSSYAMYWVRQAPGKGLEWVAIIWDDGSDQHY
                                                                                                                                                                                                                                                                                                  ELWGOGTLVTVSS 121
                                                                                                                                                                                                                                                                                                                                       ADSVKGRFTISRDNSKNTLFLQMDSLRPEDTGVYFCARDGGHGFCSSASCFGP-----
                                                                                                                                                                                                                                                                                                                                                           ADSVKGRFTISRDNILNTVYLQMNSLKPEDTAVYHCNAD-----VRPYRTSRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                               OVOLOESGGGLVOAGGSLRLSCAASGSIGSIHTMGWYROTPGTERDVVATIODGGS-TNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126
126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13718 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 328.5; DB Pred. No. 4e-26; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E4D71B52B16F8776 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                             108
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9
       DE COCCETTE DE COC
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RESULT 6
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Best Local S
Matches 66
-!- SIMILARLLI.

PIR; A02058; M3HTLY.

HSSP; P01772; 2FB4.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 1.

SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                  GLOBULIN ACTIVITY.
-!- SIMILARITY: Contains 1 immunoglobulin-like PIR; A02058; M3HULY
                                                                                                                                                                                                                                 anti-gamma globulins.";
Proc. Natl. Acad. Sci. U.S.A. 71:4
-!- MISCELLANEOUS: THIS CHAIN WAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
To heavy chain V-III region LAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV3N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region; S:
                                                                                                                                                                                                                                                                                      MEDIINE-75046755; PubMed-4139708;
Capra J.D., Kehoe J.N.;
Capra J.D., Kehoe J.N.;
of the heavy chain variable regions of two immunoglobulin M
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, I
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad.
HSSP; P01772; 2FB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson M.R., Middleton D., Warr G.W.; "Immunoglobulin heavy chain variable region gene evolution: structure and family relationships of two genes and a pseudogene in a teleost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P01775;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fish."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQPPGKGLEWVSVIYSGGSTYYA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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68
84
116
114
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); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 327; DB 1;
Pred. No. 5.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2
FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK-1
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                                                                                                                                                                                                                                     71:4032-4036(1974)
WAS ISOLATED FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
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                                                                                                                                                                                                                                         IGM WITH
                                                                                                                                                                                                                                                                                                                                                                                                                        Buteleostomi;
; Homo.
                                                                                                                                                                                                                                         ANTI-GAMMA
                                                                                                                                                                                                                                                                                                             sequence
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RESULT 7
HV3B_HUMA
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 71
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Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin V
DOMAIN 1
NON TER 119
SEQUENCE 119 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986
21-JUL-1986
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic DOMAIN
1 112 IG-LIKE
MOD RES .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goni F., Frangione B.,

"Amino acid sequence of the Fv region of a human monoclonal IgM
"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";

Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

-I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P01772; 2FB4.
GG; GG:0005576; C:extracellular; NAS.
GG; GG:0003823; F:antigen binding; NAS.
GG; GG:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=83273707; PubMed=6410398; Goni F., Frangione B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A02046; M3HUWE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WALDENSTROM'S MACROGLOBULINEMIA.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heavy chain V-III region WEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                              120
                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                              SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSVNGRFTISRNDSKNTLYLOMNGLQAZVSAIYYCARDAGPYVSPTFFAHWGQGTLVT 119
               SS 114
                                                                                                            ADSVKGRFTI
                                                                                                                                                        ADSVKGRFTISRDNILNTVYLOMNSLKPEDTAVYHCNADVRPYRTSRYLELWGQGTLVTV
                                                                                                                                                                                                                                                        OVOLOSSGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQDGGST-NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQLLESGGGLVQPGGSLRLSCAASGFTFSASAMSWVRQAPGKGLEWVAWKYENGNDKHYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      114 AA;
                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    114
.; 12256 MW;
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                                                                                                            SRNBSKNSLYLOMSSLRAEDTAVYYC--
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                                                                                                                                                                                                                                                                                                                           47.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.8%;
56.8%;
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                                                                                                                                                                                                                                                                                                    ; Score 325.5; DB 1; Pred. No. 7.1e-26; 15; Mismatches 27
                                                                                                                                                                                                            LSCSASGFTFSANDMNWVRQAPGKGLEWLSFIGGSGSTIYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 326.5;
Pred. No. 5.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                      D88294FB418A07B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D6338098794DCF5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114
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HV3M_HUMAN
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Best Local S
Matches 67
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
Immunoglobulin v region.
DCMAIN
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P01782;
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"Structure of antibodies with shared idiotypy: the complete of the heavy chain variable regions of two immunoglobulin M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region POM.
Homo sapiens (Human)
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P01774;
MEDLINE=80020921; PubMed=114209;
Steiner L.A., Garcia Pardo A., Margolies
"Amino acid sequence of the heavy-chain v
                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region DOB.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-gamma globulins.";
proc. Natl. Acad. Sci. U.S.A.
proc. NISCELANEOUS: THIS CHAIN
GLOBULIN ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=75046755; PubMed=4139708; Capra J.D., Kehoe J.M.;
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HSSP; P01772; 2FB4.
                                                                           SEQUENCE
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GO:0003823; F:antigen binding; NJ
GO:0006955; P:immune response; NJ
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                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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N -> D (PROBABLY DUE TO DEAMIDATION DURING ISOLATION).

/FTId=VAR_003966.
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Pred. No. 9.4
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WAS ISOLATED FROM
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Best Local :
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HSSP; P01772; ZFB4.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0000525; F:antigen binding; NAS.
G0; G0:0000525; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003506; Ig_v.
InterPro; IPR007110; Ig-like.
InterPro; IPR003796; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS30835; IG_LIKE; 1.
                                                                                                                                                                                    Biochemistry 16:3160-3168(1977).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region GOM.
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HV01 CAN
P01784;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
                                                                                                                                 PIR; A02067; AVDGGM.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                     MEDLINE=77242268; PubMed=407924;
Wasserman R.L., Capra J.D.;
"Primary structure of the variable regions of immunoglobulin heavy chains.";
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-!- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN
-!- HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia_Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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120 AA;
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13440 MW; 880DDE307C4B2627 CRC64;
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Pred. No. 2.4e-25;
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Best Local S
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Query Match
Best Local Similarity
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EMBL; M35415; AAAS8735.1; -
EMBL; M35415; AAAS8735.1; -
PIR; A02047; H3HUZ6.
PDB; 1HOU; 23-DEC-99.
Genew; HGNC:5545; IGHV@.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:5545; 1GHV@.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003823; F:immune response; NAS.
Interpro; IPR007110; Ig-like.
Interpro; IPR0073596; Ig_v.
                                                                                                                      NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin V region.
DOMAIN 1 112
NON TER, 114 114
SEQUENCE 114 AA; 1243
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"Structure and multiplicity of genes for the human immediate of the human immediate
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                        ofam; PF00047; ig; 1.

MART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

Immunoglobulin V region; Signal; 3D-structure.
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117 AA;
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114 AA; 12430 MW;
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                                                                                                                      12582 MW;
    46.6%;
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57.4%; Pred. No. 3.6
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                                                                                                                                                                                                  IG HEAVY
IG-LIKE.
    Score 318.5; DB 1;
Pred. No. 3.7e-25;
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                                                                                                                      E826733F1A3CB0F1 CRC64;
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RESULT 13
HV3T_HUMAN
ID H43T_HUMAN
AC P01781;
DT 21-JUL-1986
DT 21-JUL-1986
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HV3D_HUMAN
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G0; G0:0005576; C:extracellular; NAS.
G0; G0:0003823; F:antigen binding; NAS.
G0; G0:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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21-JUL-1986
21-JUL-1986
10-OCT-2003
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Wang A.-C., Wang I.Y., Fudenberg H.H.;
Wang A.-C., Wang I.Y., Fudenberg H.H.;
Wang A.-C., Wang I.Y., Fudenberg H.H.;
Proposed For the Structure and genetics. Identity be regions of a mu and a gamma2 chain.";
J. Biol. Chem. 252:7192-7199(1977).
J. Biol. Chem. 252:7192-7199(1977).
J. MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF IGN AND IGGZ ISOLATED FROM A SINGLE PATIENT CAMMODATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE AMMODATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE AMMODATHY ARE IDENTICAL.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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NON_TER
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region TIL.
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115 AA;
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115
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            sequence update)
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HSSP; P01772; ZFB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
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SMART; SS50835; IG LL...,
PROSITE; PS50835; IG LL...,
Immunoglobulin V region.
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MEDILINE-75059123; PubMed-4803843;

Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;

Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;

"The primary structure of a monoclonal IgM-immunoglobulin

"The primary structure of a monoclonal igM-immunoglobulin

(macroglobulin Gal.), II: the amino acid sequence of the H-chain

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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V region MOPC 21 precursor (Fragment).
1g heavy chain V region MOPC 21 precursor (Fragment).
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P01783;
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Submitted (JUN-1975) to
-!- MISCELLANEOUS: THIS
                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth
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Mammalia; Eutheria;
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"Heavy chain variable region antibodies: somatic mutation Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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116 AA;
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Rodentia;
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12; Mismatches
                                     contribution evident in a
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                   Imanishi-Kari T.,
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                                     gamma 2a
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21-JUL-1986
21-JUL-1986
10-OCT-2003
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                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region TRO.
Homo sapiens (Human)
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                                                                   SEQUENCE (MYELOMA PROTEIN TRO).
MEDLINE=76023781; PubMed=809331;
Kratzin H., Altevogt P., Ruban E., Kortt A., Staroscik K.
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                              "The
                                                   Kratzin H., A
Hilschmann N.
                                                                                                                                                                                                                                                                                                                                                                                             HV3A_HUMAN
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; 13; 1.
SMART; SM00406; IGv; 1.
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PDB; 11GC; 03-JUN-95.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE OF 17-136.
                                                                                                                                                                       NCBI_TaxID=9606;
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primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), The amino acid sequence of the H-chain, alpha-type, subgroup III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 VTVSS 121
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72; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIVSS 136
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bbulin V region; Signal; 3D-structure.
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136 AA;
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DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 315.5; DB 1;
Pred. No. 8.9e-25;
1; Mismatches 31;
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D SEGMENT.
JH4 SEGMENT.
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Best Local S
Matches 68
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SEQUENCE
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HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0008825; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN 1 108 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                           Structure of the complete IgA-molecule.";
Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
-i- MISCELANBOUS: THE SEQUENCE OF THE C. REGION IS ALSO GIVEN.
-i- SIMILARITY; Contains 1 immunoglobulin-like domain.
121
                          120
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                                                                                                                                                                      Similarity
                          SS 121
                                                                          ADSVKGRFTISRDNILNTVYLQMNSLKPEDTAVYHCNADVRPYRTSRYLBLWGQGTLVTV 119
SS 122
                                                  ADSVKGRFTISRDNAQKSLYLZMBSLRTZBTAVYYCAATBBFBWSTFSLBYWGZGBLVTV 120
                                                                                                      QVQLVQSGGGLVKPGGSLRLSCVASGFSFRDFYMSWIRZTPGKGLZWVSYIGGSGSTLYY
                                                                                                                              QVQLQESGGCLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQDGGST-NY
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122 AA;
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                                                                                                                                                                                                            122
13472 MW;
                                                                                                                                                                     46.0%;
                                                                                                                                                        17;
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Pred. No. 9.8e
17; Mismatches
                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                             2E21A11DA04D80F9
                                                                                                                                                                        .8e-25;
                                                                                                                                                                                 DB 1;
                                                                                                                                                          36;
                                                                                                                                                                                                             CRC64;
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Search completed: October 5, 2004, 08:01:55 Job time: 12.6358 secs The Pago Benk (Uspic)

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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                                 Score
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Match
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_hunan:*

5: sp_invertebrate:*

6: sp_mammal:*
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Gapop 10.0 , Gapext 0.5
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683
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   sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_virus:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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099TA4
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Q9ul72 homo
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Q9ha4 mus
Q9hn5k4 homo
Q9hn5k4 homo
Q9ul71 homo
Q9ul71 homo
Q9ul77 mus
Q912e1 mus
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5	44	43	42	41	40	39	38	37	36	ω G	34	ω ω	32	31	30		28		26				22				18	17
247	247.5	248	250	250.5	252	252.5	254.5	261	261.5	262	265.5	276.5	279.5	298.5	298.5	300.5	303.5	308.5	313.5	318.5	320.5	321.5	322	324.5	334	335	335.5	(L)
36.2	36.2	ω 6. ω	36.6	36.7	36.9	37.0	37.3	38.2	38.3	38.4	38.9	40.5	40.9	43.7	43.7	44.0		45.2	٠	•	٠	47.1	7.	.7	8	9	49.1	9
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Q9UL73	092400	099M22	096080	Q925S3	Q9UGP3	Q8VDC9	Q8VCX7	Q7TMT6	Q91X92	Q9UL87	Q9UL92	Q7TMK4	Q7Z351	Q8VEA0	Q9N0W4	Q9NOW6	Q725W1	Q9QYF0	Q9ULB6	Q9R1A4	Q8N4Y9	Q8R3V9	Q80ZI7	Q91Z05	Q96K68	Q9UL93	Q9UL84	ОЭНССІ
Q9u173	092400	099m22	O96gs	Q925s3	Q9ugp:	Q8vdc9	Q8vcx7	Q7tmt6	Q91x92	Q9u187	Q9u192	Q7tm)	Q7z35:	Q8ve2	. Q9n0w4	Q9n0w6	Q7z5w1	:Vbeð	Q9ulb6	Q9r1a4 r	Q8n4y!	Q8r3v9	Q80zi7	021z(	. Q96k68	Q9u19:	Q9u184	Q9hcc1
Omo	Bug	BILE.	Omo	mus	3 homo sapien	c9 mus musculu	mus	mus	Bru		homo	Q7tmk4 mus musculu		o mus	4 oryctolagus	oryc	powo	mus	omo	Bun	9 homo sapien	Snu	Bru	5 mus	homo	homo	homo s	homo

# ALIGNMENTS

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80 ADSVKGRETISRDNSRDTLYLOMNSLRAEDTAVYYCAKDPRGYSASGNYTREDYWGQGTL 139	60 ADSVKGRFTISRDNILNTVYLQMNSLKÞEDTAVYHCNADVRPYRTS-RYLELWGQGTL 116	20 EVQLIESGGGIVQPGGSLRLSCAASGFSFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYY 79	1 QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTWGWYRQTPGTERDVVATIQ-DGGSTNY 59	Query Match 54.8%; Score 374; DB 4; Length 597; Best Local Similarity 65.6%; Pred. No. 4.2e-29; Matches 82; Conservative 9; Mismatches 30; Indels 4; Gaps 3;	AYPOCHETICAI PIOCETI. SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;	)290; IG	PROSITE; PS50835; IG_LIKE; 5.	PF00047; 1g; 5	Pro; IPR003596;	IPR003006;	InterPro; IPR007110; Ig-like.	15760; AAH15760.1;	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.	Straishord	-cell	SEQUENCE FROM N.A.	NCEL TAXID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	Hypothetical protein.	(TrEMBLrel. 25, Last annotatio	(TrEMBLrel. 19,	01-DEC-2001 (TrEMBLrel. 19, Created)	6889;	Q96BB9 PRELIMINARY; PRT; 597 AA.	RESULT 1

117

VIVSS

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RESULT 3
Q99KA
ID Q99K
AC Q99K
AC Q99K
DT 01-J
DT 01-J
DT 01-G
DE Hypo
OC Mus
OC Mus
OC Mamm
OX NCB1
RN [1]
RP SEQU
RA Stra
RL Subn
DR EMBI
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ID Q9UI
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Best Local S
Matches 78
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
NOW_TER 118 118
                                                                                                Q99KA4;
01-JUN-2001 (TrEMBLrel. 17, C
01-JUN-2001 (TrEMBLrel. 17, I
01-CCT-2003 (TrEMBLrel. 25, I
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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01-MAY-2000
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MEDLINE=98277119; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L.,
Young D.C.;
        Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC004786; AAH04786.1; -.
                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035042; AAD56278.1; ..
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Mammalia; Eutheria; Primates;
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                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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HSSP; P01772; 2FB4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                118 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                            PRELIMINARY;
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                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                12872 MW;
                                                                                                                                                                                                                                                                                                                                                                                             53.5%;
                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                            Created)
Last sequence update)
Last annotation update)
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Pred. No. 3.8e
10; Mismatches
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Catarrhini; Hominidae; Homo
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                                                                              Craniata; Vertebrata; Buteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                   B4D1A5944B2D5CCA CRC64;
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SMART; SM00409; IG; 4.
SMART; SM00407; IGC1; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS900290; IG_MHC; 1.
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SEQUENCE 48
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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01-OCT-2002
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 499 AA; 53376 MW;
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InterPro; IPR003110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_wHC.
InterPro; IPR003596; Ig_wHC.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
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TLVTVSS-EPKTPKPQP 130
                                                                                                                                EVOLVESGGGVVRPGGSLRLSCATSGFTFDDSGASWVRQAPGKGLEWVSSINWNGGSTNY
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                                             ADSVKGRFTISRDNAKNSLYLOMNSLRVEDTALYYCARDPTKYCSGGSCLGYYMDVWGKG
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487 AA;
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Last annotation update)
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Pred. No. 5.9
                                                                                                                                                                                                                          Score 359.5; DB 4;
Pred. No. 9.7e-28;
8; Mismatches 35;
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Best Local S
Matches 78
                                                                                                    01-MAR-2002 (TrEMBLrel. 20, C
01-MAR-2002 (TrEMBLrel. 25, L
01-OCT-2003 (TrEMBLrel. 25, L
Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primatee;
                                                                                                                                                                   Q8WUK1;
Q8WUK1;
01-MAR-2002
EMBL; BC020240; AAH20240.1; -. PIG: PL0120; PL0120. PL0120. PIR; S15590; S15590.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
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MEDLINE=98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L.,
                                                            TISSUE=Tonsil;
                                                                                          NCBI_TaxID=9606;
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                                                                       SEQUENCE FROM N.A.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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113 AA,
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                                                                                                    Chordata;
Primates;
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Pred. No. 2e-28;
9; Mismatches
                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local S
Matches 75
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Best Local S
Matches 77
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
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Q9UL71;
01-MAY-2000
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NON TER
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EMBL; AF035043; AAD56279.1; -.
HSSP; P01772; 2FB4.
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SMART; SM00406; IGV; 1.
SPROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                            SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                  etus.";
                                                                                                                                                                                                                                                                                                                                               Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iomo sapiens (Human).
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TVSS
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                                      ADSVKGRFTISRDNSKNSLYLOMNSLRAEDTALYYC---AKGKVTTIYDRFDIWGQGTMV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADSVKGRFTISRDNILNTVYLOMNSLKPEDTAVYHCNAD----VRPYRTSRYLELWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQ-DGGSTNY
                                                             ADSVKGRFTISRDNILNTVYLOMNSLKPEDTAVYHCNADVRPYRTSRY--LELWGQGTLV 117
                                                                                       EVŐLVESGGGVVÓPGGSLRÍFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGGSTYY
                                                                                                               QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQ-DGGSTNY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKDWSEGVETF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                                                          121
121 AA;
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                             121
13154 MW; 2F045CCFA5D50736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67296 MW;
                                                                                                                                        50.7%; Score 346; DB 4; 60.5%; Pred. No. 3.6e-27; Live 15; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 348.5; DB 4;
Pred. No. 1.6e-26;
1; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60C7F5950671E315
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                                                                                                                                         28;
                                                                                                                                                                Length 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region
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RESULT 9
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Best Local S
Matches 71
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC010324; AAH10324.1; -.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003506; Ig_v.

Pfam; PP00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS00290; IG_MHC; 2.
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                   Strausberg R.;
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010798; AAH10798.1; -.
InterPro; IPR0077110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003906; Ig_V.
Pfam; PF00047; ig; 4.
PMART; SM00406; IGV; 1.
PROSSITE; PS00290; IG_MHC; 2.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 25, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 486 AA; 5
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91Z07
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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Eutheria; Rodentia;
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19,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 346; DB
Pred. No. 2.2e
L6; Mismatches
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2.2e-26;
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RESULT 11
Q9UL88
ID Q9UL8
AC Q9UL8
DT 01-MADT 01-MADT
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Q9UL88;
Q9UL88;
01-MAY-2000
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01-DBC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pterin-mimicking anti-idiotope heavy chain variable
                                                                                                                                                                                                                                                                                     NON TER
                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGV;
PROSITE; PS50835; IG
                                                                                                                                                                                                                                                                                                                                                                                                     Atkin J.D., Iape A., Jenning "Definition of the Idiotope in Mammalian Cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2000) to the EMEL; AF307937; AAL09421.1; -.
                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                    PIR; C25913; C25913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).
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75; Conserv
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                                                                                                                                                                                                                              l Similarity
76; Conserv
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                                                                                                               VTVSS 121
                                                                                                                                                          ADSVKGRFTISRDNILNTVYLOMNSLKPEDTAVYHCNADVRPYRTSRY---LELWGQGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSMKGRFTISRDNAQNTVLLQMTSLNSEDTAVYYCTRG--
                                                                                                                                     PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYC-----ARHGDYDVGFAYWGQGTL
                                                                                                                                                                                  EVOLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVROTPDKRLEWVATISSGGSYTYY
                                                                                          VTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480
                                                                                                                                                                                                                                                                           119
119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
(TrEMBLrel. 13, (TrEMBLrel. 13,
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                           119
13025 MW; F6E904044381CA7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
51936 MW;
                                                                                                                                                                                                                                                                                                            ; 1.
3_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                          Ig-like.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                          49.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.1%; Score 342; DB 11; 61.0%; Pred. No. 5.4e-26; tive 10; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                 Jennings I.G., Horaitis O., Cotton R.G.H.;
Hiotope of Pterin-Mimicking Antibodies Expr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                               10;
 Last sequence update)
            Created)
                                                                                                                                                                                                                               Score 340; DB 11;
Pred. No. 1.4e-26;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20B9234EEF2B41ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
                                    131
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                                                                                                                                                                                                                                                     Length 119;
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RESULT 12
Q9Y509
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
EMBL; S80860; AAD14339.1; ...
HSSP; P01772; 2F94.
GO; GO:0005887; C:integral to plasma membrane; NAS.
GO; GO:0005887; C:integral to plasma membrane; NAS.
GO; GO:0016489; F:immunoglobulin receptor activity;
GO; GO:0016066; F:cellular defense response (sensu \
InterPro; IPR007110; Ig-like.
InterPro; IPR0073596; Ig-v.
                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=96071149; PubMed=7475288;

MEDLINE=96071149; PubMed=7475288;

Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Le
Lichtenstein A.K., Berenson J.R.;

"A CDI0-positive subset of malignant cells is identifie
"A CDI0-positive subset of malignant cells is identifie
myeloma using FCR with patient-specific immunoglobulin
myeloma using FCR with patient-specific immunoglobulin
toukemia 9:1948-1953 (1995).
                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
Yin B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035026; AAD56262.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9Y509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S21205; S21205.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Last annotation update) M_{\underline{Y}}osin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
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InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Myosin-reactive autoantibodies in rheumatic carditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 49.6%;
Similarity 57.9%;
77; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NYADSVKGRFTISRDNILNTVYLQYNSLKPEDTAVYHCNADV------RPYRTSRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVQLVESGGGLVKPGGSLRLSCAASGFTFSKAWMSWVRQAPGKGLEWVGRIKSKTDGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQ---DGGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYAAPVKGRLTISRDSSKNTLYLRMNSLKTEDTAVYYCTTGITMIIVVITTSSKRTS--F
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PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYWGQGTLVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131
131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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Pred. No. 2e-26;
1; Mismatches
                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; l
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96E7D668E375DEA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147
                                                                                                                                                                                                                             C.H., Kim A., Lee J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
                                                                                                                                                                     is identified in munoglobulin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31;
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                                                           Vertebrata);
                                                                             NAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region
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                                                                                                                                                                     multiple primers.";
                                                           NAS
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 RESULT 14
Q8WU38
ID Q8WU3
AC Q8WU3
AC Q8WU3
DT 01-MA
DT 01-MA
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Best Local S
Matches 71
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Best Local :
 Q8WU38;
Q8WU38;
01-MAR-2002
01-MAR-2002
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 (TrEMBLrel.
                                                         PRELIMINARY;
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EMBL; BC013656; AAH13656.1; -.
InterPro; IPR007710; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 4.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001
01-DEC-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00406; IGV;
PROSITE; PS50835; IG |
NON TER 1
SEQUENCE 147 AA; 19
                                                                                                                                                                                                                                                          Hypothetical protein SEQUENCE 479 AA;
                                                                                                                                                                                                                                                                                      SMART; SM00406; IGV; 1.
pROSITE; PS50835; IG LIKE; 4.
pROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
SSEP
                               SSEP
                                                              SDIMKGRETISRDNAKSILYLOMSSLRSEDTAFYYC
                                                                                        ADSVKGRFTISRDNILNTVYLQMNSLKPEDTAVYHCNADVRPYRTSRYLELWGQGTLVTV 119
                                                                                                                          EVOLVESGGGLVKPGGSLKVSCAASGLTFSNYAMSWVRQSPEKRLEWVAAINSNGGNTYY
                                                                                                                                                         QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATI-QDGGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVTVSSASTKGPSVFP 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYYCAKDGNYFDSVGYYYAGIDYWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADSVKGRFTISRDNILNTVYLQMNSLKPEDTAVYHCNADVRPYRTSRY----LELWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVHLVESGGGVVQPGKSLRLSCEASGFTFSTYGMSWVRQAPGKGLDWVALISYDGSTQYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQDGGSTN-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 19, (TrEMBLrel. 19, 3)
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                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                             123
136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                          51603 MW;
                                                                                                                                                                                                          49.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130
                                                                                                                                                                                          19;
                                                                                                                                                                                          Score 337; DB
Pred. No. 1.7e
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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Pred. No. 2.4e-26;
9; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                          ECB2D0877748584F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8489FCAAA7BC925C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       479
                                                                                                                                                                                                          DB 11;
..7e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                              Ş.
                                                                                                                                                                                                                                                                                                                                                                                                                          databases
                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 147
                                                                                                                                                                                                                         Length
                                                              -GGYFDVWGAGTAVTV
                                                                                                                                                                                          8
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                                                                                                                                                                                          Gaps
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20,

Created) Last sequ

573

sequence update

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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RESULT 15
Q9UL91
ID Q9UL9
AC Q9UL9
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Best Local Similarity
Matches 76; Conserv
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Homo sapiens (Human).
Eukaryota; Metazoa; C
               NON_TER
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC021276, AAH21276.1; -.
PIR; S21205; S21205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                             Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035023; AAD56259.1; -
PIR; S21205; S21205.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                     Q9UL91;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein. SEQUENCE 573 AA; 62967 MW;
                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                  Wu X., Liu
Young D.C.;
                                                                                                                                                                                                            MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                    NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                   "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                           Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTVTVSSAPTKAPDVFP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADSVKGRFTISRDNAKONSLYLQMNSLRAEDTALLYYC----AKHGSGSYIGYYYGMDVWGQ 135
 118
118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.3%; Score 337; DB 4; llarity 55.1%; Pred. No. 2.2e-25; Conservative 15; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
   12843 MW;
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    D0633949F2AC149D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                 118 AA
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 116 VS 117
                     119 VS 120
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                                                           60 ADSVKGRFTISRDNILNTVYLQMNSLKPEDTAVYHC-NADVRPYRTSRYLELWGQGTLVT
                                                                                                            1 QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATTQDGGST-NY
                                                                                                                                    74; Conservative
                                                                                                                                                  Similarity
                                                                                        ADSVKGRETISRDNAKNSLYLQVINSLRAEDTAVYYCARGD----SSEAFDIWGQGTMVT 115
                                                                                                                                     49.3%; Score 336.5; DB 4
60.7%; Pred. No. 3.2e-26;
tive 13; Mismatches 28
                                                                                                                                                              DB 4;
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                                                                                                                                                           Length 118;
                                                                                                                                       Indels
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Search completed: October Job time : 69.8117 secs <u>ر</u> 2004, 08:13:46

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Gapop 10.0 , Gapext 0.5
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683
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devo of light chains.

immunoglobulin naturally devoid

WPI; 2001-572718/65.

Example 2; Page 9; 37pp; English

<b>4</b> 5	44	43	42	41	40	39	38	37	36	S S	34	ω ω	32	31	9	29	28	27	6
410.5	414	414.5	416	419.5	420.5	422.5	423	423	424.5	426.5	432.5	433	434	436.5	440	440	441	441.5	441.5
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183	130	193	125	124	133	127	194	124	205	225	153	119	134	211	198	190	190	204	μ
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AAY41166	AAE10560	ABR62884	AAY39817	AAY28615	ABG30972	ABG30617	ABR62885	AAE10562	AAY41173	AAY41165	AAE05282	AAB67779	ABG30618	AAY41172	ABR62878	ABR62880	ABR62879	AAY41167	AAISYELY
Aay41166	Aae10560	Abr62884	Aay39817	Aay28615	Abg30972	Abg30617	Abr62885	Aae10562	Aay41173	Aay41165	Aae05282	Aab67779	Abg30618	Aay41172	Abr62878	Abr62880	Abr62879	Aay41167	Ааузувту
Llama Vhh	HGL ir	Llama ant				Mouse cro	Llama ant	HGL inhib	Llama Vhh	Llama vhh	Anti-pota	Amino aci	Immunoglo	Llama Vhh	Llama ant	Llama ant	Llama ant	Llama Vhh	Prama and

## ALIGNMENTS

### Key Region Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight. 14-MAR-2000; 2000EP-00200930. Region Region AAE10554; AAE10554 standard; peptide; 130 AA. Bezemer S, 20-FEB-2001; 2001EP-00200703. 19-SEP-2001. EP1134231-A1 Lama sp. HPL inhibiting VHH fragment, HPL #14 from llama species. 10-DEC-2001 (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC. Van De Burg (first entry) /label= CDR2 /note= "Complementarity determining region 98. .110 Location/Qualifiers /label= CDR3 /note= "Complementarity determining region note= "Complementarity determining region /label= CDR1 3 De Haard JJW, Tareilus 2

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 130 AA;
           New antibody or
                                      WPI; 2001-572718/65
                                                                    Bezemer S,
                                                                                                                                            14-MAR-2000; 2000EP-00200930
                                                                                                                                                                                                         19-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              tood;
                                                                                                  (UNIL ) UNILEVER NV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody; camelid; anorectic; heavy chain variable domain; VHH; dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; human gastric lipase; HGL; cosmetic control; body weight.
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           its fragments for inhibiting
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/note= "Complementarity
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/note= "Complementarity
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                                                                    Burg
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Pred. No. 4.8e-54;
Wismatches 0;
                                                                       Haard
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                                                                       JJW,
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           human dietary enzymes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Llama antibody; camelid; human dietary enzyme inhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPL inhibiting VHH fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present peptide sequence is HPL inhibiting VHH fragment, HPL llama (camelid) species
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Pred. No. 7.1e-52;
2; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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                                                                                                                                                                                                                                                                                      Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control: hody weight
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             20-FEB-2001; 2001EP-00200703
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                                                                                                                                                                                                                                                                                       ry enzyme inhibitor; medicament; human pancreatic lipase; HPL; gastric lipase; HGL; cosmetic control; body weight.
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note= "Complementarity determining
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Pred. No. 4.4e-48;
4; Mismatches 9
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Pred. No. 2.4e-39;
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                                                                                             location/Qualifiers
                                                                                                                                                                                                             fragment, HPL #19 from llama species.
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    "Complementarity
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #19 from llama (camelid) species
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                                                                                                                                 Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control; body weight.
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                                                                                  Lama sp
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/note= "Complementarity determining region
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Pred. No. 1.7e-37;
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RESULT 8
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Best Local (
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Potato; heavy chain immunoglobulin; pathogen resistance metabolism modulator; passive immunisation; heavy chain VH; anti-potato SBEII; starch branching enzyme; SBE A.
                                                                                                                                                                                                                                                                           AAE05283 standard; protein; 152
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                                                                                                            (Clone46) VH region attached with myc and his6
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Pred. No. 7.9e-37;
9; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                          á
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a method for modifying a plant to produce an antibody or an active fragment or derivative, or a protein functional equivalent, in a cellular compartment comprises introducing a CC DNA sequence encoding a heavy chain immunoglobulin, where the DNA is compartment. The method is used for producing a heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain that is functionally equivalent for increasing the pathogen resistance in a plant or to modulate metabolism in a plant. Under some circumstances it may be desirable to retain the antibody product with the plant rather than cextracting and isolating the product. In particular, edible selected antigens may be used in a method of passively immunising an animal, preferably human, against the antigen, e.g., pathogenic organisms. The preferably human, against the antigen, e.g., pathogenic organisms. The present sequence is an anti-portato SBEII antibody (denoted Clone46) heavy chain variable domain (VH) attached to peptide linkers, myc and his6 tag.

The potato SBEII is a starch branching enzyme also designated SBE A
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequent encoding a heavy chain immunoglobulin linked to a peptide that targets cellular compartment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-2000; 2000EP-00310997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1118669-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanum tuberosum 
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 12; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD10054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frenken LGJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNIL )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric.
                                                                                 AAE10563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-427157/46.
                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                            100;
                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNILEVER PLC.
                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                              QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQDGGSTNYA
                                                                                                                                                                VIVSSEPKTPKPQP
                                                                                                                                                                                     VTVSSEPKTPKPQP 130
                                                                                                                                                                                                                            DSVKGRFTISRDNAKNTVYLQMSSLKPEDTAVYYCAAGNLLVKRPY-
                                                                                                                                                                                                                                                            DSVKGRFTISRDNILNTVYLQMNSLKPEDTAVYHCNAD----VRPYRTSRYLELWGQGTL
                                                                                                                                                                                                                                                                                            QVQLQESGGGLVQAGGSLRLSCVASGNTFSIIAMAWYRQAPGKQREVVASINSIGSTNYA
                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Der Logt CPE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99EP-00310188
                                                                                 peptide;
                                                                                                                                                                                                                                                                                                                                                                        71.6%;
                                                                                                                                                                126
                                                                                 124
                                                                                                                                                                                                                                                                                                                                                            6,
                                                                                                                                                                                                                                                                                                                                                           Score 489; DB 4
Pred. No. 2e-36;
6; Mismatches
                                                                                 Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jobling
                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SA.
                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                        Length 152;
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NA sequence
targets a
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                             116
                                                                                                                                                                                                                                                                                              60
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10-DEC-2001 AAE10563;

(first entry)

food;

HGL inhibiting

HH

fragment, HGL

#9 from llama species.

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RESULT 10
ABG30620
ID ABG30
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                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 96
                                                                                                                                                                                                                                                                                                                            The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #9 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                     The present peptide sequence is llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bezemer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2000; 2000EP-00200930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2001; 2001EP-00200703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lama sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-572718/65
                                                                       115
                                                                                               121 SEPKTPKPOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody; camelid; anorectic; heavy chain variable domain; VHH; dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                            61
                                                                                                                                                     61
                                                                                                                                                                                 μ
                                                                                                                                                                                                           Н
                                                                                                                                                                                                                                     l Similarity
96; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                       SEPKTPKPQP
                                                                                                                           DSVKGRFTISRDNIKNIMYLQMNSLKPEDIGVYYCAG-----TGAEGHYWGQGTQVTVS
                                                                                                                                                     DSVKGRFTISRDNILNTVYLOMNSLKPEDTAVYHCNADVRPYRTSRYLELWGQGTLVTVS
                                                                                                                                                                               QVQLQESGGGLVQAGGSLRLSCAASGSIGSLYVMSWYRQAPGKQREPVAALMGSGSTTYA
                                                                                                                                                                                                     QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQDGGSTNYA
                                                                                                                                                                                                                                                                                            124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van De Burg M,
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= CDR2
/note= "Complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Complementarity
                                                                                                 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                       37pp; English.
                                                                                                                                                                                                                                                  71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complementarity determining
                                                                                                                                                                                                                                  Score 488; DB 4; I
Pred. No. 1.9e-36;
7; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tareilus
                                                                                                                                                                                                                                                              Length 124;
                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                   Gaps
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ABG30620 standard; protein; 131 AA

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1 QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQDGGSTNYA 60

Matches Query Match Best Local :

95;

Conservative

10;

Similarity

70.4%;

Score 480.5; DB 5; Pred. No. 9.8e-36; 0; Mismatches 25;

Length Indels

<u>'</u>

Gaps

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The invention describes a protein array (1) comprising a number of heavy-
C chain variable domain antibodies or antibody fragments, obtainable from
C camelidae. The method is useful for removing abundant proteins from an
C extract or sample which do not provide useful information on the
C condition of a cell or tissue in the extract or sample to be
investigated. (1) is useful for detecting the presence of individual
C proteins in a sample, comparing the distribution of proteins in different
C cell types, and identification of proteins that may be of importance in
C cell types, and identification of proteins that may be of importance in
C cell types, and leavy-chain variable domain derived from an
C immunoglobulin that is naturally devoid of light chains (VHH) in (1)
C provides a number of advantages, such as an improvement of
C sensitivity/resolution in the order of 10-100 times, and detection of
C post-translationally modified proteins. The invention also describes a
C method (II) that enables the simultaneous processing of large numbers of
C target antigens in a controlled way. The incorporated phage-ELISA
C generates on-line information of the technology, based on computer-made
C allows the complete automation of the technology, based on computer-made
C decisions on the values of the phage-ELISA for continuation of a limited
C conditions can be tested, varying amounts of imput-phages can be used
C simultaneously in order to decrease the enrichment of sticky phage-
C antibodies. Micro-panning is an effective tool for selecting both naive,
Synthetic and immune libraries on large panels of antibodies in short
C time frames needed for the generation of large panels of antibodies in short
C time frames needed for the generation of arrays (proteomics). This
C antibody (VHH)
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel protein array useful for detecting the presence of individual proteins in sample, comprises heavy-chain variable domain antibodies antibody fragments obtainable from Camelidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heavy chain variable domain; antibody; immunoglobulin; sticky phage-antibody; proteomic; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-583487/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNIL )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ds snw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        De Haard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-2001; 2001WO-EP014471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-DEC-2000; 2000EP-00311142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin G specifc heavy chain variable domain antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNILEVER NV.
UNILEVER PLC.
HINDUSTAN LEVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JJW,
131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 3; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Verrips CT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein array;
micro-panning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aging; VHH; immune library;
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QVQLQESGGGLVQPGGSLRLSCAASKSIFGFGAVGWHRQAPGKQRELVARITYDSGTNYA

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                                                                                                 The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MIL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE10566
                                                                                                                                                                                                                                                                                                                Example 4; Page 14; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-572718/65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGL inhibiting VHH fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNILEVER NV.
UNILEVER PLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; peptide; 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSVKGRFTISRDNAKNTVYLQMNSLKPEDTGVYYCNAETVRATTGRFITDLWGQGTTVTV
                                                                                                                                                                                                                                                                                                                                                                           chains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR1
/note= "Complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tareilus
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                                                                                 #15 from
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Query Match

69.78;

Score 476;

DB

4

Length 124;

Sequence

124

A

present peptide sequence na (camelid) species

is HGL

inhibiting

된

fragment,

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #22 from

Example 2; Page 10; 37pp; English.

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RESULT 12
AAE10558
ID IO SX
AAE10558
AC AAE10
XX AAE10
XX AAE10
AX IO DT 10 - DI
XX L1am
XW human
XW human
XW human
XW HOOC
XX L1am
XW FT Reg

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Matches
                                                                                                                                                                                                                                                 useful for cosmetic control heavy chain variable domain of light chains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody; camelid; anorectic; heavy chain variable domain; dietary enzyme inhibitor; medicament; human pancreatic lipa human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQDGGSTNYA
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                                                                                                                                                                                                                                                                                                                                                                                                              Van
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/note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide; 129
                                                                                                                                                                                                                                                                       fragments for inhibiting human dietary enzymes, control of body weight of human beings, comprises e domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .109
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                                                                                                                                                                                                                                                                                                                                                                                                              Z
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                                                                                                                                                                                                                                                                                                                                                                                                              De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPL #22 from llama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2.467; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              Haard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.4e-35;
ches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                Tareilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        species
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llama

(camelid)

species

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RESULT 13
AAE05288
ID AAE05288
AC AAE05
AC AAE05
XX AAE05
XX AAE05
XX AAE05
XX Potat
DT 18-SH
XX Potat
KW POTAT
CO CUNII
PA (UNII
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                              The present invention relates to a method for modifying a plant to produce an antibody or an active fragment or derivative, or a protein functional equivalent, in a cellular compartment comprises introducing DNA sequence encoding a heavy chain immunoglobulin, where the DNA is linked to promoters and provided with an additional sequence encoding peptide capable of targeting heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain immunoglobulin or an active fragment or derivative, or a protein that if functionally equivalent for increasing the pathogen resistance in a place or to modulate metabolism in a plant. Under some circumstances it may increasing the pathogen resistance it may increasing the pathogen resistance in a place of the pathogen resistance.
   or to modulate metabolism in a plant. Under some circumstances it may desirable to retain the antibody product with the plant rather than
                                                                                                                                                                                                                                                                                                                                                                                                                  Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potato; heavy chain immunoglobulin; pathogen resistance; metabolism modulator; passive immunisation; heavy chain VH; anti-potato SBEII; starch branching enzyme; SBE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIND)
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                                                                                                                                                                                                                                                                                                                                                              Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                              13; Fig 28; 81pp; English
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Pred. No. 1.4e-34;
1; Mismatches 24
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                       New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control; body weight.
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Pred. No. 2.1e-34;
5; Mismatches 20
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KW Hood;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #4 from lama (camelid) species
                                                                                 (UNIL )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGL inhibiting VHH fragment, HGL #16 from llama species.
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/note= "Complementarity determining
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1; Mismatches 23
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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                                                                                                          GTLVTVSSEPKTPKPQP 130
                                                                                                                                                 DSVKGRFTISRDNARGTVYLQMNSLKPEDTAVYYCAA-----ARSLELTPTSYDYWGQ
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RESULT 2
155673
ITS heavy chain - human (fragment)
ITS heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02
C;Accession: I55673
R;Knight, G.B.; Agnello, V.; Bonagura, V.
J. Exp. Med. 178, 1903-1911, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
S05271
Ig heavy chain precursor - human (fragmen C;Species: Homo sapiens (man)
C;Species: 30-Jun-1992 #sequence revision 30
C;Accession: S05271; S04602
R;Kishimoto, T.
Submitted to the EMBL Data Library, March A;Reference number: S05270
A;Accession: S05271
A;Accession: S05271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-144 < KIS2>
A;Residues: 1-144 < KIS2>
A;Cross-references: EMBL:X14584
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19Domain: signal sequence #status predicted <SIG>F;20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-160 < KISI>
A; Cross-references: EMBL:X14584
R; Kishimoto, T.; OKajima, H.; Okumoto, T.;
Nucleic Acids Res. 17, 4385, 1989
A; Title: Nucleotide sequences of the cDNAs
A; Reference number: S04601; MUID:89296497;
A; Accession: S04602
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Similarity 66.4%;
83; Conservative 1
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                                                                       02-Jul-1996 #text_change 21-Jan-2000
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                           Barnes, J.L.; Panka, D.J.; Zhang,
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PMID:2500644
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C;Accession: S31107

C;Accession: S31107

C;Accession: F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, Eur. J. Immunol. 22, 247-251, 1992

A;Title: Restricted utilization of germ-line V(H)3 genes A;Reference number: S31104; MUID:92111633; PMID:1730252

A;Accession: S31107
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immuno
F;15-98/Domain: immunoglobulin homology <IMM>
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Ig heavy chain V region
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Best Local S
Matches 84
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;Note: the nucleotide sequence was submitted to the EMBL Data Library, Superfamily: immunoglobulin V region; immunoglobulin homology;Reywords: heterotetramer; immunoglobulin;15-98/Domain: immunoglobulin homology <IMM>
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:Species:
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Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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84; Conservative
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                  human
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; Pred. No. 2.9e-25;
12; Mismatches 25;
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Pred. No. 2.4e-25;
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 Ig heavy chain .
C; Species: Homo
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Ig heavy chain - human (Man) (C,Species: Homo Sapiens (Man) (C,Species: Homo Sapiens (Man) (C,Species: Homo Sapiens (Man) (C,Species: C,Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999 (C,Accession: S31110 R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schur. J. Immunol. 22, 247-251, 1992 Fabra. J. Immunol. 22, 247-251, 1992 Fabra. J. Fitle: Restricted utilization of germ-line V(H)3 genes and short diverse third A;Reference number: S31104; MUID:92111633; PMID:1730252 A;Accession: S31110
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A,Molecule type: mRNA
A,Residues: 1-140 <CUI>
A,CROSS-references: EMBL.Z14200, NID:g30957, PIDN:CAA78569.1,
A,Cross-references: EMBL.Z14200, NID:g30957, PIDN:CAA78569.1,
C,Superfamily: immunoglobulin V region; immunoglobulin homolo;
C,Keywords: heterotetramer; immunoglobulin
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A;Note: the mucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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Pred. No. 4.5e
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RESULT 8
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C.Species: Homo sapiens (man)
C.Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C.Accession: S31108
C.Rocession: S31108
C.Rocession: Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.I.
E.; Timmunol. 22, 247-251, 1992
Timmunol. 22, 247-251, 1992
Timmunol. 22, 247-251, 1992
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IM%>
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A;Molecule type: mRNA
A;Residues: 1-123 <RAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 02-Dec-1993 #sequence_revision C;Accession: S31114 R;Raaphorst, F.M.; Timmers, E.; Kenter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-119 < RAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31108
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;Note: the nuclectide sequence was submitted to the EMBL Data Library, ;Superfamily: immunoglobulin V region; immunoglobulin homology ;Keywords: heterotetramer; immunoglobulin ;15-98/Domain: immunoglobulin homology <IMM>
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Best Local
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Best Local Similarity
    heavy chain
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81; Conserv
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    human
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Pred. No. 7.6e-25;
2; Mismatches 21
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Ig heavy chain V region C; Species: Homo sapiens
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region

(man)

human

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCHA
A;Residues: 1-119 <SCHA
A;Cross-references: GB:M18513
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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R;Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable A;Reference number: A36005; MUID:90349571; PMID:2117273

A;Accession: C36005
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A;Molecule type: mRNA
A;Residus: 1-140 <CUI>
A;Residus: 1-140 <CUI>
A;Cross-references: RMSL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IVM>
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A;Description: Mechanisms that generate human immunoglobulin diversit A;Reference number: 831585
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C;Date: 22-Nov-1993 #sequence
C;Accession: S31686
R;Cuisinier, A.M.; Gauthier,
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Matches 83
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Best Local S
Matches 81
  117
                                          120 VSS 122
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B1; Conservative
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VSS 119
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65.9%; Pred. No. 1.3e
tive 12; Mismatches
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10; Mismatches
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1.3e-24;
1es 27;
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 C;Accession: S3166  
C;Accession: S3166  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate A;Reference number: S31585  
A;Accession: S31666  
A;Accession: S31666  
A;Accession: S31666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-114 < RRA> A;Cross-references: EMBL:X62972 A;Cross-references: EMBL:X62972 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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A;Molecule type: mRNA
A;Residues: 1-138 <CUI>
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C;Species: Homo sapiens
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Best Local S
Matches 80
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Best Local S
Matches 82
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;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman ur. J. Immunol. 22, 247-251, 1992
;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: S31120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Homo sapiens (man);Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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                       (anti-Sm,
      (man)
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                         VH3/Dxp4/JH4b) -
                                                                                                                                                                                                                                                                                                                                                                                            Score 378; DB 2;
Pred. No. 2.9e-24;
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Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change :
C;Accession: S26786
R;Mortari, F; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Bur, J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage A;Accession: S26786
A;Accession: S26786
A;Accession: S26786
A;Status: preliminary
A;Status: preliminary
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A;Residues: 1-120 <MAH>
A;Cross-references: EMBL:Z46382; NID:g562324; PIDN:CAA86521.1; PID:g1340167
A;Cross-references: EMBL:Z46382; NID:g562324; PIDN:CAA86521.1; PID:g1340167
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999 C;Accession: S48798
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A; Residues: 1-120 < MA
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision
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A; Residues: 1-128 < MOR>
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                                                                                                                                                                                                                            ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGLYCSSTSCYIWSNNWFDPWGQ
                                                                                                                                                                                                                                                                                                       QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSSSYTNY
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                                                                                                                                                                                      GTKVTVSS 122
                                                                                                                                                                                                                                                              ADSLKGRFTISRDNAKNAVYLOMNNLKPEDTAVYYCNAHITPAGSSNYVYGY-----WGH 114
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Pred. No. 3.3e-24;
.3; Mismatches 28
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October 1994
      06-Jan-1995 #text_change 16-Aug-1996
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C;Accession: S30531
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A,Reference number: S30520
A;Reference number: S30520
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-125 <MAR>
A;Cross-references: EMBL: Z18317
A;Cross-references: EMBL: Z18317
C;Superfamily: immunoglobulin V region; immunoglobulin P;15-98/Domain: immunoglobulin homology 
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A;Description: Human antibody fragments specific for human blood group antigens from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
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A;Accession: S38489
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C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Accession: 838489
C;Accession: 838489
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;Molecule type: DNA
;Residues: 1-127 <MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 54.9%; Score 377.5; DB 2; Length 127; Best Local Similarity 63.3%; Pred. No. 3.6e-24; Matches 81; Conservative 13; Mismatches 25; Indels 9;
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ID HUMAN

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AC PO1767;

AC PO1767;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-CCT-2003 (Rel. 42, Last annotation update)

DT 10-Last annotation update)

DT 10-Last annotation update

DT 10-CCT-2003 (Rel. 42, Last annotation update)

DT 10-CCT-2003 (Re
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Matches 71
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Torano A., Putnam F.W.;
Torano A., Putnam F.W.;
"Complete amino acid sequence of the alpha 2 heavy cha
IgA2 immunoglobulin of the A2m (2) allotype.";
Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
-I- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2)
REGION OF THIS WYELOWA PROTEIN IS ALSO GIVEN.
-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Similarity 58.2%;
71; Conservative 18
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                                                                                                                                                                            DSLKGRFTISRDNAKNAVYLQMNNLKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTKVTV
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                                                                                                                                                      DSVKGRFTISRDDSRBTVYLQMBSLRAEDTAVYYCARDLAAA---
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HV05 MOUSE
HV27 MOUSE
HV29 MOUSE
HV31 MOUSE
HV34 HUMAN
HV34 HUMAN
HV18 MOUSE
HV25 MOUSE
HV26 MOUSE
HV27 MOUSE
HV27 MOUSE
HV28 MOUSE
HV28 MOUSE
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Pred. No. 1.2e-26;
8; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                       208876A7DF52DCF4 CRC64;
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human

Result

Score

Query Match

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HV3F HUVAN
HV3K HUVAN
HV3K HUVAN
HV3K HUVAN
HV3K HUVAN
HV3E MOUSE
HV3E HUVAN

mus musculu mus musculu

RESULT 2 HV05\_CARAU

RLFGKGTTVTV

120 60 7;

Gaps

Database

SwissProt\_42:\*

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score greater

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

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Best Local S
Matches 69
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21-JUL-1986
21-JUL-1986
10-OCT-2003
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                                                MEDLINE=83289131; PubMed=6884994; Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; "Three-dimensional structure determination of antibodies. structure of crystallized monoclonal immunoglobulin IgG1 structure of crystallized monoclonal immunoglobulin IgG1 hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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P19181;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig heavy chain V region 5A precursor.
                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=88144476; PubMed=3125551;
Wilson M.R., Middleton D., Warr G.W.;
Wilmunoglobulin heavy chain variable region
and family relationships of two genes and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ev
Actinopterygii, Neopterygii; Teleostai; Ostariophysi;
Cyprinidae; Carassius.
                  X-RAY CRYSTALLOGRAPHY (1.9 ANGSTR
MEDLINE=81072295; PubMed=7441755;
                                                                                                         SEQUENCE,
                                                                                                                                                            Homo sapiens (Human)
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NCBI_TaxID=7957;
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InterPro; IPR003596;
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-JUL-1986 (Rel. 01, Last sequence update)
-OCT-2003 (Rel. 42, Last annotation update)
| heavy_chain_V-III_region_KOL.
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                                                                                                                                                                                                                                                                                                                                                                           69,
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PS50835; IG LIKE; 1.
bulin V region; Signal
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                                                                                                        AND DISULFIDE BONDS
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         Deisenhofer
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Primates;
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72.6%;
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       J., Huber R.,
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                            ANGSTROMS).
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Pred. No. 1.4e
8; Mismatches
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BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-1
FRAMEWORK-2.
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Catarrhini;
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Immunoglobulin V region; 3)-structure; Pyrrolidone carboxylic DOMAIN

MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
DISÜLFID 22 96
DISULFID 105 110
STRAND 3 7
STRAND 11 12
PO1783;
PO17783;
PO17783;
PO17783;
PO17783;
PO17783;
PO17783;
PO17783;
PO1788 (Rel. 01, Created)
PO1788 (Rel. 01, Last sequence update)
PO17888 (Rel. 42, Last annotation update)
PO1888 (Rel. 42, Last annotation update)
Ig heavy chain V region MOPC 21 precursor (Fr. Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulin molecule K
and 1.0-A resolution.";
J. Mol. Biol. 141:369-391
-i- SIMILARITY: Contains
PIR; A02055; GHUKL.
                                                       MOUSE
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NON TER
SEQUENCE
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PDB; 2IG2; 12-JUL-89.
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                                                                                                                                                      QVQLVESGGGVVQPGRSLRLSCSSSGFIFSSYAMYWVRQAPGKGLEWVAIIWDDGSDQHY
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                                                                                                                                      ADSLKGRFTISRDNAKNAVYLOMNNLKPEDTAVYYC---NAHITPAGSSNYVYGYWGHGT
                                                                                                                                                                      QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGS-TNY
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13718 MW;
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Pred. No. 2.3e-26;
5; Mismatches 32
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          (Fragment).
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RESULT 5

HV3C HUMAN

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AC PO175

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DT 21-JUL

DT 21-JUL

DT 10-OCT

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Best Local
HV3C_HUMAN STANDARD; PRT; 117 AA P01764; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation updat Ig heavy chain V-III region VH26 precursor.
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CONFLICT
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=77100368; PubMed=401950; Adetugbo K., Milstein C., Secher D.S.; "Molecular analysis of spontaneous somatic mutants."; Nature 265:299-304(1977).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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DOMAIN
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InterPro; IPR003596; Ig_v.
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T; SM00406; IGv;
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77; Conser
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PS50835; IG LIKE;
obulin V region; Si
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                                                                                                                                                                                                DSLKGRFTISRDNAKNAVYLOMNNLKPEDTAVYYCNAHITPAGSSNYVY---GYWGHGTK 117
                                                                                                                                                                          DTVKGRFTISRDNPKNTLFLOMTSLRSEDTAMYYC----ARWGNYPYYAMDYWGQGTS
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Rodentia;
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                                                                                                                                                                                                                                                                          Score 345; DB 1; 1
Pred. No. 3.9e-26;
0; Mismatches 28;
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D SEGMENT.
JH4 SEGMENT.
                                                                                                                                                                                                                                                                                                                                                HYAD -> DYAH (IN REF. DN -> ND (IN REF. 2). W -> H (IN REF. 2). Y -> W (IN REF. 2).
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                                                                                                                                                                                                                                                                                                Length 136;
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RESULT
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Best Local S
Matches 69
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GO; GO:0003576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal; 3D-struc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
NON TER
SEQUENCE
                                                                                                                                                           HV3B_HUMAN STANDARD; PRT; 1

P01763;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence up

10-OCT-2003 (Rel. 42, Last annotation

19 heavy chair V-III region WEA.
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EMBL; M35415; AAA58735.1; -.
PIR; A02047; H3HU26.
PDB; 1HOU; 23-DEC-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matthyssens G., Rabbitts T.H.; Procture and multiplicity of genes for the hum "Structure and multiplicity of genes for the hum many chain variable region."; Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980) -!- SIMILARITY: Contains 1 immunoglobulin-like d
Goni F., Frangione B.;
"Amino acid sequence of the Fv region of a human monoclonal 1
"Amino acid sequence of the tregion of a human monoclonal 1
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                     HUMAN
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                                                           MEDLINE=83273707; PubMed=6410398;
                                                                          SEQUENCE
                                                                                                                                                Homo sapiens (Human)
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                                                                                                                    Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                             49.3%;
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Pred. No. 1.1e
9; Mismatches
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IG-LIKE.
                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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ALD DESCRIPTION OF THE PROPERTY OF THE PROPERT
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HV3G_HUMAN
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Best Local S
Matches 73
    P01768;
21-JUL-1986 (
21-JUL-1986 (
10-OCT-2003
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MOD_RES
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region CAM.
Homo sapiens (Human)
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SMART; SM00406; IGv; I.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region; Py
DOMAIN
1 112
                                                                                                                                                                                                                                                                                                        Lehman D.W., Putnam F.W.;

"Amiho acid sequence of the variable region of a human location of a possible of segment.";

Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).

1. MISCELLANGOUS: THIS MU CHAIN WAS ISOLATED FROM THE PATISKY WITH MACROGLOBULINEMIA.

1. SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P01772; 2FB4.
HSSP, P01772; 2FB4.
GO; GO:00005576; C:extracellular; NAS.
GO; GO:0003523; F:antigen binding; NAS.
GO; GO:0005955; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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-!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                       PIR; A02051; M3HUAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=81013859; PubMed=6774332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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- SIMILARITY: Contains 1 immunoglobulin-like domain.
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114 AA;
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            PYRROLIDONE CARBOXYLIC ACID
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Best Local
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR007110; Ig-1ike.
PROS176; IPR003596; Ig-V.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50833; IG_LIKE; 1.
PROSITE; PS50833; IG_LIKE; 1.
Immunoglobulin V region; Glycoprotein;
DOMAIN
1 112 IG-LIKE
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DISULFID
CARBOHYD
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SEQUENCE
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P01773;
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                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                IgAl procease, digestion, Fab and Fc fragments, amino acid sequence of the alpha 1 heavy chain.
J. Biol. Chem. 254.2865-2874(1979).
-!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=79151016; PubMed=107164;
Putnam F.W., Liu Y.-S.V., Low T.L.K.;
"Primary structure of a human IgA1 immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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21-JUL-1986 (Rel. 01, Last s
10-OCT-2003 (Rel. 42, Last a
Ig heavy chain V-III region
                                                                                                                                                                                                                                                                                                                                                                           HSSP; P01772; 2FB4.
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                                                                                                                                   72;
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                                                                                                                                                Similarity
                                                                                                             QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGS-TNY
                                      ADSVRGRETISRBISKBILYLZMKTLRTEDTAVYYCAKLIAVAGTRB----FWGQGTLVT
                                                       ADSLKGRFTISRDNAKNAVYLQMNNLKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTKVT
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                                                                                    QVQLVESGGGVVQAGTSLRLSCTASAFNLSDYAMHWVRQAFGKGLZWVALISYGGSBTYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVELVESGGGVVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBBKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
122 AA;
                                                                                                                                                                                     119
             121
                                                                                                                                      Conservative
                                                                                                                                                                                     AA;
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Primates;
                                                                                                                                                48.8%;
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                                                                                                                                                                                                                                                   Glycoprotein;
IG-LIKE.
                                                                                                                                   14;
                                                                                                                                               Score 335.5; DB 1
Pred. No. 2.7e-25;
                                                                                                                                                                                                             N-LINKED (GLCNAC. .
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; Mismatches
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Pred. No.
                                                                                                                                                                                                                                      PYRROLIDONE CARBOXYLIC
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Matches 71
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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HV3D HUMAN
P01765;
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21-JUL-1986
10-OCT-2003
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HV3P_I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS GO; GO:0006955; P:immune response; NAS
                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
10-CCT-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region TIL.
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"Variable r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=74142702; PubMed=4522793; Capra J.D., Kehoe J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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Homo sapiens (Human)
MEDLINE=78005528; PubMed=409716; Wang A.-C., Wang I.Y., Fudenberg H.H.; "Immunoglobulin structure and genetics. regions of a mu and a gamma2 chain."; J. Biol. Chem. 252:7192-7199(1977).
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                  SEQUENCE
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6 (Rel. 01, Last se
3 (Rel. 42, Last an
hain V-III region T
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Pred. No. 3.8e-
16; Mismatches
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                                                                                                                                                                                                                                                                    Craniata; Vertebrata; i Catarrhini; Hominidae;
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on update)
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3.8e-25;
31;
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Best Local Similarity
Matches 73; Conserv
Query Match
                                                                                                                                          InterPro; ..... ig; 1.
pfam; pF00047; ig; 1.
SMART; SW00406; IGv; 1.
PROSITE; pS50835; IG_LIKE; 1.
Immunoglobulin V region.
Interpretation of the control of
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InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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P01802;
21-JUL-1986
21-JUL-1986
10-OCT-2003
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binding proteins.";
J. Immunol. 128:302-307(1982).
J. Immunol. 178:302-307(1982).
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Johnson N., Slankard J., Paul L.,
"The complete V domain amino acid
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Mammalia; Eutheria;
                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; D92811; AVMS82.
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-!- SIMILARITY: Contains 1 immunoglobulin-like
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InterPro; IPR003596; Ig_v.
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GO:0003823; F:antigen binding; NAS
GO:0006955; P:immune response; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 VSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADSLKGRETISRDNAKNAVYLQMNNIKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAFGKQRELVASITS-GGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVOLLESGGGLVOPGGSLRLSCAASGFTFSTYVMSWVRQAPGKGLZWVGAIZGLSVSZSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABSVKGRFTISRDDSKNT---
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115
115 AA;
                                                                   115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
ain V-III region W3082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12356 MW; 4DCC67D179F62326 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                   12887 MW;
                                                                                                                                   98
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   48.2%;
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Pred. No. 4.1e-25;
1; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG-LIKE
   Score 331.5;
                                                                                                                                IG-LIKE.
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                   9B4517648C121C5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNSLRAEDTAVYYC----AKGKVSAYYFBYWGZGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hood L.;
| sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOLATED FROM A MYELOMA
       BB
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   Length
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       115;
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RESULT 12
HY3T HUMM
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Best Local S
Matches 75
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Matches
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DOMAIN 1
NON_TER 116
SEQUENCE 116
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21-JUL-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A02064; M3HIGL.

HSSP; P01772; 2FB4.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.

InterPro; IPR007596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=75059123; PubMed=4803843; Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.; "The primary structure of a morclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain type), subgroup H III. Architecture of the complete IgM-molecule. Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-1975) to the PIR data -!- MISCELLANEOUS: THIS MU CHAIN WAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MACROGLOBULIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hilschmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISION TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986
10-OCT-2003
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-JUL-1986 (Rel. 01, Last sequence update)
-OCT-2003 (Rel. 42, Last annotation update)
heavy chain V-III region GAL.
               114
                                                          120
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                                                                                                                                                                                                      <u>بــ</u>
                                                                                                                                                                                                                                               1 QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGS-TNY
                                                                                                                                                                                                                                                                                                     75;
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67; Conserv
                                                                                                                                                                                                                                                                                                                            Similarity
       VST 116
                                                                                                                                       ADSLKGRFTISRDNAKNAVYLQMNNLKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTKVT
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:||:|||||||:|::|:||| :|||
HYAESVKGRFTISRDDSKSSVYLRMNNLRPEDTGIYYCTTG-------FAYWGQGTL 110
                                                        VSS 122
                                                                                                           VDSVKGRFTI
                                                                                                                                                                                                      EVOLVESGGDLVQPGRSLRLSCAASGFBFBBLGMTWVRQAPGKGLEWVANIKZBGSZZBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTVSA 115
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                                                                                                                                                                                                                                                                                                                                                                                         116
116
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                                                                                                           SRDNAKNSLYLOMNSLRVEDTALYYC-ARGWGGGD----
                                                                                                                                                                                                                                                                                                                                                                                              116
12730 MW;
                                                                                                                                                                                                                                                                                                                         48.0%;
61.0%;
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                                                                                                                                                                                                                                                                                                Score 330; DB 1;
Pred. No. 8.9e-25;
0; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 6.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                              2C67CA9AAAAA1282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bank.
ISOLATED FROM A WALDENSTROM'S
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ches 25;
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                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                              Length 116;
                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                Gaps
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REAL SECTION OF THE S
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HV02_CANFA
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HV32_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                              HV02 CANFA
P01785;

p01785;

21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 02, Last sequence update)
21-JUL-1986 (Rel. 04, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
11 fleavy chain V region MOO.
Canis familiaris (Dog).
Canis familiaris (Dog).
Canis familiaris (Dog).
Canis familiaris (Canidae; Canidae; Canidae; Canidae; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1.

Pfam; NM00406; IGv; 1.

SMART; SM00406; IG LIKE; 1

PROSITE; PS50835; IG_LIKE; 1

Immunoglobulin V region.

DOMAIN

114
SEQUENCE OF 1-112.

MEDLINE=77242268; PubMed=407924;

Wasserman R.L., Capra J.D.;

"Primary structure of the variable immunoglobulin heavy chains.";

Biochemistry 16:3160-3168(1977).
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P01801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986
21-JUL-1986
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; C92811; AVMS06.
HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=82099361; PubMed=6798111;
Johnson N., Slankard J., Paul L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation updat Ig heavy chain V-III region J606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANEOUS: THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding proteins."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               son N., Slankard J., Paul complete V domain amino
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115 AA;
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12810 MW;
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Ig_v.
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acid
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Pred. No. 9.8e-25;
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[2]
SEQUENCE OF 113-117.
MEDLINE=80077682; PubMed=117299;

McCumber L.J

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RESULT 15
HV30 MOUSE STANDARD; PRT; 113 AA.

ID HV30 MOUSE STANDARD; PRT; 113 AA.

AC P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 19 heavy chain V-III region ABE-47N.
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Best Local Similarity
Query Match
                                                                                                                                              PIR; A90400; AVMSB7.

HSSP; P01810; 2FBJ.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region.

DOMAIN 1 113 11
                                                          DOMAIN
DISULFID
NON TER
SEQUENCE
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SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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Mol. Immunol. 16:565-570(1979).
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.

MEDLINE=77134726; PubMed=402936;

Wrana M., Rudikoff S., Potter M.;

"Heavy-chain variable-region sequence from an inulin-binding myeloma protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 16:1170-1175(1977).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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- SIMILARITY: Contains 1 immunoglobulin-like domain.
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                                                             113 AA;
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                                                             12675 MW;
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47.6%; Score 327.5; DB 1; Length 113;
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BY SIMILARITY.
                                                             76658C16C779845E CRC64;
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                                                                                                                                                                                                                                       Best Local Similarity 54.5 Matches 67; Conservative
                                               111 VTV 113
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                                                                                                              61 HYAESVKGRFTISRDDSKSSVYLOMNIRAEDTAIYYCSTG---
                                                                                                                                     58 NYADSIKGRETISRDNAKNAVYLQMNNIKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTK 117
                                                                                                                                                                                                      1 QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASI---TSGGST 57
                                                                             VTV 120
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5, 2004, 08:01:55
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Search completed: October Job time: 11.7253 secs

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Title:
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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688
1 QVQLQESGGGLVQAGG
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                          sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_vriclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_mammal:*
sp_mhc:*
SUMMARIES
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Result	Score	Query Match Length	ength	DB	ID	Description
р.	381	55.4	118	42	Q9UL72	Q9ul72 homo sapien
2	379	55.1	499	4	Q8N5K4	Q8n5k4 homo sapien
ω	377.5	54.9	597	4	Q96BB9	_
4	375.5	54.6	573	4.	Q8WU38	homo
ທ	363.5	52.8	494	4	Q96K68	Q96k68 homo sapien
σ	362.5	52.7	119	11	Q920E7	Q920e7 mus musculu
7	361.5	52.5	116	4,	Q9UL93	Q9ul93 homo sapien
œ	361	52.5	487	11	Q99KA4	Q99ka4 mus musculu
9	358	52.0	118	4	Q9UL91	Q9ul91 homo sapien
10	354.5	51.5	113	4	Q9UL90	Q9ul90 homo sapien
11	354.5	51.5	131	4	Q9UL88	Q9ul88 homo sapien
12	354	51.5	112	4	Q9HCC1	Q9hcc1 homo sapien
13	350.5	50.9	480	11	Q91XE1	Q91xe1 mus musculu
14	349.5	50.8	121	4	Q9UL71	
15	348.5	50.7	487	11	Q80ZI7	
16	344.5	50.1	479	11	Q91WP5	Q91wp5 mus musculu

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1 QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGSTNYA 60

<u>.</u> 45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	ω 53	24	23	22	21	20	19	18	17	
258	260	261	265.5	265.5	268.5	268.5	274	275	275.5	276	278	280.5	283	289	301	309	313	322	323	327	328.5	329	ω u u	335	336.5	339.5	342	343	
7.	37.8	.7	œ	8	9	φ.	9	0			•							46.8		•	•	•	•	٠	•	•	•		
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4.	11	4.	4.	4.	11	4	4	片	4,								4	11	4.	4	4	11	11	11	11	4	4	4	
Q7Z374	Q8VDC9	095973	Q96KX8	Q9UL73	Q7TMT6	080960	Q9UL92	Q99NG4	Q9UGP3	Q9NOW4	Q9N0W6	Q9UL87	Q7Z351	Q91X92	Q7TMK4	Q8VEA0	Q7Z5W1	QBR3V9	QBNCL6	Q9UL84	Q9ULB6	Q9R1A4	Q91Z05	037760	Q91Z07	Q9Y509	Q8N4Y9	Q8WUK1	
Q7z374 homo sapien	sum 6	O95973 homo sapien	homo	homo	6 mus	homo	Q9ul92 homo sapien	Q99ng4 mus musculu	Q9ugp3 homo sapien	Q9n0w4 oryctolagus	Q9n0w6 oryctolagus	Q9u187 homo sapien	Q7z351 homo sapien	2 mus	Bru	Bru	Q7z5w1 homo sapien		Q8ncl6 homo sapien	homo	homo	mus	mus	mus	mus	omo	10mo	Q8wuk1 homo sapien	

# ALIGNMENTS

QSULT2  QSULT2  QSULT2  QSULT2;  DT  QSULT2;  QS
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RNN COX NOCE BERN COX NOCE BER
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Best Local S
Matches 83
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SMART; SM00409; IG; 4.

SMART; SM00409; IG; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS50835; IG MHC; 1.

Hypothetical protein.

SEQUENCE 499 AA; 53376 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC032249; AAH32249.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_mHC.
InterPro; IPR003596; Ig_w.
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Hymothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Che
Mammalia; Eutheria; Pri
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01-OCT-2002
01-OCT-2002
                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                             Hypothetical protein. Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                     Q96BB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Blood;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83;
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                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Primates;
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Last sequence update)
Last annotation updat
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Pred. No. 2.2e-27;
                                                                                                  Catarrhini;
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                                                                                                                                     Craniata;
                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                  Hominidae;
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Matches 84
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Best Local
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SVART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS508290; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 573 AA; 62967 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pram; PR00047; 19; 5.

SMART; SM00406; IGv; 1.

PROSITE; PS01835; IG LIKE; 5.

PROSITE; PS01290; IG_MHC; 3.

Hypothetical protein.

SEQUENCE 597 AA; 65039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
EMBL; BC021276; AAH21276.1; -
PIR; S21205; S21205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC015760; AAH15760.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003056; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B EDMBD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ç8WU38;
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                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Tonsil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138
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                                                                                                                                   1 QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASIT-SGGSTNY
                                                                                                                                                                                       84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83;
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                                                                                                                                                                                                             Similarity
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ADSVKGRETISRDNAKNSLYLQMNSLRAEDTALYYCAKH--
                                            ADSLKGRFTISRDNAKNAVYLOMNNLKPEDTAVYYCNAHITPAGSSNYV---YG--YWGH 114
                                                                                         EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLVTVSS 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADSVKGRFTISRDNSRDTLYLOMNSLRAEDTAVYYCAK--DPRGYSASGNYTREDYWGQG
                                                                                                                                                                                       Conservative
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Primates;
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                                                                                                                                                                                                           54.6%;
                                                                                                                                                                                                                                                                                   62967 MW;
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                                                                                                                                                                                    12;
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Last annotation update)
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                                                                                                                                                                                                           Score 375.5;
Pred. No. 5.6
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Pred. No. 3.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4FCA3AD8ECE263D9 CRC64;
                                                                                                                                                                                                                                                                                   FD072344033AC530 CRC64;
                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             databases
                                                                                                                                                                                                                                   Length
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    -GSGSYIGYYYGMDVWGQ 135
                                                                                                                                                                                                                                   573;
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115

GTKVTVSSEP-KTPKPQP 131

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RESULT 6
Q920ET
ID Q920E
AC Q920E
AC Q920E
AC Q920E
DT 01-E
DT 01-E
DT 01-E
DT 01-E
DT 01-G
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Best Local (
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG_LIKE; 4.
PR0SITE; PS508390; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Mammary gland;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Wagatsuma M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishi S., Kawai Y., Saito K.,
Watanamoto J., Wakamateu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
NIDOD human CDMA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027379; BAB55072.1; -.
PIR; S21205, S21205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Hypothetical protein FLJ14473.
Homo sapiens (Human)
                                                                                                                                                           Q920E7 PRELIMINARY; PRT; 119 AA. Q920E7; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) pterin-minicking anti-idiotope heavy chain variable (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
SEQUENCE 49
  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDSVKGRFTISRDNAKNSLYLQMNSLRVDDTAVYYC-ARDSCNGAICYGFSPWGQGTLVT
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  FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSS-EPKTPKPQP 131
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494 AA; 5
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  N.A
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Pred. No. 6.3e-26;
4; Mismatches 35;
                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9A1D7AEB5AEE4C0E CRC64;
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RESULT 7
Q9UL93
ID Q9UL93
ID Q9UL
AC Q9UL
DT 01-1
DT 01-1
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DT 01-1
DT 01-1
DT 01-1
RYO
CS HOM
CS HOM
CS WC
RN WC

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Best Local S
Matches 76
                                                                                                                          Query Match
Best Local S
Matches 78
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EMBL; AF035021; AAD56257:1; -.
PIR; PL0120; PL0120.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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InterPro; IPR007516; Ig-v.
Pfam; PR00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
NON_TER 11 11
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
" '4" B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UL93; PRELIMINARY;
Q9UL93; PRELIMINARY;
Q1-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Atkin J.D., Iape A., Jenning "Definition of the Idiotope in Mammalian Cells.";
Submitted (SEP-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF307937; AAL09421.1; PIR; C25913; C25913.
                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin-reactive immunoglobulin
                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                          78;
                                                           Ν
                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADSLKGRFTISRDNAKNAVYLQMNNLKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTKVT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARH----GDYDVGFAYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGS-TNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSS 122
VQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA
                                                       VQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGSTN-YA
                                                                                                                                                                                                                                                           116
116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 119
119 AA; 13025 MW;
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                                                                                                                                                                                                                                                           116
12434 MW;
                                                                                                                                                         52.5%;
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Hiotope of Pterin-Mimicking i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 362.5; DB 11; Pred. No. 1.3e-26; 14; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
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                                                                                                                             Score 361.5; DB 4
Pred. No. 1.6e-26;
8; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heavy
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                                                                                                                                                                                                                                                                  0DA0348154DD6061 CRC64;
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o variable
                                                                                                                                                                                                DB 4;
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                                                                                                                                 29;
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RESULT 9
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DT 01-M
DT 01-M
DT 01-M
OT 01-O
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RN [1]
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Best Local (
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                                                                                                                                                                                                                                                                                                                Q9UL91;
01-MAY-2000
01-MAY-2000
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pummitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC004786; AAH04786.1; -. HSSP; P01810; 2FBJ. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003006; Ig_MHC. InterPro; IPR003906; Ig_WHC. Ffam; PF00047; io: 4
                                            SEQUENCE FROM N.A.

MEDLINE=98277139; PubMed=9614934;

Wu X., Liu B., Van der Merwe P.L.,

Young D.C.;
                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Ro
                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 25, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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SMART; SM00406; IGv; 1.
SMART; PS50835; IG LIKE; 4.
PROSITE; PS50835; IG_MHC; 2.
                       "Myosin-reactive autoantibodies
                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                  Q9UL91
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01-OCT-2003
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01-JUN-2001
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77; Conserv
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487 AA; 52554 MW;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144
                                                                                                                                                                                             Chordata;
Primates;
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Pred. No. 1.1e-25;
5; Mismatches 28;
                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                       H.
                                                                   Kalis N.N.,
                       rheumatic
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                                                                      Berney S.M
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Matches 77
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Best Local S
Matches 78
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NON_TER
SEQUENCE
                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035023; AAD56259.1; -.
PIR; S21205; S21205.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                  EMBL; AF035024; AAI
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UL90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                         Clin.
                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 06TD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                    etus."
                                                                                                                                                                                                                                                                                                                                                                             (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110;
InterPro; IPR003596;
                                                                                                                                                                                          nterPro, IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 VS 121
                                                                                                                                                                                                                             Immunol. Immunopathol. 87:184-192(1998) AF035024; AAD56260.1; -.
             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
                                                                              77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSTIITIYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGST-NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
78; Conserv
ADSLKGRFTISRDNAKNAVYLQMNNLKÞEDTAVYYCNAHITÞAGSSNYVYGYWGHGTKVT
                                                QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGSTN-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADSLKGRFTISRDNAKNAVYLQMNNIKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYC----ARGDSSEAFDIWGQGTMVT
                                  EVOLVESGGGVVOPGGSLRLSCAASGFTFSSYGMHWVROAPGKGLEWVAFIRYDGSNKYY
                                                                                                                                                                                                       IPR007110;
                                                                                                                          113
113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118
                                                                                                                          12437 MW; ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                             Primates;
                                                                                       51.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12843 MW;
                                                                                                                                                                                                                                                                                                                                                       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig-like.
Ig_v.
                                                                                                                                                                                                      Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 358; DB
Pred. No. 3.5e
10; Mismatches
                                                                              Score 354.5; DB 4;
Pred. No. 7.1e-26;
8; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D0633949F2AC149D CRC64;
                                                                                                                                                                                                                                                               in rheumatic
                                                                                                                                                                                                                                                                                      Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
.5e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                   DB 4;
                                                                                                                                                                                                                                                               carditis and normal
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                                                                                                                                                                                                                                                                                      Berney
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                                                                                                  Length 113;
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                             Homo.
                                                                                                                                                                                                                                                                                                                                                                                         region
                                                                               11;
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                                                                              Gaps
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В

61

ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDL--

---NYWGQGTLVT 110

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Q9HCC1 12
Q9HCC1
ID Q9HCC
AC Q9HCC
D1 01-MA
D7 01-MA
D7 01-MA
D7 01-MC
D8 Singl
OS Homo
OC Sukar
OC Mamma
OX NCBI 1--
RN (1)--
RN SEQUE
RA Kikuc
RT "An a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                         Q9HCC1 PRELIMINARY;
Q9HCC1;
01-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, L
01-OCT-2003 (TrEMBLrel. 25, L
Single chain Fv (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wu X., L
Young D.
                                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UL88;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
W. X., Liu B., Van der Merwe P.L., Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF035026; AAD56262.1; PIR; S21205; S21205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.TN60
SEQUENCE FROM N.A.
Kikuchi M., Takeda C., Ts
"An antibody fragment2A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P01810; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
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                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunol. Immunopathol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASI---TSGGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WGHGTKVTVSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYAAPVKGRLTISRDSSKNTLYLRMNSLKTEDTAVYYCTTGITMIIVVITTSSKRTSFEY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYADSLKGRFTISRDNAKNAVYLQMNNLKPEDTAVYYCNAHIT-----PAGSSNYVYGY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVOLVESGGGLVKPGGSLRLSCAASGFTFSKAMMSWVRQAPGKGLEWVGRIKSKTDGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131
131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                        (Human)
                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14142 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131
Tsujimoto Y., Asada S., Nagata K.;
A3 specific for native lysozyme :Isolaion
                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 354.5; DB 4
Pred. No. 8.5e-26;
1; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87:184-192(1998)
                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96E7D668E375DEA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                       112
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                                                                                                                                                                                                                                              update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 131;
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RESULT

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RESULT 13
Q91XE1
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Best Local 9
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Best Local
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; P850835; IG_LIKE; 1.
NON TER 1.
NON TER 1.2 1.2
SEQÜENCE 112 AA; 12243 MW;
                                                                                                                                                                                                                        Pfam; PF00047; 19; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91XE1
Q91XE1;
01-DEC-2001
01-DEC-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                            TISSUE=Colon; Strausberg R.; Strausberg R.; Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; BC010798; AAH10798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Mus musculus (Mouse).
Eukaryota; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human synthetic phage display library and characterization."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB049915; BAI
HSSP; P01772; 2FB4.
                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
134
                        121
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                                                                                                                                                          75;
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                                                                                                                                                                     Similarity
                                                                        DSLKGRFTISRDNAKNAVYLQMNNLKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTKVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADSLKGRFIISRDNAKNAVYLQMNNLKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTKV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEP 124
                                                                                                    VKLVESGGGLVKPGGSLRLSCAASGFIFSNSYMSWVRQTPEKRLEWVATISNSGYATHYP
SSEP 137
                                                  DSMKGRFTISRDNAQNTVLLOMTSLNSEDTAVYYCTR---
                                                                                                                             VQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASIT-SGGSTNYA 60
                                                                                                                                                                                                             480 AA; 51936 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 112
112 AA; 12243 MW;
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAB16829.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                    50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.5%; Score 354; DB 4;
61.3%; Pred. No. 7.8e-26;
tive 11; Mismatches 27
                                                                                                                                                        13;
                                                                                                                                                        Score 350.5; DB 11
Pred. No. 1e-24;
3; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24F1A45EC3B84788 CRC64;
                                                                                                                                                                                                             20B9234EEF2B41ED CRC64;
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                                                                                                                                                                                  DB 11;
                                                                                                                                                                                                                                                                                                                                                              databases
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                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --ARRRYALDYWGQGTLV 112
                                                                                                                                                                                   Length 480;
                                                    -GDYWYFDVWGAGTTVTV
                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                          Gaps
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                                                                                                        79
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N [1]

P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

(C STRAIN=FVB/N; TISSUE=Colon;

RL Strausberg R.;

RA Strausberg R.;

RA Strausberg R.;

RI Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

BR EMBL; BC049143; AAH49143.1; -.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003597; Ig.

DR InterPro; IPR003596; Ig_MHC.

DR InterPro; IPR003596; Ig_MC.

DR InterPro; IPR003596; Ig_MC.

DR InterPro; IPR003596; Ig_MC.

DR Pfam; PF00047; Ig; 3.

CARRET: SM004409; IG; 3.
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Matches 76
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InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1
SMART; SM00406; IGv; 1.
PR0SITE; P850835; IG LIKE; 1.
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01-JUN-2003
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
Mus musculus (Mouse).
Eukaryota, Merazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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HSSP; P01772; 2FB4.
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Mammalia; Eutheria;
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01-MAY-2000 (TrEMBLrel. 25, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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121 AA;
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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t; Pred. No. 2.3e-25;
12; Mismatches 29
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PROSITE; PS00290; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 487 AA; 53019 MW;
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                         118 VTVSSEP 124
                                                                  80 HYAESVKGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTRR--GYGDPNWYFDVWGAGTT
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SM00406; IGV; 1.
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Search completed: October 5, 2004, 08:13:46
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 New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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 Example 2; Page
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### ALIGNMENTS

A.

(first entry)

lipase; HPL;

#### Key Region Region Region Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control; body weight. WPI; 2001-572718/65. Bezemer S, (UNIL ) 14-MAR-2000; 2000EP-00200930 20-FEB-2001; 2001EP-00200703. 19-SEP-2001. EP1134231-A1 Lата вр UNILEVER NV. UNILEVER PLC. Van De Burg /note= /label= CDR2 /note= "Complementarity /label= CDR1 /note= "Complementarity determining region Location/Qualifiers note= "Complementarity determining region label= CDR3 .111 × De Haard JJW, determining region Tareilus

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   New antibody or its fragments for inhibiting human dietary enzymes,
                          WPI; 2001-572718/65
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Pred. No. 1.6e-50;
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Pred. No. 2.2e-37;
1; Mismatches 17;
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/note= "Complementarity determining region
                                                                                                                                                            note= "Complementarity
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80.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     HPL #19 from llama species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 532; DB 4;
Pred. No. 2.4e-37;
6; Mismatches 17
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Best Local :
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprisheavy chain variable domain derived from immunoglobulin naturally of light chains.
                                                                                                                                                                                                                                 HPL inhibiting
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                                                                                                                                                          Lama sp
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                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                antibody; camelid; anorectic; heavy chain variable domain; dietary enzyme inhibitor; medicament; human pancreatic lipa human gastric lipase; HGL; cosmetic control; body weight.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASITATGPPNYT
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                                                /note= "Complementarity
98. .110
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                                                                                                                                 Location/Qualifiers
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                                     label= CDR3
                                                                                                                                                                                                                                                                                                        peptide;
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76.3%;
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Pred. No. 1.3e-36;
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Best Local S
Matches 100
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                                                              Region
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                                                                                                                                                                                                                                                                             t; human pancreatic lipase; HPL;
control; body weight.
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Best Local Similarity
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Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                    Lama
                                                                                                                                    Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
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                                                                                                                                                                                                                                                   HPL inhibiting VHH fragment, HPL #30 from llama species.
                                                                                                                                                                                                                                                                                                                  10-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                              AAE10559 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEPKTPKPQP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAFGKERBLVARMSSDGTTSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGSTNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGSWNDYG--GQGTQVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEPKTPKPQP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                               (first entry)
   Location/Qualifiers 31. .35
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/label= CDR3
/note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                           peptide; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 508; DB 4;
Pred. No. 2.6e-35;
1; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . JJW,
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RESULT 8
ABG30620
ID ABG3
XX
ABG3
AC ABG3
XC
ABG3
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IDT 21-C
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IDT Immu
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IMM immu
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human baings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #30 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 130 AA
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Heavy chain variable domain; antibody; protein array; immunoglobulin; sticky phage-antibody; micro-panning; proteomic; mouse.
                                                                                                                                                ABG30620 standard;
                                                                                        21-OCT-2002
                                                         Immunoglobulin G specifc heavy chain variable domain antibody #3
                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                SSEPKTPKPQP 131
                                                                                                                                                                                                                                                                         DSVKGRETISRDNTLNTVYLOMNDLKPEDTGVYYMNADVRPYRTSRYL-EIWGQGTLVTV
                                                                                                                                                                                                                                                                                                                                                           QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGSTNYA
                                                                                                                                                                                                                                                                                                       DSLKGRFTISRDNAKNAVYLOMNNLKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTKVTV 120
                                                                                                                                                                                                                                                                                                                                  QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA
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                                                                                      (first entry)
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49. .64
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                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                           73.5%; Score 505.5; DB 4
74.8%; Pred. No. 4.2e-35;
tive 11; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110
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                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 130;
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                   aging; VHH; immune library;
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121 61 61

SSEPKTPKPQP 131

131

Matches

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QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGSTNYA

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Indels

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Gaps

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60 60

QVQLQESGGGLVQPGGSLRLSCAASKSIFGFGAVGWHRQAPGKQRELVARITYDSGTNYA

DSLKGRFTISRDNAKNAVYLOMNILKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTKVTV

120 120

DSVKGRFTISRDNAKUTVYLQMNSLKPEDTGVYYCNAETVRATTGRFITDLWGQGTTVTV

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chain variable domain antibodies or antibody fragments, obtainable from CC Camelidae. The method is useful for removing abundant proteins from an CC extract or sample which do not provide useful information on the condition of a cell or tissue in the extract or sample to be condition of a cell or tissue in the extract or sample to be conditions. Using a heavy-chain variable domain derived from an CC ell types, and identification of proteins that may be of importance in CC determining the altered properties of cells in disease, aging or other conditions. Using a heavy-chain variable domain derived from an CC immunoglobulin that is naturally devoid of light chains (VHH) in (I) provides a number of advantages, such as an improvement of CC post-translationally modified proteins. The incorporated plage numbers of method (II) that enables the simultaneous processing of large numbers of target antigens in a controlled way. The incorporated plage ELISA CC generates on-line information about the success or failure of a certain CC panning condition. This feature combined with the microtiter plate format allows the complete automation of the technology, based on computer-made decisions on the values of the phage-ELISA for continuation of a limited conditions can be tested, varying amounts of input-phages can be used decisions on the values of the technology, based on computer-made conditions on the values of the technology based on computer-made conditions on the values of the technology based on computer-made conditions can be tested, varying amounts of input-phages can be used conditions on the values of the technology based on computer plate in short conditions and immune libraries on large numbers of different target conditions needed for the generation of large panels of antibodies in short can be used an expectation of large panels of antibodies in short can be used an immune generation of arrays (proteomics). This can be used to the generation of arrays (proteomics). This can be decisions and the generation of larg
                      Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel protein array useful for detecting the presence of individual proteins in sample, comprises heavy-chain variable domain antibodie antibody fragments obtainable from Camelidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-DEC-2001; 2001WO-EP014471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNIL ) UNILEVER NV.
(UNIL ) UNILEVER PLC.
(UNIL ) HINDUSTAN LEVER LTD.
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                                                                                          Sequence 131 AA;
                        Similarity
73.4%; ilarity 74.8%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Landa I,
Score 505; DB 5; Pred. No. 4.7e-35; 6; Mismatches 27;
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                                                 Length 131;
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AAE10556
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Best Local Sim:
Matches 100;
                                                                                                                                                                                          The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #18 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                    New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                   Sequence 130 AA;
                                                                                                                                                                                                                                                                                                                               Example 2; Page 10; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAR-2000; 2000EP-00200930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPL inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNIL ) UNILEVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control; body weight.
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     61
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                                                                                                                          Similarity
                                                                           QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWERQAPGKQRELVASITSGGSTNYA
                         DSLKGRFTISRDNAKNAVYLQMNNLKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTKVTV 120
  DPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYYCNALIRRKFTSBY-NBYWGQGTQVTV
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van De Burg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLC.
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/label= CDR2
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note= "Complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
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                                                                                                                         73.0%;
                                                        /QAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPNYA
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                                                                                                            Score 502.5; I
Pred. No. 7.6e
7; Mismatches
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                                                                                                                         ; DB 4;
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                                                                                                             23;
                                                                                                             Indels
                                                                                                                                      Length 130;
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                                                                                                            Gaps
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1 QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGSTNYA 60

Matches 101;

Similarity

Conservative

7;

Mismatches

18;

5

Gaps

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RESULT 10
AAE05283
                                                      The present invention relates to a method for modifying a plant to CC produce an antibody or an active fragment or derivative, or a protein CC functional equivalent, in a cellular compartment comprises introducing a CC DNA sequence encoding a heavy chain immunoglobulin, where the DNA is CC linked to promoters and provided with an additional sequence encoding a cc peptide capable of targeting heavy chain immunoglobulin to a cellular CC compartment. The method is used for producing a heavy chain to a cellular CC immunoglobulin or an active fragment or derivative, or a protein that is CC introductionally equivalent for increasing the pathogen resistance in a plant CC or to modulate metabolism in a plant. Under some circumstances it may be CC desirable to retain the antibody product with the plant rather than cextracting and isolating the product. In particular, edible selected antigens may be used in a method of passively immunising an animal, CC present sequence is an anti-potato SBEII antibody (denoted Clone46) heavy CC chain variable domain (VH) attached to peptide linkers, myc and his6 tag. The potato SBEII is a starch branching enzyme also designated SBE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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 Query Match
Best Local
                                                    Sequence 152
                                                                                                                                                                                                                                                                                                                                                                                                                               Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 12; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frenken LGJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Solanum tuberosum. Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potato; heavy chain immunoglobulin; pathogen resistance, metabolism modulator; passive immunisation; heavy chain VH; anti-potato SBEII; starch branching enzyme; SBE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-potato SBEII (Clone46) VH region attached with myc and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE05283;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein; 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEPKTPKPQP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEPKTPKPOP
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72.9%;
77.1%;
 Score 501.5; DB 4
Pred, No. 1.1e-34;
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                  DB 4;
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                  Length
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                   152;
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맑 Ş B Š

116 121

SSEPKTPKPQP

126

61 61

SSEPKTPKPOP 131

DSLKGRFTISRDNAKNAVYLOMNNLKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTKVTV

120 60

DSVKGRFTISRDNAKNTVYLQMSSLKPEDTAVYYC----AAGNLLVKRPYWGQGTLVTV

QVQLQESGGGLVQAGGSLRLSCVASGNTFSIIAMAWYRQAPGKQREVVASINSIGSTNYA

human

AAE10567; AAE10567

standard;

peptide;

130

10-DEC-2001

(first HHY

inhibiting

fragment, entry)

HGL

#16 from llama

species.

lipase; VHH;

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ARBSULT 11
ARABIO 567
ID AABIO 567
ID IO-DE 577
ID IO-SI
                                                              The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #16 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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UNILEVER PLC
                                                                                                                                                                                                                                                                                                                                                                               Page 14; 37pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van De Burg
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/note= "Complementarity
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Query

Match

72

68

Score

499 5

DB

4; Length 130;

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #4 from

Example

4

13,

37pp;

English.

Sequence

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ARESULT 12
AREJUS 11
ID AAE10
XX
XX AAE10
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AAE10
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IDT 10-DE
XX
Llama
XX
Llama
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KW Hounar
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FT Regic
FT R
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Matches
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                                                                                                                                                                                                                                                                                                                                                                    Bezemer
                                                                                                                                                                                                                                                                                                                                                                                                         (UNIL )
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                                                                                                                                                                                                                                                                                                                                                                    Van
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B; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                      Haard
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llama

(camelid) species

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RESULT 13
AABOSZ88
ID AABOS
XX AABOS
XX AABOS
XX AABOS
XX DATE:
XX Potat
YOU PR O8-DE
XX 17-DE
XX 17-DE
XX (UNII
PA (UNI
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Best Local
The present invention relates to a method for modifying a plant to produce an antibody or an active fragment or derivative, or a protein functional equivalent, in a cellular compartment comprises introducing a DNA sequence encoding a heavy chain immunoglobulin, where the DNA is linked to promoters and provided with an additional sequence encoding a peptide capable of targeting heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain immunoglobulin or an active fragment or derivative, or a protein that is functionally equivalent for increasing the pathogen resistance in a plant or to modulate metabolism in a plant. Under some circumstances it may be desirable to retain the antibody product with the plant rather than
                                                                                                                                                                                                                                                                                                                                                                                           Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequenc encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Solanum tuberosum. Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potato; heavy chain immunoglobulin; pathogen resistance; metabolism modulator; passive immunisation; heavy chain variable VH; anti-potato SBEII; starch branching enzyme; SBE A.
                                                                                                                                                                                                                                                                                                                                         Example 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD10059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Frenken LGJ, Van Der
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-2001
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UNILEVER NV.
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                                                                                                                                                                                                                                                                                                                                         Fig 28; 8lpp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Logt CPE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 498;
Pred. No. 1
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                                                                                    Bezemer S,
                                                                                                                                          14-MAR-2000; 2000EP-00200930
                                                                                                                                                             20-FEB-2001; 2001EP-00200703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          extracting and isolating the product. In particular, edible selected antigens may be used in a method of passively immunising an animal, preferably human, against the antigen, e.g., pathogenic organisms. The present sequence is an anti-potato SBEII antibody (denoted Clone68) heavy chain variable domain (VH) attached to peptide linkers, myc and his6 tag. The potato SBEII is a starch branching enzyme also designated SBE A
                                                                                                                                                                                   19-SEP-2001
                                                                                                                                                                                                         EP1134231-A1
                                                                                                                                                                                                                                                  Region
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                                                                                                                                                                                                                                                                                                                                                                    Llama antibody;
human dietary er
food; human gast
                                                                                                                                                                                                                                                                                                                                                                                                             HGL inhibiting VHH fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE10563
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                                                                                                          UNILEVER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGSTNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASEPKTPKPQP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEPKTPKPQP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSLKGRFTISRDNAKNAVYLOMNNLKPEDTAVYYCNAHITPAGSSNYVYGYWGHGTKVTV
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                                                                                   Van De Burg
                                                                                                                                                                                                                                                                                                                                                                   ody; camelid; anorectic; heavy chain variable domain;
ry enzyme inhibitor; medicament; human pancreatic lip;
gastric lipase; HGL; cosmetic control; body weight.
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                                                                                                          PLC.
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                           note= "Complementarity determining
                                                                                                                                                                                                                                                                                        label= CDR1
note= "Complementarity determining
                                                                                                                                                                                                                                                           note= "Complementarity determining
                                                                                                                                                                                                                                                                     label= CDR2
                                                                                                                                                                                                                                      label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide;
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                                                                                    JJW,
                                                                                                                                                                                                                                                                                                                                                                                                            from llama species.
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                                                                                                                                                                                                                                                                                                                                                                             lipase; HPL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Example 4;

Page 13; 37pp; English.

# X 6 6 6 6 6 6 6 6 6 8 8 8 8

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #9 from lama (camelid) species

Query Match Best Local S

Sequence 124 AA;

Matches

Similarity 97; Conserv

Conservative

72.2%;

Score 496.5; DB 4; Pred. No. 2.3e-34; 0; Mismatches 17;

DB 4;

Length 124; Indels

7;

Gaps

2

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AABSULT 15
AAABSO64
ID AABSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGL inhibiting VHH fragment, HGL #10 from llama species
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                                                                                                                                                                                                                                                                                                           20-FEB-2001;
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                                WPI; 2001-572718/65
                                                                                          Bezemer S,
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                                                                                          Van De Burg
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/note= "Complementarity determining region
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/note= "Complementarity determining region 1"
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FFFFXSXSSSSSSSSSXX
                                                                                                                                                     New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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Example 4; Page 13; 37pp; English.

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HFL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #10 from The present peptide sequence llama (camelid) species

Sequence 129 A

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Matches 97
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            120 VSSEPKTPKPQP 131
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97; Conserv
                                                                           DSLKGRFTISRDNAKNAVYLOMNNIKPEDTAVYYCNAHITPAGSSNY-VYGYWGHGTKVT 119
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                                                                                                                   QVQLQESGGGLVQAGGSLRLSCAASGSISSINVMGWFRQAPGKQRELVASITSGGSTNYA`60
                                                                                                                                                        Conservative
                                                                                                                                                                   71.8%;
 129
                                                                                                                                                       Score 494; DB 4;
Pred. No. 3.9e-34;
1; Mismatches 20
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  51.2
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  S20782
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  A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
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347	347.5	347.5	347.5	347.5	348	348.5	348.5	349	349	349	349.5	350	350	350	350.5
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A;Map position: 1432.33-14322.33
C;Superfamily: immunoglobulin v region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Knight, G.B.; Agnello, V.; Bonagura, V.; Barnes, J.L.; Panka, D.J.; Zhang, J. Exp. Med. 178, 1903-1911, 1993
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            );Species: Homo sapiens (man)
;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
;Accession: S31114
;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.P.
;Urr. J. Immunol. 22, 247-251, 1992
;Title: Restricted utilization of germ-line V(H)3 genes and short diverse tyReference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Status: preliminary; translated
;Molecule type: mRNA
;Residues: 1-121 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reference number: I55673; MUID:94065558; PMID:8245772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g heavy chain - human (fragment)
;Species: Homo sapiens (man)
;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
Status:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:M87268; NID:g186197;
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                                                                                         Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.;
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Pred. No. 3.8e-25;
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Pred. No. 3.7e-25;
0; Mismatches 28
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Ig heavy chain precursor - human (fragment)
(;Species: Homo sapiens (man)
(;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996
(;Accession: S05271; S04602
R;Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A;Reference number: S05270
A;Accession: S05271
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
S31108
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A;Title: Restricted utilization of germ-line V(H)3 genes A;Reference number: S31104; MUID:92111633; PMID:1730252 A;Accession: S31108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain - human
[;Species: Home sapiens (man)
[;Species: Home sapiens (man)
[;Date: 02-Dec-193 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
[;Accession: S31108
[;Racaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.R.
[;Raaphorst] [;Raapho
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A;Residues: 1-123 <RNA>
A;Residues: 1-123 <RNA>
A;Cross-references: EMBL:X62963
A;Cross-references: EMBL:X62963
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin references: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                     RESULT
S05271
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-119 < RAA>
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Best Local
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Best Local Similarity
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Pred. No. 5.5e
11; Mismatches
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A;Residues: 1-160 <KIS1>
A;Cross-references: EMBL:X14584
R;Kishimoto, T; Okajima, H; Okur
Nucleic Acids Res. 17, 4385, 1989
RESULT 8
D36005
Ig heavy
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A;Title: Restricted utilization of germ-line V(H)3 genes A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Recession: S31109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiene (man)
C;Date: 02-Dec-1993 #sequence revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31109
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.I.
Eur. J. Immunol. 22, 247-251, 1992
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A; Residues: 1-144 <KIS2>
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                                                                                                                 TVSS
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Pred. No. 9.2e-25;
                                                                                                                                                                                                                                                                                                                                                                                               Score 362; DB 2;
Pred. No. 2.2e-24;
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                                                                                                                                                                                                    -TYYFDYWGQGTLV 113
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RESULT 9
$46391
Ig heavy chain V region - human
C:Spēcies: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
C;Accession: $46391
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on A;Paference number: $46390; MUID:94254092; PMID:8196048
                                                                                                                                                                                                                                                                                                 A;Reference number: S46391
A;Accession: S46391
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <FIG-
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A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IVM>
                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z31687; NID:g509784; PIDN:CAA83492.1; C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>.
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A,Residues: 1-119 <SCH>
A,Cross-references: GB:M34024
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                                                                 ADPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYYCNALIRRKFTSEYNEYWGQGTQVTV 119
                                                                                                                                QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPN-Y
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   SS 121
                                     ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC--
                                                                                                    QVNIRESGGGIVQPGGSIRISCSASGFTFSSYAMHWVRQAPGKGLEWVAVIWYDGSNKYY 60
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                                                                                                                                                                    Score 360.5; DB 2;
Pred. No. 2.8e-24;
8; Mismatches 28;
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Pred. No. 2.2e-24;
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A; Residues: 1-119 < SCH >
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C;Species: Homo sapiens (man)
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31588
C;Accession: S31588
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
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RESULT 12
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                                                                                                                                                                                                                       1 QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATES-GSPNY
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                                                   SS 119
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Pred. No. 4.8e-24;
1; Mismatches 23
                                                                                                                                                                                                                                                                          Score 357;
Pred. No. (
                                                                                                                                                                                                                                                                        6e-24;
                                                                                                                                                                                                                                                                                         DB 2;
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A;Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IM%>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31686
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A;Cross-references: EMBL:Z18317
C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotestramer; immunoglobulin E;15-98/Domain: immunoglobulin homology <IMM>
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A; Accession: 830531
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A; Accession: S31686
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79; Conserv
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                                                                                 SDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC---AKCPFAGGSPSFDYWGQGTLV
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62.7%;
                                                                                                                                                                                                                                                                   52.1%; Score 357; DB 2; 63.7%; Pred. No. 7.1e-24;
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RESULT 14 S31666 Ig heavy chain V region -

human (fragment)

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C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31120
C;Accession: S31120
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31120
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X62972
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-138 <CUI>
A;Residues: 1-138 <CUI>
C;Coss-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
A;Accession: S31666
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Best Local Similarity
Matches 79; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA A;Residues: 1-114 <RAA>
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ALIGNMENTS

#### GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:anttgen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like. InterPro; IPR007110; Ig-like. InterPro; IPR00396; Ig\_v. Pfam; PF00047; Ig; 1. SMART; SM00406; IGv; 1. SMART; SM00406; IGv; 1. PROSITT; PS50835; IG\_LIKE; 1. Immunoglobulin V region; 3D-structure; Py DOMAIN 1 112 IG\_LIKE. SEQUENCE, AND DISULFIDE BONDS. MEDLINE=83289131; PubMed=6884994; Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I,"; Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983). X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS). MEDLINE=81072295; PubMed=7441755; Marquart M., Deisenhofer J., Huber R., Palm W.; "Crystallographic refinement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment and 1.0-A resolution."; J. Mol. Biol. 141:369-391(1980). -!- SIMILARITY: Contains PIR; A02055; G1HUKL. PDB; 2FB4; 12-JUL-89. PDB; 2IG2; 12-JUL-89. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Ig heavy chain V-III region KOL. STANDARD; Н 3D-structure; Pyrrolidone carboxylic immunoglobulin-like domain PYRROLIDONE CARBOXYLIC ACID 126 A at . Þ

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Matches
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Best Local :
  PIR; A91668; GHUNI.
HSSP; P01772; 2F84.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0005823; F:antigen binding; NAS.
G0; G0:0008955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
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NON TER
SEQUENCE
                                                                                                                                                                                                                               MEDIINE-77070267; PubMed=1002129; Dreker L., Schwarz J., Reichel W., Hilschmann N.; Dreker L., Schwarz J., Reichel W., Hilschmann N.; "Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."; Hoppe-Seyler's Z. Physiol. Chem. 357:L515-L540(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HELIX
STRAND
STRAND
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"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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STRAND
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Mammalia; Eutheria;
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21-JUL-1986
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                           DISULFIDE BOND
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TURN
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(Rel.
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Primates;
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Pred. No. 6.5e
13; Mismatches
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RESULT 3
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Best Local
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P01765;
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MOD RES
DISULFID
NON TER
SEQUENCE
                                                                                                                                                        SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region.

DOMATN
                                                                                                                                                                                                           GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NJ
GO; GO:0006955; P:immune response; NJ
InterPro; IPRO07110; Ig-1ike.
InterPro; IPRO03596; Ig_v.
                                                                                                                                                                                                                                                                                                                                         "Immunoglobulin structure and genetics. regions of a mu and a gamma2 chain.";
J. Biol. Chem. 252:7192-7199(1977)
-i- MISCELLANEOUS: THE SEQUENCES OF THE OF IGM AND IGG2 ISOLATED FROM A SING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-UUL-1986 (Rel. 01, Last sequence up
10-CCT-2003 (Rel. 42, Last annotation
Ig heavy chair V-III region TIL.
                                                                                                                                                     DOMAIN
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SMART; SM00406; IGV;
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HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                        Wang A.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=78005528; PubMed=409716;
Wang A.-C., Wang I.Y., Fudenberg
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                                                                                                                                                                                                                                                                                                                              GAMMOPATHY ARE IDENTICAL.
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                                                                         . Similarity 72; Conserv
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ADPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYYCNALIRRKFTSEYNEYWGQGTQVTV 119
                                              QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATE-SGSPNY
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                         EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYVMSWVRQAPGKGLZWVGAIZGLSVSZSY
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119
119 AA;
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                                                                          Conservative
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1 112 IG-LIKE.
1 1 PYRROLIDONE CARBOXYLIC ACID
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12356 MW;
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13242 MW;
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                                                                        Score 329; DB
Pred. No. 1.1e
.4; Mismatches
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Pred. No. 2.5e
12; Mismatches
                                                                                                                                                    IG-LIKE
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L.1e-24;
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RESULT 5
HY3G HUMAN
ID HY3G HUMAN
AC P01768;
DT 21-JUL-1986
DT 21-JUL-1986
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HV3T_HUMAN
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Best Local S
Matches 72
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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P01781;
21-JUL-1986
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SEQUENCE
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Submitted (JUN-1975) to the
Submitted (JUN-1975) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MACROGLOBULIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like
PIR; A02064; M3HUGL.
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Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
"The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), II: the amino acid sequence of the H-chain (mutype), subgroup H III. Architecture of the complete IgM-molecule.";
Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region GAL.
Homo sapiens (Human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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116 AA;
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Pred. No. 1.6e
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L.6e-24;
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ID HV01_C
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Best Local
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11 heavy chain V region GOM.
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:00055/6; C:extracellular; NAS.
GO; GO:0003523; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-1like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; I.
SMART; SM00406; IGv; I.
PROSITE; PS50835; IG_LIKE; 1.
Inmunoglobulin V region; Pyrrolidone carboxylic acid.
DOWATM:
                      Wasserman R.L., Capra J.D.;
"Primary structure of the variable regions of two canine immunoglobulin heavy chains.",
Biochemistry 16:3160-3168(1977).
-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02067; AVDGGM.
HSSP; P01772; 2FB4.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                MEDLINE=77242268; PubMed=407924; Wasserman R.L., Capra J.D.;
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11; Mismatches
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Best Local :
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InterPro; IPA.
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PMART; SM00406; IGV; 1.
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NON TER 114 114
SEQUENCE 114 AA; 12430 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-78137069; PubMed=416441;
Torano A., Putnam F.W.;
Torano A., Putnam F.W.;
"Complete amino acid sequence of the alpha 2 heavy chain of a human IgA2 immunoglobulin of the A2m (2) allotype.";
Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
-!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A02050; A2HUBU.
HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986
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21-JUL-1986 (Rel. 01, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region BUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO:0005576; C:extracellular; NAS. GO:0003823; F:antigen binding; NAS GO:0006955; P:immune response; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
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                  DPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYYC--NALIRRKFTSEYNEYWGQGTQVT
                                                                                                                                                                      QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPNYA
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                                                                                                                              EVŐLVETGGGLI ÓPGGSLRLSCAÁSGFTVSBHSMSWVRÓAPGKALZWVSAI YRGGTTYYA
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115
115 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                  12379 MW; 208876A7DF52DCF4 CRC64;
                                                                                                                                                                                                                                                                                         47.3%;
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Pred. No. 3.4e-24;
7; Mismatches 27;
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Pred. No. 3e-24;
1; Mismatches
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on update)
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Best Local
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SMART; SM00406; IGV; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 1.

Immunoglobulin V region; Pyrrolidone carboxylic acid.

Immunoglobulin V region; IG-LIKE.

DOMAIN

1 108 PYRROLIDONE CARBOXYLIC ACID.
                                                                         HV40 MOUSE
P01810;
         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Ig heavy chain V region J539.
Mus musculus (Mouse)
                                                                                                   MOUSE
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NON_TER
SEQUENCE
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P01762;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence up

10-OCT-2003 (Rel. 42, Last annotation

Ig heavy chain V-III region TRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NP
GO; GO:0006955; P:immune response; NP
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tr II. The amino acid sequence of the H-chair, alpha-type, subgroup structure of the complete IgA-molecule."
Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kratzin H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE (MYELOMA PROTEIN TRO).
MEDLINE=76023781; PubMed=809331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - SIMILARITY:
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                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                    SSA
                                                                                                                                                                            VSS 121
                                                                                                                                                                                                                             YADPVKGRFTISRDNGKLTVYLOMNSLKPEDTAVYYCNALIRRKFTSEYNEYWGQGTQVT 118
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122 AA;
                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contains 1 immunoglobulin-like domain
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122
; 13472 MW;
Chordata;
                                                                                                                                                                                                      46.5%;
55.3%;
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                                                                                                                                                                                                                                                                                                      Score 318.5; DB 1
Pred. No. 1.2e-23;
9; Mismatches 33
 Craniata;
                                                                                       PRT;
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on update)
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  Vertebrata;
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  Euteleostomi;
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RESULT 10
HV3J_HUMAN
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Best Local S
Matches 67
HUMAN
-HV3J HUMAN
P01771;
21'-JUL-1986
21-JUL-1986
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STRAND 3
STRAND 10
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PRELIMINARY SEQUENCE.

MEDLINE=79223895; PubMed=111245;

Rao D.N., Rudikoff S., Krutzsch H., Potter M.;

Rao D.N., Rudikoff S., Krutzsch H., Potter M.;

"Structural evidence for independent joining re;

immunoglobulin heavy chains from anti-galactan its potential role in generating diversity in complementarity-determining regions.";

Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979)
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NCBI TaxID=10090;
[1]
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PDB; 2FBJ; 15-OCT-90.
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InterPro; IPR003596; Ig_v.
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67; Conserv
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Pred. No. 1.5e-23;
7; Mismatches 34;
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Pyrrolidone carboxylic ac:
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IG-LIKE.
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NON_TER
SEQUENCE
                                                                                                             HV3C_HUMAN STANDARD; PRT; 117 AA.

P01764;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region VH26 precursor.
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A02054; G1HUHL.
HSSP; P01772; 2FB4.
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MEDLINE-79124695; PubMed=420800;
MEDLINE-79124695; PubMed=420800;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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10; Mismatches
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21-JUL-1986
21-JUL-1986
10-OCT-2003
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=80020921; PubMed=114209;
Steiner L.A., Garcia Pardo A., Margolies M.N.;
"Amino acid sequence of the heavy-chain variable
crystallizable human myeloma protein Dob.";
Biochemistry 18:4068-4080(1979).
       -!- SIMILARITY: Contains 1 immunoglobul PIR; A90431, G1HUDB.
HSSP; P01772; 2FB4.
G0; G0:00005576; C:extracellular; NAS.
G0; G0:0001823; F:antigen binding; NAS.
G0; G0:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                            Biochemistry 18:4054-4067(1979).
-!- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELI
HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY
                                                                                                                                                                                                                                                                                                                                                                         CRYSTALLIZATION.
MEDLINE=80020920; PubMed=114208;
Steiner L.A., Lopes A.D.;
"The crystallizable human myelom
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EMBL; M35415; AAA58735.1; -.
PIR; A02047; H3HU26.
PDB; 1HOU; 23-DEC-99.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2003 (Rel. 42, Last annot Ig heavy chain V-III region DOB. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                       deletion."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0005576; C:extracellular; NAS
GO:0003823; F:antigen binding; NJ
GO:0006955; P:immune response; NJ
                                                                                                                                                                                                               DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00047; ig; 1.; SM00406; IGV; 1.
TE; PS50835; IG_LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:5545; IGHV@.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVOLLESGEGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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V region; Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
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117
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                                                                                                                                                                                                                                                                                                                                                                                 human myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12582 MW;
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                                                                                                                                                                           immunoglobulin-like
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Pred. No. 1.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .8e-23
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                                                                                                                                                                                                                                                   CHAIN
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                                Query Match
Best Local S
Matches 70
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Best Local S
Matches 71
                                                                              CARBOHYD
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986
21-JUL-1986
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                 MOD_RES
                                                                                                                                                                                                                                                                             SEQUENCE (MYELOMA PROTEIN BUR).

MEDIINE=79151016; PubMed=107164;

Putnam F.W., Liu Y.-S.V., Low T.L.K.;

"Primary structure of a human IgAl immunoglobulin.

"Brimary structure of a human IgAl immunoglobulin.

"IgAl protease, digestion, Fab and Fc fragments, and amino acid sequence of the alpha 1 heavy chain.";

J. Biol. Chem. 254:2865-2874(1979).

J. BIOL. Chem. 254:2865-2874(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
SEQUENCE
                                                                                                                                                                                                                      GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V-III region BUR. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                      Immunoglobulin
DOMAIN
                                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                       PIR; A02056; A1HUBR.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV3L_HUMAN
P01773;
                                                                                                                                       PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Glyc
DOMAIN 1 112
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'fam; PF0004', '45'; 1.

MART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE;

PROSITE; PS50835; IG LIKE;

Immunoglobulin V region.
                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                             Similarity
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QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTWAWHRQAPGKERELVASATESGSPN-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSS 121
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119
119
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120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 01, Last sequence update)
(Rel. 42, Last annotation updat
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                               AA;
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Primates;
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28
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57.7%;
                                           45.7%;
                                                                                12981 MW;
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                                                                                                                                        Glycoprotein; Pyrrolidone carboxylic acid. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                 Score 313; DB
Pred. No. 4e-2
L2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 313.5;
Pred. No. 3.
                                                                                                     N-LINKED (GLCNAC. . .).
                                                                                                                              PYRROLIDONE CARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                               12A709A75344D024 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                            4e-23;
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                                                         Length 119;
                                  Indels
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                                  Gaps
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RESULT 14
HV3E_HUMAI
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   SSEPPPRE
                                                                                                                                                                                                                                                               RESULT 15
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Best Local S
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003823; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR00396; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparative studies on monotypic IgM lambda and IgG kappa from an individual patient. III. The complete amino acid sequence of the VH region of the IgM paraprotein.";
Immunochemistry 13:995-99(1976).
ITHE WISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
To heavy chain V-III region BRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                             HV3B HUMAN STANDARD; PRT; 1

P01763;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence up

10-OCT-2003 (Rel. 42, Last annotation

19 heavy chain V-III region WEA.
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PIR; A02049; M3HUBW.
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Homo sapiens (Human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                           Homo sapiens (Human)
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120 AA;
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InterPro; IPR003596; Ig_v.
Pfam; PR00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN 1 112 IG-LIKE.
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(Goni F., Frangione B.;

"Amino acid sequence of the Fv region of a human monoclonal IgM

"Amino acid sequence of the Fv region of a human monoclonal IgM

(protein wRA) with antibody activity against 3,4-pyruvylated

galactose in Klebsiella polysaccharides K30 and K33.";

proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

--- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY

--- AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS GO; GO:0006955; P:immune response; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A02046; M3HUWE. HSSP; P01772; 2FB4.
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MEDLINE=83273707; PubMed=6410398;
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Pred. No. 4.
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PYRROLIDONE CARBOXYLIC ACID
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Copyright (c) 1993 - 2004 Compugen Ltd.
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096k68 homo sapien
Q9u191 homo sapien
Q901207 mus musculu
Q9u184 homo sapien
Q99k84 mus musculu
Q91wp5 mus musculu
Q9u193 homo sapien
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Q8n5k4
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Matches 80
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Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pi
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TISSUE=B-cell;
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Q924q6	Q924q9	Q96qs0 homo	Q924p9	Q991a6	Q8k172	Q9ul92 homo	Q924q1 mus	Q91x92 mus	Q921a6	Q9ugp3 ]	Q7z351 k	Q9n0w4 c	Q9n0w6 oryctolagus	Q9ul87 homo	Q7tmk4 mus	Q7z5wl homo	Q8vea0 mus	Q8n4y9 homo	Q8ncl6 homo	Q8r3v9 mus	03Vb60	Q9ulb6 homo	Q91xe1 mus	Q80zi7 mus	Q9y509 homo	Q9rla4 mus	Q920e7 mu	Q91z05 mus

## ALIGNMENTS

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Opensy

ID Q96BB9

ID Q96BB9

AC Q96BB9

AC Q96BB9

DT Q1-DEC-2001 (TERMELIFEL 19, Created)
DT Q1-DEC-2001 (TERMELIFEL 19, Last sequence update)
DT Q1-DEC-2001 (TERMELIFEL 25, Last annotation update)
DE Hypothetical protein.

OS Home sapiens (Human).

OS NCB1_TaxID=9606;

RN [1]

RA STRUBSD-9606;
RN [1]

RA STR
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01-MAR-2002
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50818.
                     Submitted (JAN-2002)
                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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MEDLINE=98277139; PubMed=9614934;
MEX., Liu B., Van der Merwe P.L.,
                                       Strausberg R.;
                                                                 TISSUE=Tons
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HSSP; P01772; 2FB4.
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EMBL; AF035042; AAD56278.1; -.
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Mammalia; Eutheria; Primates;
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01-MAY-2000 (TrEMBLrel. 25, Last annotation update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Myosin-reactive autoantibodies
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118 AA;
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12872 MW; B4D1A5944B2D5CCA CRC64;
                                                                                                                                                   Chordata;
Primates;
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                  the EMBL/GenBank/DDBJ databases
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Last annotation updat
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Pred. No. 5.5e-29;
3; Mismatches 30
                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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SEQUENCE
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wu X., Liu B., Van Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003596; Pfam; PF00047; ig; 4. SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Myosin-reactive autoantibodies in rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                    nterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR007110;
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                                                                                                          Similarity
76; Conserv
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ADSVKGRFTISRDNSKNSLYLOMNSLRAEDTALYYC---AKGKVTTIYDRFDIWGQGTMV
                                     ADPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYYCNALIRRKFTSEYNEY--WGQGTQV
                                                                                       EVOLVESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGGSTYY
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121 AA;
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573 AA; 6
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                                                                                                                                                                                                                                                                   13154 MW; 2F045CCFA5D50736 CRC64;
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Ig_v.
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Pred. No. 2.2e
10; Mismatches
                                                                                                                                                                                            Score 351; DB 4;
Pred. No. 3.4e-28;
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                                                                                                                                                                           Mismatches
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.2e-27;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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MEDLINE=98277139; PubMed=9614934;
MUX., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06TD60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF035024; AAD
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
Strauberg R.;
Strauberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ
EMBL; BC032249; AAH32249.1; -.
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                SEQUENCE FROM N.A. TISSUE=Blood;
                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8N5K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nterPro; IPR007110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYC-----AKDLN-YWGQGTLVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYYCNALIRRKFTSEYNEYWGQGTQVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113
113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
12437 MW; ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 349; DB 4; Length 113; Pred. No. 4.9e-28; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
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Best Local S
Matches 79
                                                                                                                                                                          Matches
                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 4.

SMART; SM00409; IG; 4.

SMART; SM00407; IGC1; 2.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS508290; IG_MHC; 1.
                                                                                                                                                                                                                                                                    NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9UL88 PRELIMINARY; PRT; 131 AA.

Q9UL88;

01-MAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-CCT-2003 (TrEMBLrel. 25, Last annotation update)

Myosin-reactive immunoglobulin heavy chain variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wu X., Liu B., Van Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S21205; S21205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF035026; AAD56262.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunol. Immunopathol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79;
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                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTOVIVSS-EPKTPKPOP
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NYADPVKGRETISRDNGKLTVYLQMNSLKPEDTAVYYCNALI-----
                                                                                                                   QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVA---SATESGSP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTVTVSSASPTSPKVFP
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                                                                          50.3%;
milarity 57.2%;
Conservative 14
                                                                                                                                                                                                                                                                      131
131 AA;
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499 AA; 53376 MW;
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                         14142 MW;
                                                                                                                                                                          50.1%; Score 343; DB 4;
57.4%; Pred. No. 2.5e-27;
tive 10; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Merwe
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                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 344.5; DB 4
Pred. No. 1.1e-26;
4; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                         96E7D668E375DEA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berney
                                                                                                                                                                                                                        Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                 --- RRKFTS 105
                                                                                                                                                                            Gaps
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RESULT 9

OBWUK1

ID WWU

AC Q8WU

DT 01-W

DT 01-W

DT 01-W

OC Buk

OC Buk

OC Mam

OX NCB

RN [1]

RN [1]

RR EM

DR EM

DR EM

DR EM

DR III

DR III

DR III

DR PJ

DR PJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
Q9HCC1
ID Q9HCC1
AC Q9HCC2
AC Q9HCC2
AC Q9HCC2
DT 01-M
DT 01-
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Best Local S
Matches 72
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InterPro; IPR003596; Ig v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG LIKE; 1.
NON TER.
1 1 11
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020240; AAH20240.1; -.
PIR; PL0120; PL0120.
PIR; S15590; S15590.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "An antibody fragment2A3 specific for native lysozyme :Isolaion human synthetic phage display library and characterization."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB049915; BAB16829.1; -.

INSEP; P01772, 2FB4.
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01-MAR-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8WUK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8WUK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Kikuchi M., Takeda C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single chain Fv (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                   FISSUE=Tonsil;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQLVESGGGVVRPGGSLRISCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADSVXGRETISRDNAKNSLYLQMNSLRAEDTAVYYC---ARRRYAL---DYWGQGTLV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYYCNALIRRKFTSEYNEYWGQGTQV 117
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112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Primates;
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Last sequence update)
Last annotation update)
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; l
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESULT 10
Q96K68
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Best Local S
Matches 79
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Isogai T., Ota T., Hayashi K., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamata Y., Nagahari K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 494 AA; 53088 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
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Mammalia; Eutheria; Primates;
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PROSITE; PSS0835; IG_IKE; 5.
PROSITE; PSS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67296 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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TQVTVSS-EPKTPKPQP 130
                                                                                         RDSVKGRFTISRDNAKNSLYLOMNSLRVDDTAVYYCARDSCNGAICYGFSP-----WGQG
                                                                                                                                              ADPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYY-----CNALIRRKFTSEYNEYWGQG
                                                                                                                                                                                                      EVQLVESGGGLVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGKGLEWVSSISSRSDYIYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                           53088 MW;
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                                                                                                                                                                                                                                                                                                                      Score 339; DB Pred. No. 3.9e. 12; Mismatches
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Last annotation update)
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Pred. No. 3.6e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           9A1D7AEB5AEE4C0E CRC64;
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                                                                                                                                                                                                                                                                                                                                                        DB 4;
1.9e-26;
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01-MAY-2000
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Strausberg R.;
Straus
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01-MAY-2000 (TYEMBLYE). 13, Last sequence update)
01-CCT-2003 (TYEMBLYE). 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Mammalia, Eutheria, Rodentia, NCBI_TaxID=10090;
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Q91Z07; TrEMBLrel 19;
01-DEC-2001 (TrEMBLrel 19;
01-DEC-2003 (TrEMBLrel 25;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; 1.
SPROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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62.0%; Pred. No. 6.2e-27;
bive 12; Mismatches 29
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Sciurognathi;
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InterPro; IPR003596; Ig-v.
Pfam; PE00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NOW TEP
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SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Tin B., Van der Merwe P.L.,
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Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae;
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PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC;
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SMART; SM00406; IGv;
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SEQUENCE 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myosin-reactive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF035030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Myosin-reactive autoantibodies in rheumatic carditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSP; P01772; 2FB4.
InterPro; IPR007110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116
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         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunol. Immunopathol. 8 AF035030; AAD56266.1; -.
                                                       61
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                                                                                                                                                                                   1 QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPN-Y
                                                                                                                                                                                                                                     74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 53.5
58; Conservative
                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPNYA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITVSSE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPYKGRFTISRDNGKLTVYLOMNSLKPEDTAVYYCNALIRRK-----FTSEYNEYWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVHLVBSGGGLVKPGGSLKLSCVVSGFSFTSYDMSWVRQTPERRLEWVAAITSGGNTYYP
                                                                                          ADPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYYCNALIRRKFTSEYNEYWGQGTQVTV
                                                                                                                                          EVOLVESGGGVVÓPGRSLRLSCAASRFTFSNÝGMHWVRÓAPGKGLEWVÁAISNDGSNKFÝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVTVSSE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNVKGRFTVSRDNAKYTLYLOMSSLKSEDTAMYYC---VRPEIPIYYYSGSYFDSWGOGT
         SS 121
                                                    ADSVKGRFTIFRDNSKNMMDLOMNSLRAEDTAVYYCAKDERGRLVGTYFDYWGQGTLVTV
                                                                                                                                                                                                                                                                                                                         122
122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al protein
486 AA; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TYEMBLrel. 13, Created)
(TYEMBLrel. 13, Last sequence update)
(TYEMBLrel. 25, Last annotation update)
ive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                              13579 MW;
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                                                                                                                                                                                                                                                           Score 334.5; DB 4
Pred. No. 1.7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87:184-192(1998)
                                                                                                                                                                                                                                                                                                                              36054D41366545B8 CRC64;
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                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kalis
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.8e-26;
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                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                        38;
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                                                                                                                                                                                                                                                                              Length 122;
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RESULT 15
Q91WP5
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Q99KA4
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Best Local S
Matches 73
                                                                              TISSUE=Colon;
Strausberg R.;
Sthmitted (SEE-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013656; AAH13656.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-V.
R Pfam; PF00047; ig; 4.
R PROSITE; PS50835; IG LIKE; 4.
R PROSITE; PS50835; IG LIKE; 4.
R PROSITE; PS50835; IG LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003056; Ig_v.
Pfam; PF000407; 1d; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS00335; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 487 AA; 52554 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001
01-JUN-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91WP5;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004786; AAH04786.1; -.
HSSP; P01810; 2FBJ.
                                               Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata,
Mammalia, Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q91WP5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q99KA4
                                                                                                                                                                                                                                                                                                                                                                                                                                               VCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 EVQLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVATISDGGSYTYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGS-PNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADPVKGRFTISRDNGKLTVYLOMNSLKPEDTAVYYCNALIRRKFTSEYN-----EYWGQG
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                                               al protein.
479 AA; 5
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                               51603 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52554 MW; 7DC8E96DB333077B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.7%; Score 333.5; DB 11; Length 57.0%; Pred. No. 1.4e-25; tive 13; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                               ECB2D0877748584F CRC64;
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Best Local Similarity 55.6%
Matches 69; Conservative
133 SSEP 136
                           120 SSEP 123
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                                                                                                                20 EVQLVESGGGLVKPGGSLKVSCAASGLTFSNYAMSWVRQSPEKRLEWVAAINSNGGNTYY
                                                        80 SDTMKGRFTISRDNAKSTLYLQMSSLRSEDTAFYYC-----VRGGYFDVWGAGTAVTV 132
                                                                                                                                            1 QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASA-TESGSPNY
                                                                         ADPVKGRFTISRDNGKLTVYLOMNSLKPEDTAVYYCNALIRRKFTSEYNEYWGQGTQVTV
                                                                                                                                                                                     48.3%;
                                                                                                                                                                         16; Mismatches
                                                                                                                                                                    Score 331; DB 11; L
Pred. No. 2.5e-25;
Mismatches 31;
                                                                                                                                                                                                  Length 479;
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Search completed: October 5, 2004, 08:13:47 Job time: 69.8117 secs

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Perfect score:
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                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Query
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                                                                                                                                                                                                                                                                                          A_Geneseq_29Jan04:*
L: geneseqp1980s:*
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Copyright (c) 1993 - 2004 Compugen Ltd
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geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
                                                                                                                                                      geneseqp2004s:*
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geneseqp1990s:*
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                                         SUMMARIES
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440	440.5	442	443	43.	443.5	451	51	54	59	56	w	473.5	482	487	491	491.5	494	500	502.5	513	518.5	N	563	685	Score
							65.9		67.1			69.1		71.1	71.7		٠		73.4		٠	76.2		100.0	Match
134	124	190	190	383	377	128	133	129	149	129	129	131	130	152	124	129	124	130	131	130	129	130	130	130	Length
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ABG30618	AAY28615	ABR62882	ABR62883	AAE05287	AAE05286	AAE10565	ABG30972	AAE10551	AAE05288	AAE10564	AAE10561	ABG30620	AAE10567	AAE05283	AAE10566	AAE10558	AAE10563	AAE10559	AAE10555	AAE10554	0	1055	AAE10557	AAE10556	ID
	m	Abr62	Abr62	Aae05	Aae05	Aae1056!	Abg30	Aae10	Aae05	Aae10564	Aae10	Abg30	Aae10	Aae05283	Aae10	Aae10	Aae10	Aae10	Aae10	Aae10	Aae10	5	Aae10	Aael0	Descr
618 Immunoglo	615	882 Llama	883 Llama ant	287 I	286 Llama HCV	51	N	551 HPL	288 Anti-pota	564 HGL inhib	HGL	620 Immunoglo	HGL	Anti	)566 HGL inhib	558 HPL	563 HGL inhib	559 HPL	555 HPL	554 HPL :	553 HPL	552 HPL	557 HPL 1	556 HPL	Description

45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	26
419.5	419.5	422.5	423	423.5	423.5	425	427.5	428	429	429.5	430	431	432	434	435.5	436	436.5	437	440
61.2	61.2	61.7	61.8	61.8	61.8	62.0	0,									63.6	63.7	63.8	64.2
500	500	205	130	193	118	119	204	119	124	127	119	198	138	194	219	190	225	190	190
4	ω	N	4	7	Ŋ	4,	N	4.	4	ហ	4	7	ທ	7	Ŋ	7	N	7	7
AAB72413	AAB07654	AAY41173	AAE10560	ABR62884	AAY39819	AAB67779	AAY41167	AAB67778	AAE10562	ABG30617	AAB67777	ABR62878	ABG30619	ABR62885	AAY41176	ABR62880	AAY41165	ABR62879	ABR62881
Aab72413	Aab07654	Aay41173	Aae10560	Abr62884	Aay39819	Aab67779	Aay41167	Aab67778	Aae10562	Abg30617	Aab67777	Abr62878	Abg30619	Abr62885	Aay41176	Abr62880	Aay41165	Abr62879	Abr62881
Llama bi-	Llama ant	Llama Vhh	HGL inhib		Llama ant	Amino aci	Llama Vhh		HGL inhib	Mouse cro	Amino aci	Llama ant	Immunoglo	Llama ant	Llama Vhh	_	Llama Vhh	_	Liama ant

### ALIGNMENTS

HPL inhibiting VHH fragment, HPL #18 from llama species.

AAE10556;

10-DEC-2001

(first entry)

AAE10556 standard; peptide; 130 AA.

#### ARESULT 1 ARESUL Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight. EP1134231-A1 Region Region WPI; 2001-572718/65. Bezemer S, 14-MAR-2000; 2000EP-00200930 20-FEB-2001; 2001EP-00200703. Region Lama sp. (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC. 19-SEP-2001. Van De Burg /label= CDR1 /note= "Complementarity determining region 1" 50...64 Location/Qualifiers note= "Complementarity determining region 'label= CDR3 /label= CDR2 /note= "Complementarity determining region .110 3 De Haard JJW, Tareilus

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Example 2; Page 10; 37pp; English.

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RRESULT 2
AABE10557
ID AABE1
XX AABE1
XX AABE1
XX AABE1
XX AABE1
XX IO-I
XX ILlam
XX Equi
XX Equi
XX Equi
XX Regi
FT Regi
FT Regi
FT Regi
FT Regi
FT Regi
FT Regi
YX II-I
XX Epll
XX E
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Best Local S
Matches 130
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                New antibody or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE10557 standard; peptide; 130
                                                                WPI; 2001-572718/65
                                                                                                                Bezemer S,
                                                                                                                                                                (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
                                                                                                                                                                                                                                            14-MAR-2000; 2000EP-00200930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody; camelid; anorectic; heavy chain variable domain; VHH; dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; human gastric lipase; HGL; cosmetic control; body weight.
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                                                                                                                Van De Burg
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                  its
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/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50. .64
/label= CDR2
/note= "Complementarity
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Pred. No. 2.3e-53;
Mismatches 0;
                for inhibiting
                                                                                                                   Haard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determining
                  human dietary enzymes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 130;
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RESULT 3
ADE10552
ID ADE1
XX AAE1
AC AAE1
XX Llan
AC Llan
KW Llan
KW food
XX Lama
XX Lama
XX ET Regi
FT Regi
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HPL) which are useful for the cosmetic control of body weight of human beings.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 130 AA;
                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                          Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-DEC-2001
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                                                           14-MAR-2000; 2000EP-00200930
                                                                                                                                                    EP1134231-A1
                                                                                                                                                                                                                                                                                                                                                    Lama sp.
                                                                                                                                                                                                                                                                                                                                                                                                Llama antibody; camelid;
human dietary enzyme inhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present peptide sequence is HPL inhibiting VHH fragment, HPL #19
                                                                                        20-FEB-2001; 2001EP-00200703
                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                   food;
              (UNIL ) UNILEVER
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                                                                                                                                                                                                                                                                                                                                                                             lantibody; camelid; anorectic; heavy chain variable domain; VHH; dietary enzyme inhibitor; medicament; human pancreatic lipase; human gastric lipase; HGL; cosmetic control; body weight.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                   note= "Complementarity determining region"
                                                                                                                                                                                                                             /label= CDR2
/note= "Complementarity
                                                                                                                                                                                                                                                                        /label= CDR1
/note= "Complementarity determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.2%;
                                                                                                                                                                                                                  110
                                                                                                                                                                                                   CDR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                             HPL #12 from llama species.
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Pred. No. 1.
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1.7e-42;
                                                                                                                                                                                                                              determining
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Bezemer

Van

De

Burg

Z De

Haard

JJW,

Tareilus

2001-572718/65

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RRESULT 4
AAB10553
ID AAB10553
ID AAB10553
AC AAB11
XX AAB10-C
XX AAB10
DT 10-C
XX Llam
XW huma
XX Key
FT Regi
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HFL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #12 from llama (camelid) species
                                                                                                                                                                                                                                                                                                      Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-2001
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                20-FEB-2001;
                                               19-SEP-2001.
                                                                                                                                     Region
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                                                                                                                                                                                                                                                                             Lama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; peptide; 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEPKTPKPQP 130
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                                                                                                                                                                                                                                                                                                                                                                       HH
                                                                                                                                                 /label= CDR2
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                                                                                                                                                                                                note= "Complementarity
                                                                                                                                                                                                                                                                                                                                                                    fragment,
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77.7%;
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Pred. No. 7.9e-39;
9; Mismatches 20
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Best Local
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                                                                                                                                                                                                     Llama antibody; camelid; anorectic; heavy chain variable domain; human dietary enzyme inhibitor; medicament; human pancreatic lipafood; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                               HPL inhibiting
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                                                                                                                                                                                                                                                                                                                                               peptide;
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Pred. No. 1.6e-38;
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Pred. No. 5e-38;
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numan dietary er
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEPKTPKPQP
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                                                                                                                               ody; camelid; anorectic; heavy chain variable domain; VHH;
ry enzyme inhibitor; medicament; human pancreatic lipase;
gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Van De Burg
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                                                                                                                                                                                                                                                                                             (first entry)
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/label= CDR3
  Location/Qualifiers 31. .35
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                                                                                                                                                                                                                                       fragment,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 502.5; DB 4
Pred. No. 4.3e-37;
7; Mismatches 23
                                                                                                                                                                                                                                             HPL #30 from llama species
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                                                                                                                                                                 lipase; HPL;
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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                         The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of-light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #30 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
Llama antibody; camelid; anorectic; heavy chain variable domain; human dietary enzyme inhibitor; medicament; human pancreatic lipfood; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                 10-DEC-2001
                                                                                                                                   AAE10563
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 130 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 10; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-572718/65
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                                                     inhibiting VHH fragment,
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98; Conserv
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                                                                                                                                    standard;
                                                                                                                                                                                                                               SEPKTPKPQP 130
                                                                                                                                                                                                                                                                                                                                  QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPNYA
                                                                                                                                                                                                                                                       DSVKGRFTISRDNTLNTVYLOMNDLKPEDTGVYYWNADVRPYRTSRYLEIWGQGTLVTVF 120
                                                                                                                                                                                                                                                                               DPVKGRFTISRDNGKLTVYLOMNSLKPEDTAVYYCNALIRRKFTSEYNEYWGQGTQVTVS 120
                                                                                                                                                                                                                                                                                                           QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA
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                                                                               (first entry)
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/note= "Complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note=
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                                                                                                                                  peptide; 124
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                                                     HGL
                                                                                                                                                                                                                                                                                                                                                              Score 500; DB 4;
Pred. No. 7.2e-37;
8; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haard
                                                     #9 from llama species.
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              lipase; HPL;
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Best Local :
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               10-DEC-2001
                                          AAE10558
                                                                  AAE10558
                                                                                                                                                                                                                                                                                                                                              Sequence 124
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                                                                 standard;
                                                                                                                                                           SEPKTPKPQP 130
                                                                                                                                                                                                            DPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYYCNALIRRKFTSEYNEYWGQGTQVTVS
                                                                                                                                                                                                                                                        QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPNYA
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                                                                 peptide;
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                                                                                                                                                                                                                                                                                                          72.1%;
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                                                                                                                                                                                                                                                                                          Score 494; DB
Pred. No. 2.3e
8; Mismatches
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HPL inhibiting

HHV

fragment,

HPL #22 from llama species

human Llama

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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    AAE10566
                                                                                                                                                                                                                                                                           Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2;
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UNILEVER
                                                                                                                                                                                                                                      Similarity
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     standard;
                                                                                                                                                                                                QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPNYA
                                                                                                                      DSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALI-SSYDGSWNDYGGQGTQVTVS
                                                                                                                                            DPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYYCNALIRRKFTSEYNEYWGQGTQVTVS
                                                                                                                                                                       QVQLQESGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGTTSYT
                                                                   SEPKTPKPQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 10; 37pp; English
                                                                                                                                                                                                                        Conservative
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/note= "Complementarity determining
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    peptide; 124
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                                                                   129
                                                                                                                                                                                                                                     71.8%;
73.8%;
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                                                                                                                                                                                                                        Score 491.5; DB 4;
Pred. No. 4.1e-36;
1; Mismatches 22;
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Best Local Similarity
                                                                                                                                                                                                                        The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #15 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                         New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control; body weight.
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                                                                                                                                                                                                  Sequence 124 AA;
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                                                                                                                  QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPNYA
                                                                                                                                                                                                                                                                                                                                                                                   chains
                        SEPKTPKPQP 130
                                                 DSVKGRFTISRDNEKNTMYLOMNSLTPEDTGVYYCAG-----
                                                                                                QVQLQESGGGLVQAGGSLRLSCAASGSIGSMYVMSWYRQAPGKEREPIAALMGSGSTTYA
SEPKTPKPQP
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                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLC.
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/note= "Complementarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fragment,
                                                                                                                                                              71.7%;
73.8%;
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                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGL #15 from llama species
                                                                                                                                                   Score 491; DB 4;
Pred. No. 4.3e-36;
8; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         determining
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                                                                                                                                                                            Length 124;
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                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for modifying a plant to produce an antibody or an active fragment or derivative, or a protein functional equivalent, in a cellular compartment comprises introducing a DNA sequence encoding a heavy chain immunoglobulin, where the DNA is peptide capable of targeting heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain that is functionally equivalent for increasing the pathogen resistance in a plant or to modulate metabolism in a plant. Under some circumstances it may be casirable to retain the antibody product with the plant rather than extracting and isolating the product. In particular, edible selected antigens may be used in a method of passively immunising an animal, preferably human, against the antigen, e.g., pathogenic organisms. The preferably human, against the pathogenic organisms. The preferably human, against the potato SBEII antibody (denoted Clone46) heavy chain variable domain (VH) attached to peptide linkers, myc and his6 tag.
                                                                                                                                                                                                                Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potato; heavy chain immunoglobulin; pathogen resistance metabolism modulator; passive immunisation; heavy chain VH; anti-potato SBEII; starch branching enzyme; SBE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE05283 standard; protein; 152
                                                                                                                                                                                                                                                                                                                                       Sequence
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Unidentified.
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                                   61
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UNILEVER NV.
                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                          152
DPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYYC---NALIRRKFTSEYNEYWGQGTQV 117
                                                                                                                                                      QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPNYA 60
                                                                                             QVQLQESGGGLVQAGGSLRLSCVASGNTFSIIAMAWYRQAPGKQREVVASINSIGSTNYA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 12; 81pp; English
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                       AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99EP-00310188
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                                                                                                                                                                                                                Score 487; DB Pred. No. 1.2e 7; Mismatches
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                                                                                                                                                                                                                                             DB 4;
.2e-35;
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                                                                                                                                                                                                                                                                       Length 152;
                                                                                                                                                                                                                   Indels
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QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPNYA 60

Query Match Best Local S Matches 96

Similarity

70.4%; ilarity 73.8%; Conservative 1

10;

Score 482; DB Pred. No. 2.9e 10; Mismatches

DB 4; .9e-35;

Length 130; Indels

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FFT Regi
                                                      The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #16 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                        New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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                                                                                                                                                                                                                                                                                                                                                                     Example 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNIL ) UNILEVER NV.
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                                                                                                                                                                                                                                                                                                                                                                     Page 14; 37pp; English.
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      AA;
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ARESULT 13
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investigated. (I) is useful for detecting the presence of individual proteins in a sample, comparing the distribution of proteins in different cell types, and identification of proteins that may be of importance in determining the altered properties of cells in disease, aging or other conditions. Using a heavy-chain variable domain derived from an climmunoglobulin that is naturally devoid of light chains (VHH) in (I) comparity/resolution in the order of 10-100 times, and detection of proteins an improvement of constitivity/resolution in the order of 10-100 times, and detection of post-translationally modified proteins. The invention also describes a method (II) that enables the simultaneous processing of large numbers of target antigens in a controlled way. The incorporated phage-ELISA companing condition. This feature combined with the microtiter plate format allows the complete automation of the technology, based on computer-made decisions on the values of the phage-ELISA for continuation of a limited number of selections. In (II), due to the fact that many different conditions can be tested, varying amounts of input-phages can be used conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a protein array (I) comprising a number of heavy-chain variable domain antibodies or antibody fragments, obtainable from Camelidae. The method is useful for removing abundant proteins from an extract or sample which do not provide useful information on the condition of a cell or tissue in the extract or sample to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel protein array useful for detecting the presence of individual proteins in sample, comprises heavy-chain variable domain antibodies or antibody fragments obtainable from Camelidae.
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RESULT 14
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ACC AAE10
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                                              New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                         (NIL)
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                                                                                                                                                       WPI; 2001-572718/65
                                                                                                                                                                                                     Bezemer S,
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/note= "Complementarity determining region
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/note= "Complementarity determining region
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72.5%;
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Pred. No. 1.7e-34;
6; Mismatches 29
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Example 4; Page 13; 37pp; English.

SXSSSSSSSSXX SXSSSSSSSSXXX

Sequence 129 AA;

129;

5

Gaps

60 60 N The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #4 from llama (camelid) species

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RESULT 15
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Best Local
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                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                           Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                          10-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                 AAE10564 standard;
        WPI; 2001-572718/65
                                                                                                 20-FEB-2001; 2001EP-00200703
                                                                                                                      19-SEP-2001.
                                                                                                                                        EP1134231-A1
                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                          Lama sp.
                                                                                                                                                                                                                                                                                                                                    HGL inhibiting VHH fragment,
                           Bezemer S,
                                                                             14-MAR-2000; 2000EP-00200930
                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
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                                               UNILEVER NV.
UNILEVER PLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPNYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSVKGRFTIARENAKNÍVÝLOMSSLKPEDTAVÝÝCKG---RGGLTQÝSEHDÝWGOGTOVT 117
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                            Van De Burg
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                                                                                                                                                                                                              /label= CDR1
/note= "Complementarity determining
50. .64
                                                                                                                                                                                                                                            Location/Qualifiers 31. .35
                                                                                                                                                                                                   /label= CDR2
                                                                                                                                                                                         /note= "Complementarity determining region
                                                                                                                                                           note= "Complementarity determining region 3"
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                            Σ,
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Pred. No. 1.3e-33;
2; Mismatches 23
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                            Haard
                            MCD,
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Best Local S
Matches 92
                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HFL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #10 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 13; 37pp; English.
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                                                                            118 VSSEPKTPKPQP 129
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                                                                                                                                                      NSVKGRFTISRENAKNTVYLOMNSLKPEDTAVYYCKG---RGGLTQYSEHDYWGQGTQVT 117
                                                                                                                                                                                                                           QVQLQESGGDLVQAGGSLRLACAASGSTFSFNAMGWYRQVPGKQRELVAAIGNDGSTYYV
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                      2004,
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## ALIGNMENTS

RESULT 2  \$31114  Ig heavy chain - human  C/Species: Homo sapiens (man)  C/Species: Homo sapiens (man)  C/Accession: \$31114  R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,  Eur. J. Immunol. 22, 247-251, 1992  A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third compleme  A;Reference number: \$31104; MUID:9211633; PMID:1730252  A;Accession: \$31114  A;Status: preliminary; nucleic acid sequence not shown; translation not shown  A;Foross-references: EMBL:X62963  A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991	1 QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQRENVASITATGPPN-Y 59	RESULT 1 Syation V region (anti-Sm, VH3/Dxp4/JH4b) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999 C;Accession: S48798 R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D. submitted to the EMBL Data Library, October 1994 A;Description: Molecular characterization of natural human anti-Sm autoantibodies. A;Reference number: S48797 A;Recession: S48798 A;Status: preliminary A;Molecular type: mRNA A;Cression: S48797 A;Cross-references EMBL:Z46382; NID:g562324; PIDN:CAA88521.1; PID:g1340167 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology < IMM> Query Match Best Local Similarity 67.2%; Pred. No. 1.9e-25; Matches 82; Conservative 10; Mismatches 27; Indels 3; Gaps 3;

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C;Superfamily: i
C;Keywords: hete
F;15-98/Domain:
                                                           C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31107
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.J. Bur. J. Immunol. 22, 247-251, 1992
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse
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                          A;Reference number: S31104; MUID:92111633; A;Accession: S31107
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J. Exp. Med. 178,
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Species: Homo sapiens (man)
Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change
  Status:
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Ig heavy chain V region - human (fragment)
(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
(;Accession: $31686
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonn
submitted to the EMBL Data Library, June 1992
A;Bescription: Mechanisms that generate human immunoglobulin div
A;Reference number: $31585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain - human
C; Species: Homo sapiens (man)
C; Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_
C; Accession: S31108
C; Accession: S31108
C; Accession: S31108
C; Accession: S31108
Eur. J. Immunol. 22, 247-251, 1992
Bur. J. Immunol. 22, 247-251, 1992
A; Title: Restricted utilization of germ-line V(H) 3 genes
A; Reference number: S31104; MUID:92111633; PMID:1730252
A; Accession: S31108
A; Accession: S31108
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A;Note: the nuclectide sequence was submitted to the ENC;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-119 <RNA-A
A;Residues: 1-119 <RNA-A
A;Cross-references: EMBL:X52955
A;Cross-references: EMBL:X52955
A;Note: the nucleotide sequence was submitted to the EMBL Data Library,
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;15-98/Domain: immunoglobulin homology <IMM>
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S31686
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R;Kishimoto, T.
submitted to the EMBL Data Library,
submitted number: S05270
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-160/Product: Ig heavy chain (fragment) #status predicted <IF;20-160/Product: Ig heavy chain (fragment) #status predicted <IF;20-160/Production (fragment) #status predicted <IF;20-160/Production (fragment) #status predicted <IF;20-160/Production (fragment) 
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R;Kishimoto, T.; Ckajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1980
A;Title: Nucleotide sequences of the cDNAs encoding the
A;Reference number: S04601; MUID:89296497; PMID:2500644
A;Accession: S04602
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                                                                                RESULT
S31588
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A; Residues: 1-140 < CUI>
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A; Residues: 1-144 < KIS2>
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A; Residues: 1-160 <KIS1>
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                Ig heavy chain V region - hum C; Species: Homo sapiens (man)
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Best Local
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                                               human (fragment)
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Pred. No. 1.6e-24;
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Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-114 <FIG>
A;Cross-references: EMBL:231687; NID:g509784; PIDN:CAA83492.1;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;15-98/Domain: immunoglobulin homology <IMM>
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S46391
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A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
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A; Reference number:
A; Accession: S31588
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Matches
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                                                                          ADSVKGRFT
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Pred. No. 2.8e
8; Mismatches
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C;Accession: S20782
R;Mortari, F; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of the IgA and IgG rearranged VH
A;Reference number: S20765
A;Accession: S20782
A;Status: preliminary
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A;Residues: 1-124 <MCP.
A;Residues: 1-124 <MCP.
A;Cross-references: EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:g33898
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Keywords: hete
F;15-98/Domain:
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A;Residues: 1-119 <SCH>
A;Cross_references: GB:M18513
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                                                                                                RESULT 12
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roc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
;Title: Preferential utilization of conserved immunoglobulin heavy chain ;Reference number: A36005; MUID:90349571; PMID:2117273
;Accession: C36005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g heavy chain V region (30p1) - human
|Species: Homo sapiens (man)
|Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
|Accession: C36005
,Species: Homo sapiens (man)
;Bate: 22-Nov-1993 #sequence_revision 10-Nov-1995
;Accession: S31666
                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: immunoglobulin V region; immunoglobulin; Keywords: heterotetramer; immunoglobulin; 15-98/Domain: immunoglobulin homology < IMM>
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Best Local Similarity
Matches 78; Conserv
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                                                        heavy chain V region - human (fragment)
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                                                                                                                                                                                                                                                                                                                   EVOLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches
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Pred. No. 3.9e-24;
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                #text_change 23-Jul-1999
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RESULT 14 F36005

Ig heavy chain V

region

(M49)

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C;Superfamily: ımmunoy.cc...
C;Keywords: heterotetramer; immunoglobul
F;15-98/Domain: immunoglobulin homology
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Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved imm
A;Reference number: A36005; MUID:90349571; PMID:21
A;Accession: D36005
A;Status: preliminary
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A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1;
A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1;
C;Superfamily: immunoglobulin V region; immunoglobulin homolog
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region (M43) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990
C;Accession: D36005
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M34024
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A;Residues: 1-119 <SCH>
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Best Local S
Matches 77
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Best Local
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77; Conserv
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                                                                        ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYC
                                                                                                            TDSVKGRFTISRDNDKVTEYLOMNULKPEDTAVYYCNAQVRVRESSDYTNYWGQGTQVTV 119
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                                                                                                                                                                                                                                         52.1%; Score 362; DB 2; 62.3%; Pred. No. 4.8e-24;
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Pred. No. 4.6e-24;
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PMID:2117273
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A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-120 <RAA>
A, Residues: 1-120 <RAA>
A, Residues: 1-120 <RAA>
A, Rosidues: The mucleotide sequence was submitted to the EMBL Data Library, October 1991
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
F, 15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S31112

R;Raaghorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992

A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252

A;Accession: S31112
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A;Gene: GDB:IGH@; GDB:ILB731; OMIM:146910
A;Cross-references: GDB:ILB731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: F36005
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S31112
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A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: GB:M34026
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;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
;Accession: F36005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man);Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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                                                                                             60 TDSVKGRFTISRDNDKNTEYLOMNULKPEDTAVYYCNAQVRVRFSSDYTNYWGQGTQVTV 119
                                                                                                                                                                                                                                                                                                 ch 52.0%; l Similarity 65.6%; 80; Conservative
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                                                                                                                                                                                                   ÓVÓLVESGGGVVÓÞGRSLRÍSCAÁSGFTFSSÝAMHWVRÓÁÞGKGLEWVÁVÍSYDGSNKYÝ 60
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                                                                                                                                                                                                                                                                                                 Score 361.5; DB 2; Length Pred. No. 5.3e-24; 8; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                 Length 120;
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Search completed: October Job time: 22.0648 secs 'n 2004, 08:17:16 This Page Blazk (Uspig)

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Result
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1 QVQLQDSGGGLVQTGGSLRL.....wGQGTQVTVSSEPKTPKPQP 130
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P01805 rattus norv
P01812 mus musculu
P018177 homo sapien
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ID HV3K_HUMAN
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<b>,4</b> U1	44	43	42	41	40	39	კ 8	37	36	IJ G	₩ 4
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P01780 home	P01794 mus	P01791 mus	P01786 mus	P18526 mus	P01789 mus	P01776 home	P01811 mus	£18524 mus	P18527 mus m	P01774 homo	P01798 mus
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### ALIGNMENTS

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Best Local
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SEQUENCE
                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                   989
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MEDILINE=78005528; PubMed=409716;

Wang A.-C., Wang I.Y., Fudenberg H.H.;

"Immunoglobulin structure and genetics.";

"Immunoglobulin structure and genetics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region TIL.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                         regions of a mu and a gamma2 chain.";

J. Biol. Chem. 252:7192-7199 (1977).

-i- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
GAMMODATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                   HSSP; P01772;
                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                          nterPro;
                                                                                                                                                                                                                                                                              GO:0005576; C:extracellular; NAS. GO:0003823; F:antigen binding; NAS GO:0006955; P:immune response; NAS
                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 PVTVSS
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                                                                                                                                                                                                                                   IPR007110; Ig-like
IPR003596; Ig_v.
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115 AA;
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58.2%;
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                    Score 340; DB 1;
Pred. No. 4.6e-26;
                                                                                                                                 IG-LIKE
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Pred. No. 4.
                                                                                      4DCC67D179F62326 CRC64;
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Mismatches
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DISULFID
NON TER
SEQUENCE
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IG LIKE; 1.
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GO; GO:0003823; F:antigen binding;
GO; GO:0006955; F:immune response;
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dreker L., Schwarz J., Reichel W., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclon
IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
characterization of the protein, the L- and H-chains, the
cyanogen bromide cleavage products, and the disulfide bridges.",
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=77070267; PubMed=1002129; Dreker L., Schwarz J., Reichel W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."; Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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Ponsting1 H., Hilschmann N.;
"The rule of antibody structure. The primary structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
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21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region NIE.
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P01770;
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  60 TDSVKGRFTISRDNDKNTEYLQMNNLKPEDTAVYYCNAQVRVRFSSDYTNYWGQGTQVTV 119
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                                                                                   QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASITATG-PPNY
                                                                                                                                                                                                                                                                                                                                                                PS50835; IG LIKE; 1.
obulin V regin; Pyrrolidone carboxylic acid.
                                                    QVQLVQSGGGVVQPGRSLRLSCAASGFTFSRYTIHWVRQAPGKGLEWVAVMSYBGBBKHY
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119
119 AA;
                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                  13242 MW;
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                                                                                                                                                      Score-338; DB
Pred. No. 7.5e
14; Mismatches
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PYRROLIDONE CARBOXYLIC
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Matches 74
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InterPro; IPRO355..
InterPro; IPRO355..
Pfam; PF00047; 19; 1
SMART; SM00406; IGv; 1.
SMART; SM01406; IGv; 1.
SMART; SM01406; IGv; 1.
112
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21-JUL-1986
21-JUL-1986
10-OCT-2003
                                                           -HV3F HUMAN
P01767;
21-JUL-1986
21-JUL-1986
10-OCT-2003
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10-OCT-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region CAM.
Homo sapiens (Human).
                                                                                                                                                   HUMAN
HV3F_F
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HSSP; P01772; 2FB4.
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                         Homo
                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last Sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
1g heavy chain V-III region BUT.
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122 AA;
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13668 MW; A42D0F17D252F1C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.3%;
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Pred. No. 1.3e-25;
4; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID
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    Euteleostomi;
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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NON TER
SEQUENCE
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21-JUL-1986
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"Complete amino acid sequence of the alpha 2 heavy chai
"ga2 immunoglobulin of the A2m (2) allotype.";

Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).

-!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2)

REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.

-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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P01781;
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                                                                                                                                                                                                                                                                                                              MEDIINE=75059123; PubMed=4803843; Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.; Watanabe S. Barnikol H.U., Horn J., Bertram J., Hilschmann N.; "The primary structure of a monoclonal IgM-immunoglobulin (mu-(macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-type), subgroup H III. Architecture of the complete IgM-molecule."; Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last Sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region GAL.
                                                                                                                                                                              Hilschmann N.;
Submitted (JUN-1975)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
-!- SIMILARITY: Contains PIR; A02064; M3HUGL. HSSP; P01772; 2FB4.
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                                                                                                                                                                                                                                                     REVISION TO
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                                                                                                      MACROGLOBULIN.
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F.W.;
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                                                                    immunoglobulin-like
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Pred. No. 2e-24;
7; Mismatches
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                                                                                                                                               bank.
ISOLATED FROM A WALDENSTROM'S
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Matches 74
                   InterPro; IPkv.,
InterPro; IPkv.,
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
10bulin V region; 3D-structure.
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GO; GO:0003523; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; 1g; 1.
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PROSITE; PS50835; IG LIKE; 1.
IMMUNGJObulin V rejion.
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1 112 IG-LIKE.
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PDB; 2FBJ; 15-OCT-90.
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Proteins 1:74-80(1986)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complementarity-determining regions.";
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY SEQUENCE.

MEDILINE=79223895; Pubmed=111245;

Rao D.N., Rudikoff S., Krutzsch H., Potter M.;

"Structural evidence for independent joining region immunoglobulin heavy chains from anti-galactan myelous potential role in generating diversity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                        "The galactan-binding immunoglobulin Fab J539: study at 2.6-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                            Davies D.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986
28-FEB-2003
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74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             Bhat T.N., Navia M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 41, Last annotation update)
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60.7%; Pred. No. 2.36
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Cohen G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
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                                                                                                                                                                                                                                                                                                               FROM A MYELOMA PROTEIN
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1 myeloma pr
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RESULT
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Query Match
                                           PIR; A02054; G1HUHL.

HSSP; P01772; 2F84.

G0; G0:0005576; C:extracellular; NAS.

G0; G0:0005576; C:extracellular; NAS.

G0; G0:0005853; F:antigen binding; NAS.

G0; G0:0006955; P:immune response; NAS.

InterPro; IPR003710; Ig-like.

InterPro; IPR003356; Ig_v.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

SMART; SM00406; IGV; 1.

Immunoglobulin V region; Pyrrolidone carboxylic ac DOMAIN

1 112 IG-LIKE.
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Best Local
                            MOD_RES
                                                                                                                                                                                                                                                                                       P01771;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
If heavy chain V-III region HIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAND
STRAND
SEQUENCE
                                                                                                                                                                                             Chiu Y.-Y.H., Lopez de Castro
"Amino acid sequence of the V
cryoimmunoglobulin IgG Hil."
                   SEQUENCE
                                                                                                                                                                              Biochemistry 18:553-560(1979)
                                                                                                                                                                                                                 MEDLINE=79124695; PubMed=420800;
                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                          HV3J_HUMAN
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HELIX
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                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TDSVKGRFTISRDNDKNTEYLQMNNLXPEDTAVYYCNAQVRVRFSSDYTNYWGQGTQVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASI-TATGPPNY
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                  121 AA;
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PA;
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                                                                                                                                                                                                        Lopez de Castro J.A., Pequence of the VH region
                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.48;
 46.38;
                                                                                                                                                                              CHAIN WAS
Score
                                    PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 322.5;
Pred. No. 2.4
                                                                                                                                                                                                                                                                                                                                         PRT;
                  480FC53610EF5DAB CRC64;
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                                                                                                                                                                                                         Poljak R.J.;
on of human m
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                                                                                                                                                           domain
                                                                                                                                                                                                         myeloma
Length 121;
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RESULT 10
HV3C_HUMAN
ID HV3C_HUMAN
AC P01764;
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Best Local S
Matches 69
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SMART; SM00406; IGv; 1.
SMART; SM00406; IG LIKE, 1
Immunoglobulin V region.
117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining region gene
immunoglobulin heavy chains from anti-galactan myeloma pr
its potential role in generating diversity in
complementarity-determining regions.";
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
--- WISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MY
THAT BINDS GALACTAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HV37_MOUSE STANDARD; PRT; 119 AA. P01807; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Ig heavy chain V region X44.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A02077; AVMSX4.
HSSP; P01810; 2FBJ.
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MEDLINE=79223895;
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InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
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73; Conservative
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119 }
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                              STANDARD;
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13246 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 321.5; DB 1
Pred. No. 2.9e-24;
5; Mismatches 34
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HV3B_HUMAN
ID HV3B HUMAN
ID HV3B HUMAN
AC P01763;
AC P01763;
DT 21-UUL-1986
DT 21-UUL-1986
DT 10-OCT-2003
DE IG heavy cha
OS Homo sapiens
OC Eukaryota;
NCB LTAXID=
RN SEQUENCE.
RX MEDLINE=832;
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Query Match
Best Local S
Matches 66
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EMBL; M35415; AAAB3735.1; -.
PIR; M35415; AAAB3735.1; -.
PIB; H0U; 23-DEC-99.
Genew; HGNC:5545; IGHV@.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:anntigen binding; NAS.
GO; GO:0008955; F:immune response; NAS.
InterPro; IPR007710; Ig-like.
InterPro; IPR00356; Ig-like.
Pfam; PF00947; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IGLIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
ITMUNOGLOBULIN V region; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                          DOMAIN
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matthyssens G., Rabbitts T.H.;
"Structure and multiplicity of genes for the human heavy chain variable region.";
Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region VH26 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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80
                                              60 TDSVKGRFTISRDNDKNTEYLOMNNLKPEDTAVYYC 95
                                                                                             20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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GDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC
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115
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P01783; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Ig heavy chain V-III region WEA.

STANDARD;

114

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Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.

NCBI\_TaxID=9606;

MEDLINE=83273707; PubMed=6410398

Homo sapiens

(Human).

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Best Local S
Matches 70
                          PIR; A02045; A1HUTR.
HSSP; P01772; 2FB4.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0003823; F:antigen binding; NAS.
G0; G0:0006955; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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21-JUL-1986
10-OCT-2003
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"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";

Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

-I MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
ACAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.

-I- SIMILARITY: CONTAINS 1 immunoglobulin-like domain.
                                                                                                                                                                                                      "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tr II. The amino acid sequence of the H-chain, alpha-type, subgroup structure of the complete IgA-molecule.",
Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
-!- MISCELLANBOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
-!- SIMILARITY. Contains 1 immunoglobulin-like domain.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN
1 112 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE (MYELOMA PROTEIN TRO).
MEDLINE=76023781; PubMed=809331;
Kratzin H., Altevogt P., Ruban E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding; NAS.
GO:0006955; P:immune response; NAS.
erPro; IPR007110; Ig-like.
erPro; IPR003596; Ig_v.
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(Rel. 42, Last annotation
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Pred. No. 4.
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunglobulin V region.
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21-JUL-1986
21-JUL-1986
10-OCT-2003
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HV33 !
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PROSITE;
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HSSP; P01810; 2FBJ.
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Johnson N., Slankard J., Paul L.,
"The complete V domain amino acid
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Mammalia; Eutheria;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-QCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region W3082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY:
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                                                                             58 NYTDSVKGRETISRDNDKNTEYLQMNNLKPEDTAVYYCNAQVRVRESSDYTNYWGQGTQV
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E; PS50835; IG_LIKE; 1.
globulin V region; Pyrr
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                                        HYAESVKGRFTISRDDSKSSVYLRMNNLRPEDTGIYYCTTGFA--
                                                                                                                        = VKLEESGGGLVQPGGSMKLSCVASGFTFSNYWMNWVRQSPEKGLEWVAEIRLKSHNYAT
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122 AA;
                                                                                                                                                                                                                                                                                  115 AA;
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22
115
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                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
13472 MW;
                                                                                                                                                                                                                                                                                  115
12887 MW;
                                                                                                                                                                                                                                                                                                                                                114
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                                                                                                                                                                                                                        45.6%;
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                                                                                                                                                                                                     16;
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                                                                                                                                                                                                                        Score 317;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                           IG-LIKE.
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 318.5;
Pred. No. 5.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                    9B4517648C121C5A CRC64;
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                                                                                                                                                                                                                        DB 1;
7.7e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of two
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                                                                                                                                                                                                                                         Length 115;
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                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN THAT
                                                                                                                                                                                                     12;
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RESULT 15
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                       RRRRROCCOSETIO
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Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPRO07110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PP00047; ig; 1.
SWART; SW00406; IGv; 1.
PROSITE; PS5085; IG LIKE; 1.
Immunoglobulin V region.
DOMAIN 1 111 IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P01766;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
To heavy chain V-III region BRO.
                                                                                                                                                                                                                                 P01769;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region GA.
Homo sapiens (Human)
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HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding, NAS.
GO; GO:0008955; P:immune response; NAS.
SEQUENCE.
MEDLINE=74175307; PubMed=4208843;
Florent G., Lehman D., Putnam F.W.;
"The switch point in mu heavy chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Comparative studies on monotypic IgM lambda and IgG kappa from an individual patient. III. The complete amino acid sequence of the VH region of the IgM paraprotein.";
Immunochemistry 13:995-999(1976).
-!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V-III region BRO.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Capra J.D., Hopper J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=77117674; PubMed=65324;
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                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DSVKGRFTISRDNDKNTEYIQMNNLKPEDTAVYYCNAQVRVRFSSDYTNY-----WGQGT
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ilarity 57.5%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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13227 MW; D3F0428F7C2E6410 CRC64;
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Pred. No. 8.1e
10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                    of human
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nes 35;
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                 IgM immunoglobulins.";
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Best Local S
Matches 66
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MOD RES
NON TER
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plant, prool47; ig; 1.
smarr, smoo406; IGv; 1.
smarr, smoo406; IGv; 1.
prostre; pssoss; IG LIKE; 1.
Immunoglobulin v region; Pyrrolidone carboxylic acid.
Immunoglobulin v region; Pyrrolidone Carboxylic & PyrroLIDONE CARBOXYLIC &
                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- MISCELLANEOUS:
MACROGLOBULIN.
-i- SIMILARITY: Cor
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A02052; M3HUGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 13:2482-2498(1974)
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                        121
                                                                                    120
                                                                                                                 61 AASVKGRFTISRBBSKBTMYLEMNSLRAENTAVYYCARSGIALGSVAGTDYWGZGTLVTI 120
                                                                                                                                           60 TDSVKGRETISRDNDKNTEYLOMNNLKPEDTAVYYCNAQVRVRESSDYTNYWGQGTQVTV 119
                                                                                                                                                                                                                              66;
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                                                                                                                                                                                                                                               Similarity
                                                        SS 122
                                                                                    SS 121
                                                                                                                                                                        QVZLVZSGGGAVZPGRSLRLSCAASGFSFSTYAYHWVZQAPGKGLZWLSVISYBGBBZYY
                                                                                                                                                                                                    QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASITATGPPN-Y
                                                                                                                                                                                                                                                                                         122
122 AA;
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                         13166 MW; 74E5B6959E84100A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
                                                                                                                                                                                                                              45.5%; Score 316.5; DB 1
54.1%; Pred. No. 9.2e-24;
live 17; Mismatches 38
             5
               2004, 08:01:56
                                                                                                                                                                                                                                                                                                                      CARBOXYLIC ACID
                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                38;
                                                                                                                                                                                                                                                           Length 122;
                                                                                                                                                                                                                                <u>1</u>
                                                                                                                                                                                                                                Gaps
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Result
No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*
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    GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
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Q91wp5 mus musculu
Q91z07 mus musculu
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## ALIGNMENTS

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YTNYWGOGTQ 116	ASITATGPPN-Y 59 :: : :  SAISGSGGSTYY 79	7; 4; Gaps 3;											•	Euteleostomi;						

VIVSS

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RESULT 3
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Q9UL72;
01-MAY-2000
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
Tin B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                        Q9UL90;
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MEDLINE=98277139; PubMed=9614934;
Tim B., Van der Merwe P.L.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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EMBL; AF035042; AAD56278.1; -
PIR; S21205; S21205.
HSSP; P01772; 2F34.
                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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Mammalia; Eutheria;
                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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12872 MW;
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Primates;
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Primates;
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7; Mismatches
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                           Kalis N.N.,
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and fetus.";
                                                                                                                                                                                                                                               Hypothetical protein. seQUENCE 573 AA; 62967 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.; Submitted (JAN-2002) to the EMBI/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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HSSP; P01772; 2FB4.
InterPro; IPR007110;
                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 4. SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC021276; AAH21276.1; -. PIR; S21205; S21205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               SMARI; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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78; Conserv
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                                                                                   EVOLVESGGGLVOPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
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Last annotation update)
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                                                                                                                                                                                         Score 352; DB 4
Pred. No. 2e-28;
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Pred. No. 6.5e-30;
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Matches 97
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                                                                                                                           Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control; body weight.
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                                                                                                                                                                                                                                                       AAE10559 standard;
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Pred. No. 5.9e-34;
8; Mismatches 24
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                                                                                                                                                                                                                                                                                                                                    HPL
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Pred. No. 1.2e-33;
8; Mismatches 25
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                                                                                                                                                                                                                                                                                                                                    #14 from
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Key Region

Location/Qualifiers 31. .35

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                 20-FEB-2001; 2001EP-00200703
                                                  19-SEP-2001.
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                                                                                                                                                                                                                                                                                                                              Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
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                                                                                                                                                                                                             /label= CDR1
/note= "Complementarity
                                                                                                                                                              'label= CDR2
note= "Complementarity
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76.3%;
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Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                    Region
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                                                                                                                                                                                                  Llama antibody; camelid; anorectic; heavy chain variable domain; VHH, human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                      HPL inhibiting
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UNILEVER
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                                                                                                                                                                                                                                                                                                                                      standard;
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                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                      VHH fragment,
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                                                                                                                       'label=
                                                                                                                                            Cocation/Qualifiers
                          note= "Complementarity"
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                                                                 "Complementarity
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120 120 60 60 0;

EP1134231-A1.

HPL;

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The patent discloses antibodies or their fragments comprising a heavy deviation domain (WHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human distary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human distary enzymes especially human panoreatic lipsas (HPL) or human gastric lipsas (HGL) which are tweful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting WHH fragment, HPL #19 from land (camelid) species
                                                                                                                                                                                                                                                                                                                      61 DSVKGRFTISRDNDKATEYLQMANLKPEDTAVYYCNAQVRVRFSSDYTNYWGQGTQVTVS 120
                                                                                                                                                                                                                                                                                                                                                  DSVKGRFTISRDNDKNTEYLOMNNIKPEDTAVYYCNAQVRVRFSSDYTNYWGQGTQVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Llama antibody, camelid, anorectic, heavy chain variable domain, VHH; human dietary enzyme inhibitor, medicament, human pancreatic lipase, HPL; food; human gastric lipase, HGL; cosmetic control; body weight.
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|label= CDR2
|note= "COmplementarity determining region 2"
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label= cDR1
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Matches 130;
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"Complementarity determining region 1"

CDR3

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Gaps

0,

Length 130; Indels

100.0%; Score 695; DB 4; 100.0%; Pred. No. 1.7e-49; Live 0; Mismatches 0;

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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human distary enzyméps. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human distary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HPL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL HPL inhibiting VHH fragment, HPL HPL inhibiting VHH fragment,
                                                                                                                                                                                                                                                                                                                                                                                       61 DSVKGRPTISRDNDKNTBYLOMMIKPEDTAVYYCNAQVRVRFSSDYTNYWGGGTQVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                         61 DPVKGRFTISRDNGKLTVYLQMNSLKPEDTAVYYCNALIRRKFTSEYNBYWGQGTQVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Llama antibody; camelid; anorectic; heavy chain variable domain; VH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight:
                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                           90
useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                                                                  QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASITATGPPNYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                        81.0%; Score 563; DB 4; Length 130; 80.0%; Pred, No. 1.2e-38; tive 10; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPL inhibiting VHH fragment, HPL #15 from llama species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2001; 2001EP-00200703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE10555 standard; peptide; 131 AA.
                                                               Example 2; Page 10; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2000; 2000EP-00200930
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/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                       Best Local Similarity 80.0
Matches 104; Conservative
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                                                                                                                                                                                                                                             Sequence 130 AA;
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New antibody or its fragments for inhibiting human dietary enzymes,

De Haard JJW, Tareilus E;

Bezemer S, Van De Burg M,

WPI; 2001-572718/65.

(UNIL ) UNILEVER NV.

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Copyright
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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OM protein -92 protein search, using sw model October 5, 2004, 07:04:10 ; search time 98.9043 Seconds (without alignments) 371.381 Million cell updates/sec

Title: Perfect score: Sequence: US-09-805-290A-24 695

QVQLQDSGGGLVQTGGSLRL......WGQGTQVTVSSEPKTPKPQP 130

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A\_Geneseq\_29Jan04:\* geneseqp2003e:\*
geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2001s:\*
geneseqp2003ae:\*
geneseqp2003ae:\*
geneseqp2003be:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

2 563 81.0 130 4 AABIO555 3 523.5 75.3 131 4 AABIO555 4 505.5 72.7 129 4 AABIO555 502 72.2 130 4 AABIO559 8 492 70.8 132 4 AABIO559 9 487.5 70.1 129 4 AABIO559 9 487.5 70.1 129 4 AABIO556 10 47.6 68.5 130 4 AABIO556 11 47.6 68.5 130 4 AABIO567 11 47.5 68.4 131 AABIO567 12 475.5 68.9 131 AABIO5283 14 467.5 67.9 132 4 AABIO5283 14 467.5 67.9 134 AABIO5283 15 463.5 66.7 129 4 AABIO5281 16 463.5 66.7 129 4 AABIO5281 17 463.5 66.7 129 4 AABIO568 18 460.5 66.3 129 4 AABIO568 19 459 65.8 190 7 ABR62883 20 457 65.6 190 7 ABR62883 21 456 65.5 130 5 ABG30972 22 455.5 65.7 134 5 ABG30972 23 454 65.3 134 5 ABG30972 24 453 65.2 190 7 ABR62883 25 452 65.0 190 7 ABR62881	Query  Query  Attach Length DB ID
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## ALIGNMENTS

RESULT 1 AAE10557 AAE10557; AAE10557 standard; peptide; 130 ጅ

10-DEC-2001 (first entry)

HPL inhibiting VHH fragment, HPL #19 from llama species.

Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.

Lama sp

КeУ EP1134231-A1 Region Region Region 19-SEP-2001. Location/Qualifiers /label= CDR1
/note= "Complementarity determining region /note= "Complementarity determining region /label= CDR2 /note= "Complementarity determining .110 CDR3 region

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20-FEB-2001; 2001EP-00200703

14-MAR-2000; 2000EP-00200930

(UNIL ) UNILEVER NV.

Bezemer S, Van De Burg Z De Haard JJW, Tareilus M

WPI; 2001-572718/65.

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Example 2; Page 10; 37pp; English

밁 á

43 5

DSVKGRFTISKDNSKNTLYLOMNSLRAEDTANYYCAGGGGLGL-----GYWGQGTLVTVS 115 DSVKGRFTISRDNDKNTEYLQMNNLKPEDTAVYYCNAQVRVRFSSDYTNYWGQGTQVTVS

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RESULT 14

Q99KA4

ID Q99KA

ID Q99KA

ID Q99KA

AC Q90KA

AC Q90K
Q91WPS
Q91WP
ID Q91WP
ID Q91WP
AC Q91WP
DT 01-DE
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Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003006; Ig_v.
R Pfam; PF00047; 1g; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS05235; IG_LIKE; 4.
PROSITE; PS05230; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 487 AA; ESECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       G91WP5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004786; AAH04786.1; -.
HSSF; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC013656; AAH13656.1; -.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                 SEQUENCE FROM N.A.
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Mus musculus (Mouse).
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; Pred. No. 1.1e-26;
13; Mismatches 32
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                  Query Match 47.8%;
Best Local Similarity 57.3%;
Matches 71; Conservative 1
                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; 2.
                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;
133 SSEP 136
                         120
                                                                                 60
                                                                                                             20
                                                      80 SDTMKGRFTISRDNAKSTLYLOMSSLRSEDTAFYYC-----VR--GGYFDVWGAGTAVTV 132
                                                                                                                            1 QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASITATGPPN-Y
                                                                                                             SSEP 123
                                                                                TDSVKGRFTISRDNDKNTEYLOMNNLKPEDTAVYYCNAQVRVRFSSDYTNYWGQGTQVTV
                                                                                                                                                                  %; Score 332; DB 11;
%; Pred. No. 2e-26;
17; Mismatches 28;
                                                                                                                                                                                             DB 11;
                                                                                                                                                                                               Length 479;
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119 79 59

Search completed: October Job time: 69.8117 secs σ, 2004, 08:13:48

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RESULT 12
Q9HCC1
ID Q9HCC
AC Q9HCC
DT 01-MAD
DT 01-MAD
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HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Ffam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
SMCSITE; PS50835; IG_LIKE; 1.
                   Q9HCC1;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
Single chain Fy (Fragment).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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Liu B., Van der Merwe P.L.,
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Pred. No. 5.1e-28;
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NCBI_TaxID=9606;
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Q9UL9; C19UL9; C19UL9
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
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Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

"An antibody fragment2A3 specific for native lysozyme :Isolaion

human synthetic phage display library and characterization.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AB049915; BAB16829-1; -.

HSSP; P01772; 2FB4.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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IPR003596; Ig_v.
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112 AA;
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                                                                                                                                     Score 337; DB
Pred. No. 8.8e
7; Mismatches
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Pred. No. 5.8
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                                                                                                                                                                                                                                                                             CRC64;
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                                                                                                                                                                                                         Length 116,
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                                                                                                                                            Indels
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                                                                                                                                            Gaps
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RESULTION OF THE CONTROL OF THE CONT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local s
                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa; C
Mammalia, Eutheria, R
NCBI_TaxID=10090;
                                                                                                                                                                                                         01-MAY-2000
01-MAY-2000
01-0CT-2003
                                                                                                                                                                                                                                                                      Q9R1A4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; 19; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 5
PROSITE; PS00290; IG MHC; 3.
                                                                                                                                                                                  Gammal heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                               IGH-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; PL0120; PL0120.
PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (DEC-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8WUK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8WUK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CBI_TaxID=9606;
           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00
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                                                                                                                                                                                                                                                                                                                                                                                               132
                                                                                                                                                                                                                                                                                                                                                                                                                                           114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eco20240; AAH20240.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
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                                                                                                                                                                                                                                                                                                                                                                                             GIMVIVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADSVKGRÉTISRDNSKNTLÝLOMNSLRAEDTAVÝÝC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDSVKGRFTISRDNDKNTEYLOMNNLKPEDTAVYYCNAQVRVRFSSDYT-----NYWGO
                                                                                                                                                                                                                                                                                                                                                                                                                                    SSALADIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYEQAPGKQREMVASITATGPPN-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTQVTVSS-EPKTPKPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTVTVSSASPTSPKVFP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDSVKGRFTISRDNDKNTEYLOMNNIKPEDTAVYYCNAQVRVRFSSD-----YTNYWGQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADSVKGR
                                                                                                                                                                           ) (TrEMBLrel. 13, () (TrEMBLrel. 13, I) (TrEMBLrel. 25, I) 3 (TrEMBLrel. 25, I) vy chain of Mab7 ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TransLrel. 20, Created)
(TransLrel. 20, Last sequence update)
(TransLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                      121
         Ekramoddoullah A.K.M.,
                                                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISRDNAKUSLYLOMNSLRVEDTALYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67296 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.3%;
                                                                                                                                                                         (Fragment).
                                                                                                                                                                                           Created)
Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 342.5; DB 4
Pred. No. 2.2e-27;
9; Mismatches 27
                                                                                         Craniata; Vertebrata; Buteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60C7F59S0671E315 CRC64;
                                                                                                                                                                                                                                                                                      437
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      Misra
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                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
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      S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --AKDWSEGVETFDIWGQ
                                                                                    Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141
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RESULT 10
Q9UL9
D1 Q9UL9
D2 01-MA
D7 01-MA
D8 MAMMA
D7 01-MA
D8 MAMMA
D7 01-MA
D8 MAMMA
D8 MA
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Best Local S
Matches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
NON TER
SEQUENCE
                                           Interfro, 17, 19, 1.
Ffam, PF00047, 19, 1.
SMART; SM00406, IGV; 1.
SMART; SM00406, IGV; 1.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                             Clin. Immunol. Immunopathol. EMBL, AF035023; AAD56259.1; - PIR; S21205; S21205.
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human),
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM0040&; ĪGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UL91;
01-MAY-2000
                                                                                                                                                                   HSSP; P01772;
                                                                                                                                                                                                                                                                                        Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myosin-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UL91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like InterPro; IPR008006; Ig_MHC. InterPro; IPR093596; Ig_v.
                                                                                                                       InterPro; IPR007110;
InterPro; IPR003596;
                                                                                                                                                                                                                                                 etus."
                                                                                                                                                                                                                                                                Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fragment)
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MGI:96446; / Tgh-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 AKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 EPKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVKGRFTISRDNDKNTEYLOMNNIKDEDTAVYYCNAQVRVRFSSDYTNYWGQGTQVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASITATGPPNYTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVKGRFTIYKDKDRNILSLQMSSLRSEDTAMYYC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQLQBSGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASFSSGGIIYYTD
  118
118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel 13, Created)
(TrEMBLrel 13, Last sequence update)
(TrEMBLrel 25, Last annotation update)
cive immunoglobulin heavy chain variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437
  12843 MW;
                                                                                                                   Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48142 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for anti-white and heavy chain v).";
                                                                                                                                                                                                                         87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 341.5; DB
Pred. No. 1.8e-27
4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Catarrhini; Hominidae;
D0633949F2AC149D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                            in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                     Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           white pine blister rust chains) and construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33,
                                                                                                                                                                                                                                                                                                     Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ARGDYSAYWGPGTLVTVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Query Match Best Local Similarity

49.0%;

Score 340.5; DB 4; Pred. No. 3.8e-28;

Length

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114

GTQVTVSSEP-KTPKPQP

130

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Q96KB ID Q96K AC Q96K DT 01-D DT 01-D DT 01-D DT Hypo OS Homo OC Mamm OX NCBII RN [1] 
                                                                                                                                                                                                                                        Q96K68
Q96K68;
f Q1-DEC-2001 (TrEMBLrel. 19, Last ser
T Q1-DEC-2001 (TrEMBLrel. 25, Last an
T Q1-DCT-2003 (TrEMBLrel. 25, Last an
DE Hypothetical protein FLJ14473.
OS Homo sapiens (Human).
OC Sukaryota; Metazoa; Chordata; Crar
Mammalia; Eutheria; Primates; Cat;
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Best Local S
Matches 76
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TISSUE=Mammary gland;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9UL71;
Q9UL71;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
Tin B., Van der Merwe P.L.,
                                                                                                                                                                                                                         EQUENCE
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Young D.C.;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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AF035043; AAD56279.1; -.
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                                                                                                                                                                                                                 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASITATGPPN-Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3.1e
2; Mismatches
                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153
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Catarrhini; Hominidae;
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annotation update)
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                                                                                                                                                                                                                                                                                                                          Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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RESULT 7
VORNSKA
VORNS
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                                                                                                           Query Match
Best Local S
Matches 78
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Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                Strauberg R.;
Sthauberg R.;
Sthauberg R.;
Sthauberg R.;
Sthauberg R.;
InterPro; IPR003599; Ig.:
InterPro; IPR003599; Ig.-1:
InterPro; IPR003597; Ig.-1:
InterPro; IPR003067; Ig.-Wi.;
InterPro; IPR003596; Ig_-Wi.;
InterPro; IPR003596; Ig_-W.;
InterPro; IPR003596; Ig_-W.;
Sthaupergrouperscripts Research Researc
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01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                             PROSITE; PS50835; IC_LIKE; 4. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
Homo sapiens (Human).
Eukalyota, Metazoa; Chordata;
Mammajia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR007110;
Interpro; IPR003006;
Interpro; IPR003596;
Interpro; IPR003596;
Pfam; PF00047; 19; 4
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003
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"NEDO human cDNA sequencing project.";
submitted (MAY-2001) to the EMBL/GenBank/DDBJ EMBL; AKO27379; BAB55072.1; -..
PIR; S21205; S21205.
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PROSITE; PS50835; IG LIKE; 4.

PROSITE; PSC02290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TaxID=9606;
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78;
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                                                                                                                                         Similarity
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80; Conservative
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                                                                                                                                                                                                                          11 protein
499 AA;
                                                                                                           49.3%;
ilarity 56.5%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                          53376 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig-like.
Ig_c1.
Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53088 MW;
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Ig_MHC.
Ig_v.
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                                                                                                        Score 342.5;
Pred. No. 1.7e
L5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                       93A5C89582054F32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9A1D7AEB5AEE4C0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351; DB 4;
No. 2.1e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ishii S., Kawai
Y., Nagahari K.,
                                                                                                                                   ; DB 4
.7e-27;
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                                                                                                                                                              4.
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                                                                                                                                                           Length
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Masuho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494;
                                                                                                                                                                 499;
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                                                                                                        9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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LRLSCA:TSGFTFDDSGASWVRQAPGKGLEWVSSINWNGGSTNY

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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #14 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                          New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQDGGSTNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DSVKGRFTISRDNILNTVYLOMNSLKPEDTAVYHCNADVRPYRTSRYLELWGQCTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 OVOLODSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASITATGPPNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DSVKGRFTISRDNDKNTEYLQMNNLKPEDTAVYYCNAQVRVRFSSDYTNYWGQGTQVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
label= CDR1
note= "Complementarity determining region 1"
                                                              71.9%; Score 500; DB 4; Length 130; 73.8%; Pred. No. 1.7e-33; tive 10; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGL inhibiting VHH fragment, HGL #9 from llama species.
                                                                                                                                                                                                                                                                                                                          Tareilus E;
                                                                                                                                                                                                                                                                                                                            De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 9; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE10563 standard; peptide; 124
                                                                                                                                                                                                                                            14-MAR-2000; 2000EP-00200930
                               50. .64
/label= CDR2
                                                                                                                                                                                                             20-FEB-2001; 2001EP-00200703
                                                                                                                                                                                                                                                                                                                            Van De Burg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96; Conservative
                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-572718/65.
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Best Local Similarity
                                                                                                                                                                                                                                                                          UNIL ) UNILEVER
UNIL ) UNILEVER
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                                                                                                                                               EP1134231-A1
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                                                                                                                                                                                                                                                                                                                            Bezemer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #9 from lama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DSVKGRFTISRDNDKNTEYLQMNNIKPEDTAVYYCNAQVRVRFSSDYTNYWGQGTQVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASITATGPPNYT 60
                                                                                                                                                                                                                                                                                                                                                                                               New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSVKGRFTISRDNIKNTMYLQMNSLKPEDTGVYYCAG-----TGAEGHYWGQGTQVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGGGLVQAGGSLRLSCAASGSIGSLYVMSWYRQAPGKQREPVAALMGSGSTTYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                98. .104
/label= CDR3
/note= "Complementarity determining region 3"
                                                                             "Complementarity determining region 1"
                                                                                                                    /note= "Complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 492; DB 4; Length 12
Pred. No. 7.2e-33;
9; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                           Tareilus E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
                                                                                                                                                                                                                                                                                                                                            De Haard JJW,
                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide; 129
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                                                                                                                                                                                                                                             20-FEB-2001; 2001EP-00200703
                                                                                                                                                                                                                                                                        .4-MAR-2000; 2000EP-00200930
                                                       1. .35
|label= CDR1
                                                                                                         /label= CDR2
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Best Local Similarity
'-heq 95; Conserve
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                                                                                                                                                                                                                                                                                                  (UNIL ) UNILEVER (UNIL ) UNILEVER
                                                                                                                                                                                                                                                                                                                                                                                                                                           of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 124 AA,
                                                                                                                                                                                         EP1134231-A1
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              Lama sp.
                                                    Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #22 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
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                                                                                                                                                                    /label= CDR3
/note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 129;
                                                                                                                 "Complementarity determining region 1"
                                                                                                                                                "Complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
HPL inhibiting VHH fragment, HPL #22 from llama species.
                                                                                                                                                                                                                                                                                                                       Tareilus E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.1%; Score 487.5; DB 4; 71.5%; Pred. No. 1.8e-32; ive 14; Mismatches 22;
                                                                                                                                                                                                                                                                                                                      De Haard JJW,
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 10; 37pp; English.
                                                                                                                                                                                                                                                                 14-MAR-2000; 2000EP-00200930.
                                                                                                                                                                                                                                             20-FEB-2001; 2001EP-00200703
                                                                                                                                      /label= CDR2
                                                                                                        /label= CDR1
                                                                                                                                                                                                                                                                                                                      Bezemer S, Van De Burg M,
                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 71.5 93; Conservative
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                                                                                                                                                   'note=
                                                                                                                                                                                                                                                                                       (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC
                                                                                                                                                                                                                                                                                                                                           WPI; 2001-572718/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 129 AA;
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                                                               Lama sp.
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #15 from lama (camelid) species
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                                                                                                                Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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                                                                                                                                                                                                                                                                                                                                                                                                        "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complementarity determining region
                                                              HGL inhibiting VHH fragment, HGL #15 from llama species.
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                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                         50. .64
/label= CDR2
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/label= CDR3
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/label= CDR1
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(first entry)
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les 92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1134231-A1
   10-DEC-2001
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115 SEPKTPKPÓP 124

AAE10566 ID AAE10566 standard, peptide, 124 AA.

RESULT 10

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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #10 from llama (camelid) species
                                                                                                                                                Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                                                                   98. .110
/label= CDR3
/note= "Complementarity determining region 3"
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                                                                                                                                                                                                                                                                                        'note= "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                    /label= CDR2
/note= "Complementarity determining region
                                                                                                                      HGL inhibiting VHH fragment, HGL #16 from llama species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tareilus E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De Haard JJW,
                                                                                                                                                                                                                                              Location/Qualifiers
                             AAE10567 standard; peptide; 130 AA.
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                                                                                                                                                                                                                                                             31. .35
/label= CDR1
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                                                                                       (first entry)
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                                                                                         10-DEC-2001
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                                                            AAE10567;
                                                                                                                                                                                                               Lama sp.
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RESULT 11
                AAE10567
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The invention describes a protein array (I) comprising a number of heavychain variable domain antibodies or antibody fragments, obtainable from chain variable domain antibodies or antibody fragments, obtainable from camelidae. The method is useful for removing abundant proteins from an extract or sample which do not provide useful information on the condition of a call or tissue in the extract or sample to be investigated. (I) is useful for detecting the presence of individual proteins in a sample, comparing the distribution of proteins in different call types, and identification of proteins that may be of importance in determining the altered properties of calls in disease, aging or other conditions. Using a heavy-chain variable domain derived from an immunoglobulin that is naturally devoid of 11940 times, and detection of provides a number of advantages, such as an improvement of sensitivity/resolution in the order of 10-100 times, and detection of post-translationally modified proteins. The invention also describes a method (II) that enables the simultaneous processing of large numbers of target antigens in a controlled way. The incorporated phage-ELISA callows the complete automation about the success or failure of a certain panning condition. This feature concline with the microtiter place format allows the complete automation of the technology, based on computer-made
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        decisions on the values of the phage-ELISA for continuation of a limited number of selections. In (II), due to the fact that many different conditions can be tested, varying amounts of input-phages can be used simultaneously in order to decrease the enrichment of sticky phage-antibodies. Micro-panning is an effective tool for selecting both naive, synthetic and immune libraries on large numbers of different target molecules, enabling the generation of large panels of antibodies in short time frames needed for the generation of arrays (proteomics). This sequence represents an immunoglobulin (IgG) heavy chain variable domain
61 DSVKGRFTISRDNARGTVYLQMNSLKPEDTAVYYCAAARSLELTPTSYDYWGQGTQVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel protein array useful for detecting the presence of individual proteins in sample, comprises heavy-chain variable domain antibodies or antibody fragments obtainable from Camelidae.
                                                                                                                                                                                                                                                                                                                                                                                                    Heavy chain variable domain; antibody; protein array; aging; VHH; immunoglobulin; sticky phage-antibody; micro-panning; immune library;
                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin G specifc heavy chain variable domain antibody #3.
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                                                                                                                                                                                                                ABG30620 standard; protein; 131 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-DEC-2000; 2000EP-00311142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-DEC-2001; 2001WO-EP014471.
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(UNIL ) HINDUSTAN LEVER LTD.
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                                                SEPKTPKPQP 130
                                                                                           SEPKTPKPQP 130
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68.5%; Score 476; DB 4; Length 130; 72.3%; Pred. No. 1.6e-31; ive 9; Mismatches 27; Indels

94; Conservative

Local Similarity

Best Loca Matches

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Query Match

9

DSVKGRFIISRDNDKNIEYLOMANLKPEDTAVYYCNAQVRVRFSSDYINYWGQGTQVTVS 120

61

1 QVQLQESGGGLVQAGGSLRLSCAASGSDFRYNAMAWYRQAPGKQRKLVATITYTYRTNYA 60 1 QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASITATGPPNYT

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Sequence 152 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
                                                                                                                                        61 DSVKGRFTISRDNDKNTEYLQMNNLKPEDTAVYYCNAQ-VRVRFSSDYTNYWGQGTQVTV 119
                                                                                                                                                               61 DSVKGRFTISRDNAKNIVYLQMNSLKPEDIGVYYCNAETVRATIGRFITDLWGQGTIVTV 120
                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                Potato; heavy chain immunoglobulin; pathogen resistance;
metabolism modulator; passive immunisation; heavy chain variable domain;
VH; anti-potato SBEII; starch branching enzyme; SBE A.
                                                                                                           1 QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASITATGPPNYT
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                           Anti-potato SBEII (Clone46) VH region attached with myc and his6 tag.
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                                               Length 131;
                                                                     27; Indels
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                                               DB 5;
                                              68.4%; Score 475.5; DB 5 73.3%; Pred. No. 1.7e-31;
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                                                                     7; Mismatches
                                                                                                                                                                                                                                                                      AAE05283 standard; protein; 152 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Van Der Logt CPE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99EP-00310188,
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                     96; Conservative
                                                                                                                                                                                        SSEPKTPKPOP 130
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                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               Solanum tuberosum.
Unidentified.
Chimeric.
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                        Sequence 131 AA;
 antibody (VHH)
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                                               Query Match
Best Local S
                                                                     Matches
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extracting and isolating the product. In particular, edible selected antigens may be used in a method of passively immunising an animal, preferably human, against the antigen, e.g., pathogenic organisms. The present sequence is an anti-potato SBEI antibody (denoted Clone46) heavy chain variable domain (VH) attached to peptide linkers, myc and hisé tag. The potato SBEII is a starch branching enzyme also designated SBE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSVKGRFTISRDNDKNTEYLQMNNLKPBDTAVYYCNA-QVRVRFSSDYTNYWGQGTQVTV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
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                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGGGLVQAGGSLRLSCVASGNTFSIIAMAMYRQAPGKQREVVASINSIGSTNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSVKGRFTISRDNAKNTVYLQMSSLKPEDTAVYYCAAGNLLVK-----RPYWGQGTLVTV
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/label= CDR3
/note= "Complementarity determining region 3"
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                                                                                                                                                                                                                                                                      Length 152;
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                                                                                                                                                                                                                                                                Score 472; DB 4; Length 15
Pred. No. 3.9e-31;
8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGL inhibiting VHH fragment, HGL #4 from llama species.
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                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.5%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .35
label= CDR1
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/label= CDR2
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The patent discloses antibodies or their fragments comprising a heavy devoid of light chains specific for inhibiting human distary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human panoreatic lipse (HPL) or human gastric lipse (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting WHH fragment, HGL #4 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                           61 DSVKGRFTIARENAKNIVYLQMSSLKPEDTAVYYCKGRGGLTQYSEH-DYWGGGTQVIVS 119
                                                                                                                                                                                                                                                                                                                         61 DSVKGRFTISRDNDKNTEYLOMNNLKPEDTAVYYCNAOVRVRFSSDYTNYWGOGTOVTVS 120
                                                                                                                                                                                                                                                                                  1 QVQLQESGGGLVQAGGSLRLSCAASGSTFSFNAMGWYRQVPGKQRELVAAIGNDGATYYV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potato; heavy chain immunoglobulin; pathogen resistance; metabolism modulator; passive immunisation; heavy chain variable domain; WH; anti-potato SBEII; starch branching enzyme; SBE A.
                                                                                                                                                                                                                                                                 QVQLQDSGGGLVQTGGSLRLSCAASGPIGDVYLMGWYRQAPGKQREMVASITATGPPNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-potato SBEII (Clone68) VH region attached with myc and his6 tag
                                                                                                                                                                                                       Length 129;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                      67.3%; Score 467.5; DB 4; 70.8%; Pred. No. 7.7e-31; ive 12; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE05288 standard; protein; 149 AA.
Example 4; Page 13; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-2000; 2000EP-00310997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-00310188
                                                                                                                                                                                                   Query Match
Best Local Similarity 70.8%
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   121 SEPKTPKPQP 130
                                                                                                                                                                                                                                                                                                                                                                                                              120 SEPKTPKPOP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanum tuberosum.
Unidentified.
                                                                                                                                                                           Sequence 129 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE05288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
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Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a

Teh Y;

Jobling SA,

Frenken LGJ, Van Der Logt CPE,

WPI; 2001-427157/46. N-PSDB; AAD10059.

UNIL ) UNILEVER PLC (UNIL ) UNILEVER NV.

The present invention relates to a method for modifying a plant to

Example 13; Fig 28; 81pp; English

cellular compartment.

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Uncrional equivalent, on a callular compartment comparises introducing a DNA sequence encoding a heavy chain immunoglobulin, where the DNA is linked to prometers and provided with a additional sequence encoding a peptide capable of targeting heavy chain immunoglobulin to a callular compartment. The method is used for producing a heavy chain compartment. The method is used for producing a heavy chain to a callular compartment. The method is used for producing a heavy chain to a collular compartment. The method is used for producing a heavy chain to a collular compartment is functionally equivalent for increasing the pathogen resistance in a plant or to modulate metabolism in a plant. Under some circumstances it may be carriachle to retain the antibody product with the plant rather than carriachle to retain the antibody product with the plant rather than artigens may be used in a method of passively immunising an animal, preferably human, against the antigen, e.g., pathogenic organisms. The preferably human, against the antigen, e.g., pathogenic organisms. The present sequence is an anti-potato SBEII attibody (denoted Clone60) heavy chain variable domain (VH) attached to peptide linkers, myc and his6 tag. The potato SBEII is a starch branching enzyme also designated SBE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSVKGRFTISRDNAKUTIYLQMSLKPEDTAVYYCTAG-----GSYWGQGTQVTVA 113
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produce an antibody or an active fragment or derivative, or a protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.0%; Score 465.5; DB 4; 72.3%; Pred. No. 1.3e-30; iive 9; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: October 5, 2004, 08:00:13 Job time: 99:9043 secs
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Best Local Similarity 72.38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 149 AA;
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1; Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 5, 2004, 07:36:16; Search time 20.9028 Seconds (without alignments) 593.639 Million cell updates/sec Run on:

US-09-805-290A-25 674 1 QVQLQESGGGLVQAGGSLRL......GGQGTQVTVSSEPKTPKPQP 129 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 2

Ig heavy chain V region pe20 - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999
C.Accession: S5536
R.Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995 #concolonal anti-proenkephalin antibodies using utations in the variable region genes.
A.Feference number: S55526; MUID:95239763; PMID:7536850
A.Accession: S5536
A.Accession: S5536
A.Accession: S5536
A.Accession: S1528
A.Fetus: preliminary
A.Molecule 'rype: mRNA
A.Residues: 1-120 < COSE>
A.Residues: 1-120 < COSE>
A.Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305

53

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C'Species Homo sapiens (man)
C'Accession: Discology #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C'Accession: Discology Homo for the follogy is the following following the following followi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gibecies: Mus musculus (house mouse)
CiSpecies: Musculus (house mouse)
CiAccession: S5539
RiBoettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
RiBoettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
RiBoettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A. Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using utations in the variable region genes.
A. Pateriance number: S5529
A. Accession: S5539
A. Residues: 1-120 cBOE.
A. Cross-references: EMBL: X82593; NID: 9854312; PIDN: CAAS7929-1; PID: 9854313
C; Superfeanily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 14-97/Domain: immunoglobulin homology < INM>
                                                                                                                                                                                              61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC-AKDRGFWSGYKDYWGQGTLVTVS 119
                                            60 TDSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGSWNDYGGQGTQVTVS
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C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: 331110
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: 331104; MUID:92111633; PMID:1730252
A;Accession: S31110
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule_type: mRNA,
A;Residues: 1.116 < RAAA>,
A;Cross-references: EMBL.X62958
A;Cross-references: EMBL.X62958
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology < IMM>
F;15-97/Domain: immunoglobulin homology < IMM>
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R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S48798
A;Status: preliminary
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A.Residues: 1-120 «MAH»
A.Cross-references: EMBL:246382; NID:9562324; PIDN:CAA86521.1; PID:91340167
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                           1 VQLQESGGGLVKPGGSLKLSCAASGFTFSTYAMSWVRQTPEKRLEWVATISSGGSYTYYP
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                                                                                                                                                     Length 120;
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llarity 65.3%; Pred. No. 4.1e-25;
Conservative 12; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 116;
        C, Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                 // Score 368.5; DB 2; Length
// Pred. No. 3e-25;
11; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 368; DB 2;
Pred. No. 3.2e-25;
14; Mismatches 26;
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C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
                                        C; Keywords: heterotetramer; immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                         54.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 63.3%;
Matches 76; Conservative 14
                                                                                                                                                 Query Match
Best Local Similarity 65.0
Matches 78; Conservative
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Best Local Similarity
Matches 79; Conserv
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CjAccession: S55540
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
Nol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using utations in the variable region genes.
A;Reference number: S55528; MUID:95239763; PMID:7536850
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R;Mortari, F.; Newton, U.A.; Wang, U.Y.; Schroeder Ur., H.W.

Bur. J. Immunol. 22, 241-245, 1992

A;Title: The human cord blood annibody repertoire. Frequent usage of the V(H)7 gene famil A;Reference number: S26786; MUID:92111632; PMID:1730251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region pel3 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct_1995 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .Species: Homo sapiens (man)
.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
                                                                      60 TDSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYC---KALISSYDGSWNDYGGQGTQV
                                                                                                                                                                            61 ADSVKGRFTISRDNSKYLYLQMNSLRAEDTAVYYCAKDRRLTGTF-----DYWGQGTLV
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                                     QVQLQESGGGLVQAGGSLRLSCAASGS1RS1S1MTWYRQAPGKERELVARMS-SDGTTSY
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A;Residues: 1-121 <BOE>
A;Cross-references: EMBL:X82582; NID:g854288; PIDN:CAA57918.1; School-serences: EMBL:X82582; NID:g854288; PIDN:CAA57918.1; School-serences: Employed in white immunoglobulin C;Keywords: heterotectamer; immunoglobulin F;14-97/Domain: immunoglobulin homology <INM>
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53.7%; Score 362; DB 2;
Best Local Similarity 63.6%; Pred. No. 1.1e-24;
Matches 77; Conservative 14; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region - human
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Best Local Similarity 64.2
Matches 79; Conservative
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R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31107
A;Accession: S31107
A;Accession: S1107
A;Molecule type: mRNA
A;Residues: 1-19 - KRAA
A;Cross-references: EMBL:X62955
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin
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Cy Species: Homo sapiens (Man)
Cy Species: Homo sapiens (Man)
Cy Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
Cy Accession: S1108
Ry Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
A) Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A) Reference number: S31104; MUID:92111633; PMID:1730252
A) Accession: S3108
A) Accession: S3108
A) Accession: S1108
A) Molecule type: mENA
A) Residues: 1-119 eRAA>
A) Coss-references: EMBL:X62956
A) Cross-references: EMBL:X62956
A) Cross-references: EMBL:X62956
C) Superfamily: immunoglobulin V region; immunoglobulin homology
C) Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IVM>
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Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
                                                                                                                                                       1 VQLQESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVATISSSGSYTYYP
                                                                                                                                                                                                                                                             61 DSVKGRFTMSRDNAKNTLYLQMSSLRSEDTAMYYCVRLYYDYDPYVMDYWGQGTTVTVSS
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     54.1%; Score 364.5; DB 2;
64.2%; Pred. No. 6.7e-25;
ive 12; Mismatches 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.9%; Score 363.5; DB 2
66.4%; Pred. No. 8.1e-25;
iive 12; Mismatches 24
Query Match
Best Local Similarity 64.2%
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 66.4
Matches 81; Conservative
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C) Species: Homo saptens (man)

C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996

C; Accession: 805271; 804602

R; Kishimoto, T.

Submitted to the EMBL Data Library, March 1989

A; Reference number: 805270

A; Accession: 805271

A; Molecule type: mRNA

A; Accession: 805271

A; Molecule type: mRNA

A; Cross -references: EMBL:X14584

A; Cross -references: EMBL:X14584

A; Cross -references of the cDNAs encoding the V-regions of H- and L-chains of s

A; Accession: 804601; MUID:89296497; PMID:2506644

A; Reference number: 804601; MUID:89296497; PMID:2506644

A; References: EMBL:X14584

A; Accession: 804602

A; Molecule type: mRNA

A; Residues: 1-144 - KKIS2>

A; Molecule type: mRNA

A; Residues: 1-144 - KKIS2>

A; Cross -references: EMBL:X14584

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>
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C;Species: Homo sapiens (max)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 1992
A;Refusion: Machanisms that generate human: immunoglobulin diversity operate from the {
A;Recession: S1686
A;Residues: Dreliminary
A;Nolecule type: mRNA
A;Residues: 1-140 <CUI>A;Residues: 1-140 <CUI>A;Residues: 1-140 <CUI>A;Residues: 1-140 <CUI>A;Cross-references: ENBL: Z14205; NID:330969; PIDN:CAA78574:1; PID:330970
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                            61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYC-ARSRNYDSSGYYSHYFDYWGQGT 119
                                 TDSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGS-----WNDYGGQGT
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1 OVOLOESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGTT-SY
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C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
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A.Residues: 1-123 cRAA-
A.Cross-references: EMBL:X62963
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C.Superfamily: immunoglobulin v region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mana
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C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30531
R;Mariette, X.
                                                                         1 QVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMS-SDGTTSY
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A;Reference number: 830520
A;Accession: 830531
A;Accession: 830531
A;Accession: 830531
A;Accession: 123531
A;Moss-references: EMBL:218317
A;Cross-references: EMBL:218317
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Superfamily: incertramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <1MM>
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Ig heavy chain - human
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F;20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                     Query Match 53.6%; Score 361.5; DB 2; Length 160; Best Local Similarity 64.8%; Pred. No. 1.7e-24; Matches 81; Conservative 12; Mismatches 27; Indels 5;
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g heavy chain V region - human Species: Homo sapiens (man) Species: Homo sapiens (man) Species: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000 Species: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000 Mortari, F.; Newron, J.A.; Wang, J.Y.; Schroeder Jr., H.W. Mr. J. Immunol. 22, 241-245, 1995 Species: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene familizeference number: S26786; MUID:92111632; PMID:1730251

A;Status: preliminary A;Wolecule type: mRNA A;Residuse: 1-121 <MOR> A;Cross-references: EMBL:X61015; NID:g32795; PIDN:CAA43349.1; PID:g1335126 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin

Search completed: October 5, 2004, 08:17:17 Job time : 21.9028 secs

60 TDSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGSWNDYGGQGTQVTVS 119

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1 QVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGT-TSY 59 

Ouery Match 53.5%; Score 360.5; DB 2; Length 121; Best Local Similarity 63.6%; Pred. No. 1.5e-24; Matches 77; Conservative 10; Mismatches 33; Indels 1;

F,15-98/Domain: immunoglobulin homology <IMM>

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1 QVQLQESGGGLVQAGGSLRL.....GGQGTQVTVSSEPKTPKPQP 129
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P01811 mus musculu	HV41 MOUSE	Н	117	43.8	295.5	44
P18528 mus muscul	HV57 MOUSE	-	86	44.0	296.5	43
P18525 mus muscul	HV54_MOUSE	Н	117	44.1	297.5	42
P01775 homo sapie	HV3N_HUMAN	Н	119	44.2	298	41
P01776 homo sapie	HV30_HUMAN	н	117	44.2	298	40
P01787 mus muscul	HV18_MOUSE	Н	123	44.3	298.5	39
P01796 mus muscul	HV27 MOUSE	Н	113	44.3	298.5	38
P01804 mus musculu	HV35_MOUSE	Н	111	44.4	299	37
P01793 mus muscul	HV24 MOUSE	Н	123	44.4	299.5	36
P01789 mus muscul	HV20 MOUSE	Н	122	44.7	301	35
P01791 mus muscul	HV22_MOUSE	Ħ	123	44.7	301.5	34

## ALIGNMENTS

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.7	ANDLINE-81289131; PubMed=684994; Schmidt W.E., Jung HD., Palm W., Hilschm "Three-dimensional structure determination structure of crystallized monoclonal immun structure of crystallized monoclonal immun [2] X-RAY CRYSTALLOGAMPHY (1-9 ANGSTROMS). MATQUART W., Deisenhofer J., Huber R., Pallimunoglobulin molecule Kol and its antige and 1.0-A resolution."; J. Mol. Biol. 141:369-391 (1880).  PIR, A02055; GHUKL.	PDB; 2FB4; 12-JUL-89. PDB; 2G2; 12-JUL-89. G0; G0:0005576; C:extri G0; G0:0005823; F:antig G0; G0:0005823; F:antig G0; G0:0006823; F:antig G0; G0:0006823; F:antig G0; G0:0006823; F:antig G0; G0:0008823; F:antig G0; G0:000823; F:antig G0; G0:000823; F:antig Enterpro; IPR003296; Ig FRANT; SM0406; IGV; I. FROSITE; PSS0835; IG I. FROMAIN MOD RES I mmunoglobulin V region DOMAIN MOD RES I mmunoglobulin V region DOMAIN MOD RES I mmunoglobulin V region FRANT I I I I I I I I I I I I I I I I I I I	STRAND
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MEDLINE=78137069; PubMed=416441;

Torano A., Putnam F.W.;

Torano A., Putnam F.W.;

"Complete amino acid sequence of the alpha 2 heavy chain of a human 19A2 immunoglobulin of the A2m (2) allotype.";

"Complete amino acid sequence of the alpha 2 heavy chain of a human 19A2 immunoglobulin of the A2m (2) allotype.";

"In ISACELIANDOONS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C. I. MISCELLANDOONS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C. I. SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR, AGOSOO, ASTUBUR.

RHSSP, PO1789; F:antlugen binding; NAS.

GO; GO:0005876; C:extracellular; NAS.

GO; GO:0005876; P:immune response; NAS.

RICETO: IPRO07110; Ig-like.

RICETO: IPRO07110; Ig-like.
                                                                                                          1 QVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGT-TSY
                                                                                                                                                                                                              60 TDSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGSW--NDYGGQGTQVT
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                                                                                                                                                      1 BVQLVESGGDLVQPGRSLRLSCAASGFBFBBLGMTWVRQAPGKGLEWVANIKZBGSZZBY
                                                       Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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49.1%; Score 331; DB 1; Length 116; 59.3%; Pred. No. 1.5e-25; ive 11; Mismatches 29; Indels
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115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homo sapiens (Human)
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(Rel. 01, Last sequence update)
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
        Query Match
Best Local Similarity 59.33
Matches 73; Conservative
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Best Local Similarity
Matches 69; Conserv
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P01770;
21-JUL-1986 (
21-JUL-1986 (
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HV3F HUMAN
ID HV3F HUMAN
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SEQUENCE
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submitted (JUN-1975) to the PIR data bank.
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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12730 MW; 2C67CA9AAAA1282 CRC64;
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PIR, A02064; M3HUGL.
HSSP, P01772; PEB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                 13718 MW; E4D71B52B16F8776 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   ; Score 334; DB 1;
; Pred. No. 8.2e-26;
13; Mismatches 33;
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21-UUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10 heavy chain V-III region GAL.
Homo sapiens (Human)
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PEAM, PF00047; 19; 1.
SWART, SM00406; IGV; 1.
PROSTIE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                         49.6%;
58.7%;
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Query Match
Best Local Similarity
74; Conservative ....
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73
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                66
68
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1109
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1126
126
84,
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NCBI_TaxID=7957;
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P01765;
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HVOS CARAU STANDARD; PRT; 116 AA.
P19181;
01-NOV-1990 (Rel. 16, Last sequence update)
11-VUL-1999 (Rel. 38, Last annotation update)
11-Vul-1999 (Rel. 38, Last Sequence update)
11-Vul-1999 (Rel. 38, Last Sequence update)
11-Verinopterypii, Nectorial (Annotate)
12-Verinopterypii, Nectorial (Annotate)
13-Verinopterypii, Nectorial (Annotate)
14-Verinopterypii, Nectorial (Annotate)
15-Verinopterypii, Nectorial (Annotate)
16-Verinopterypii, Nectorial (Annotate)
17-Verinopterypii, Nectorial (Annotate)
18-Verinopterypii, Nectorial (Annotate)
                                                                                                                                                                                                                                                                                                                                                             Dreker L., Schwarz J., Reichel W., Hilschmann N.; Rule of antibody structure. The primary structure of a monoclonal 1991 immunoglobulin (myeloma protein Nie). I: Purification and characterization of the protein, the L- and H-chains, the characterization of the protein, the L- and H-chains, the Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

-I. MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA.
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region NIE.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                         Ponstingl H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.", Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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48.4%; Score 326.5; DB 1; Length 119;
Best Local Similarity 58.5%; Pred. No. 4.1e-25;
Matches 72; Conservative 15; Mismatches 29; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
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-- SIMILARITY: Contains 1 immunoglobulin-like domain.
-- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSSP, A91668; GIHUNI
HSSP, 201772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005555; F:antigen binding; NAS.
GO; GO:006555; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
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119 119
119 AA; 13242 MW; C96935A6B55E165B CRC64;
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
Immanoglobulin 1 112. IG-LIKE.
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                 MEDLINE=88144476; PubMed=3125551; Wilson W.; Middleton D., Warr G.W.; "Immunoglobulin heavy chain variable region gene evolution: structure and family relationships of two genes and a pseudogene in a teleost fish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=78005528; PubMed=409716;
Wang A.-C., Mang I.Y., Fudenberg H.H.;
"Immunoglobulin structure and genetics. Identity between variable regions of a mu and a gamma2 chain.";
J. Biol. Chem. 252:7192-7199(1977).
-!- MISCELLANBOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS OF IGM AND 16G2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL GALMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                          IG HEAVY CHAIN V REGION 5A.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 48.4%; Score 326; DB 1; Length 116; Similarity 67.4%; Pred. No. 4.5e-25; 64; Conservative 12; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12808 MW; 9C2279E2DF199B12 CRC64;
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR, A02048; H3HUTL.
HSSP; P01772: 2PEA
                                                                                                                 Proc. (Matl. Acad. Sci. U.S.A. 85:1566-1570(1988)
HSSP; P01772; ZFB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; MO0040; ig; 1.
Immunoglobulin V region; Signal.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11g heavy chain V-III region Til.
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SEQUENCE FROM N.A.
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us-09-805-290a-25.rsp

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IG HEAVY CHAIN V-III REGION VH26. IG-LIKE.
                                                                                                                                        13240 MW; 577B4F1DB675C1F1 CRC64;
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SMART; SM00406; IGy; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
SIGNAL
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EMBL, M35415; AAA58735.1; -.
PIR, A02047; H3HU26.
PDB, 1HOU, 23-DEC-99.
Genew, HGNC:5545; IGHV@.
GO, GO:0005576; C:extracellular; NAS.
GO, GO:0005823; P:antigen binding; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR007110; IG-like.
                                                                                                                                                                            Query Match
Best Local Similarity 58.23
Matches 71; Conservative
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                                                                                                                                                                                  1 QVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSS-DGTTSY
                                                                                                                                                                                                             Gaps
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MEDLINE-7922895; PubMed=111245;

Rao D.N., Rudixoff S., Krutzsch H., Potter M.;

Rao D.N., Rudixoff S., Krutzsch H., Potter M.;

"Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential roll in generating diversity in complementarity-determining regions.";

Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction study at 2.6-A resolution."; Proteins 1:74-80(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE=88217852; PubMed=3449853;
Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
Davies D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
29-FEB-2004 (Nel. 41, Last annotation update)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus.
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                                                                                                           48.3%; Score 325.5; DB 1; Length 115; 58.2%; Pred. No. 5e-25;
                                                         115 115 115 115 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;
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                                                                                                                                                 17; Mismatches
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PDB; ZFBJ; 15-CCT-90.
InterPro; IPR007110; Ig-like.
InterPro; IPR007396; Ig_v.
Pfam; PF00047; ig; 1.
PROSITE, PS08035; IG LIKE; 1.
Imwunoglobulin V region; 3D-structure.
ONN TER 119 119 119
STRAND 3 7
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 PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
DOMAIN 1 108
                                                                                                                                                 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                          119
                                                                                                                                                                                                                                                                                                                                                                                                                       61 TPSLKDKFIISRDNAKNSLYLQMSKVRSEDTALYYCARL--HYYG-YNAYWQQGTLVTVS 117
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                                                                                                                                                                             1 QVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSD-GTTSY
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11 heavy chain V-III region VH26 precursor.
12 heavy chain V-III region CH26 precursor.
13 heavy chain Melacona (Charata, Craniata, Vertebrata, Buteleostomi, Manalla, Butheria, Primates; Catarrhini, Hominidae, Homo.
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BEDLINES allo10909.

Matchyssens G., Rabbitts T.H.;

"Structure and multiplicity of genes for the human immunoglobulin
"Structure and multiplicity of penes for the human immunoglobulin
Bery chain variable region.";

Proc. Nall. Acad. Sci. U.S.A. 77:6561-6565(1980).

-! SIMILARITY: Contains 1 immunoglobulin-like domain.
48.2%; Score 325; DB 1; Length 119; 58.2%; Pred. No. 5.8e-25; ive 17; Mismatches 30; Indels
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PRT;

STANDARD;

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HV16 MOUSE
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The main acid sequence of the variable region of a human mu chain:

I cation of a possible with segment, ", amino acid sequence of the variable region of a human mu chain:

I cation of a possible with segment, ", and the sequent, ", and the sequent, ", and the sequent, ", and the sequent, ", and the with sequent sequ
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                                                                                                                                                 1;
                                                                                      DB 1; Length 117;
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47.5%; Score 320; DB 1; Length 12:
Best Local Similarity 56.5%; Pred. No. 1.8e-24;
Matches 70; Conservative 16; Mismatches 32; Indels
                                                                                                                                              Indels
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117
12582 MW; E826733F1A3CB0F1 CRC64;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                   ch 18:1%; Score 324.5; DB 1; Similarity 69.8%; Pred. No. 6.36-25; 67; Conservative 10; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                    80 GDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC 115
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21-UU-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homo sapiens (Human).
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117 AA;
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RESULT 10 HV16\_MOUSE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGSWNDYGGQGTQVTVSS
                                                                                                                                                                                                                                                                                                                                                     "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGTT-SYT
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MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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D SEGMENT:
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15071 MW; 2276A98DBDBF7016 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 17-136.
MEDLINE=77100368; PubMed=401950;
Adetudpo K., Milstein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
Nature 265:299-304(1977).
                                        21.JUL-1986 (Rel. 01, Created)
21.JUL-1986 (Rel. 01, Last sequence update)
10.GCT-2003 (Rel. 42, Last annotation update)
11 heavy chain V region MOPC 21 precursor (Fragment).
Mus musculus (Mouse).
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DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).
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PROSITE; PS50835, IG_LIKE; 1.
IMMUNOGlobulin V region; Signal; 3D-structure.
SIGNAL <1 16
136 AA
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig v.
Pfam; PF00047; ig; 1.
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Obst Local Similarity 60.00,
Dest Local Similarity 60.00,
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136 AA;
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HV02_CANFA
ID HV02_CANFA
AC F01785;
DT 21-JUL-1986 (
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InterPro, IPR007110; Ig-like.
InterPro, IPR005596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
I 117 IG
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HV3B_HUMAN
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Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
Ista Doublin heavy Chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-determining regions. "I Scorpilamentarity-determining regions."
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).
-! MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN THAT BINDS GALACTAN.
-! SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR, A02077; AVMSX4.
HSSP; P01810; 2FBJ.
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                                                                                                                                                                                                                          MEDINES 80077682; PubMed=117299; MCCumber L.J., Capra J.D.; McCumber L.J., Capra J.D.; "The complete amino-acid sequence of a canine mu chain."; Mol. Immunol. 16:565-570(1979).

-i. MISCELLANEOUS: THIS WIN CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
-i. SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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10-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V region X4.
Ig heavy chain V region X4.
Buks muscalus (Mouse).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                             Eukaryota, Metazoa, Čhordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Carnivora, Fissipedia; Canidae, Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.4%; Score 319.5; DB 1; Length 58.3%; Pred. No. 2e-24; ive 15; Mismatches 32; Indels
                                                                                                                                            Wasserman R.L., Capra J.D.;
"Primary structure of the variable regions of two canine immunoglobulin heavy Chains."
Biochemistry 16:3160-3168(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                   117 117 117 117 AA; 12703 MW; FCE07309E0A84B35 CRC64;
           21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10 heavy chain V region MOO.
Canis familiaris (Dog).
                                                                                                                                  MEDLINE=77242268; PubMed=407924;
                                                                                                                                                                                                                                                                                                         PIR, A90403; MHDGMO.
HSSP, P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Ffam; PF00047; ig, 1.
SMART; SM0406; IGV, 1.
Immunoglobulin V region. IG
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                                                                                                                     SEQUENCE OF 1-112.
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                                                                                          NCBI_TaxID=9615;
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HV37_MOUSE
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A GOIN F., Frangions B.;

A GOIN F., Frangions B.;

The protein WEA) with antibody activity against 3,4-pyruvylated

The protein WEA) with antibody activity against 3,4-pyruvylated

The proc. Natl. Acad. Soi. U.S.A. 80:1837-4841(1983).";

Proc. Natl. Acad. Soi. U.S.A. 80:1837-4841(1983).";

Proc. Natl. Acad. Soi. U.S.A. 80:1837-4841(1983).";

AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A MONOCLONAL ANTIBODY

AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH

WALDENSTROW'S MACROGLOBULINEMIA.

- :- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR, A02046; M3HUWE.

C -:- SIMILARITY: Contains 1 immunoglobulin-like domain.

PRSP; PO1772; PERSP;

R O; GO:0005576; C:extracellular; NAS.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:000555; P:immune response; NAS.

R InterPro; IPR007110; IG-11ke.

DR InterPro; IPR007110; IG-11ke.
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                                                                                                          47.3%; Score 319; DB 1; Length 119; 57.4%; Pred. No. 2.2e-24; ive 18; Mismatches 30; Indels
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                             119 119 AA; 13246 MW; BC34FC8F31CD41B3 CRC64;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homo sapiens (Human)
IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
MEDLINE=83273707; PubMed=6410398;
Goni F., Frangione B.;
                                                                                             Query Match
Best Local Similarity 57.1.
Best Local Similarity 57.1.
These 70; Conservative
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                                                                                 61 ADSVKGRFIISRNBSKNSLYLQMSSLRAEDTAVYYCAR-----GWLLNWGQGTLVTVS 113
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QVQLVDSGGGLVEPGGSLRLSCSASGFTFSANDMNWVRQAPGKGLEWLSFIGGSGSTIYY 60
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-I MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN THAT BINDS GALACTAN.

-I SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR; A02078; AVMST6.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

PEam; PE00047; Ig.,

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region.
                                                60 TDSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGSWNDYGGQGTQVTVS
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Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
Ravo D.N., Rudikoff S., Krutzsch H., Potter M.;
Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-determining regions.";
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21-UUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V region T601.

Mus musculus (Mouse).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
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HUMAN
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Biochemistry 18:4054-4067(1979).
-!- MISCELLARBOUS: THIS GAWA-1 MYELOWA PROTEIN HAS A DELETION IN THE
HINDE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
DISULFIDE BONDS.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NOBL_TRXID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                        Steiner L.A., Lopes A.D.;
"The crystallizable human myeloma protein Dob has a hinge-region
deletion.";
                                                                                                                                                                                Steiner L.A., Garcia Pardo A., Margolies M.N.;
"Anino acid sequence of the heavy-chain variable region of the
crystallizable human myeloma protein Dob.";
Biochemistry 18:4068-4080 (1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 46.7%; Score 315; DB 1; Length 120; Best Local Similarity 58.2%; Pred. No. 5.5e-24; Matches 71; Conservative 14; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 AA; 13440 MW; 880DDE307C4B2627 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A90431; G1HUDB.
HSSP; P01772; 2FB4.
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003596; IG-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG-LIKE.
                                                                                                                                                         MEDLINE=80020921; PubMed=114209;
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=80020920; PubMed=114208;
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SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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SMART; SM00406
PROSITE; PS508:
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Q9y509 homo sapien Q9y16 mus musculu Q9ulb6 homo sapien Q91205 mus musculu Q9ulB4 homo sapien Q8nc1 homo sapien Q8nc1 homo sapien Q9r124 mus musculu Q8r3v9 mus musculu Q8r3b homo sapien Q2r3b homo sapien Q91x92 mus musculu Q9now oryctolagus Q9now oryctolagus Q9now oryctolagus Q9ng9 homo sapien Q91173 homo sapien Q91192 homo sapien Q91192 homo sapien Q9149 mus musculu Q92449 mus musculu Q92449 mus musculu Q92449 mus musculu

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60 TDSMKGRFTISRDNAKNTVYLHMANLKPEDTAVYYCKALISSYDGSWN----DYGGQGTQ 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMWWVRQAPGKGLEWVSAISGSGGSTYY
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.6%; Score 361.5; DB 4; Length 597; 63.2%; Pred. No. 3.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Straubberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
InterPro; IPR00110; Ig-11ke.
InterPro; IPR00110; Ig-MC.
InterPro; IPR003596; Ig-MC.
InterPro; IPR003596; Ig-V.
FAGM; PR0047; ig; 5.
FAMRT; SM0466; Ig-V.
FROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
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SEQUENCE 597 AA, 65039 MW, 4FCA3AD8ECE263D9 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             597 AA
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09Y509
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08YEAO
07TWK4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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TISSUE=B-cell;
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Q9ul72 homo sapien
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674
1_QVQLQESGGGLVQAGGSLRL......GGQGTQVTVSSEPKTPKPQP
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gaps

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RESULT 29UL72

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61 DSMKGRPTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGSWNDYGGQGTQVTVSS 120
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                                                                                                                                                                                                                                                                                                          20 VKLVESGGGLVKPGGSLRLSCAASGFIFSNSYMSWVRQTPEKRLEWVATISNSGYATHYP 79
                                                                                                                                                                                                                                                                                 2 VQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDG-TTSYT
                                                                                                                                                                                50.7%; Score 341.5; DB 11; Length 480; 63.1%; Pred. No. 2.5e-25; ive 9; Mismatches 31; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC004786; ARH04786.1; -. HSSP, PO1810; 2FBJ. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MFC. InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS00390; IG_MHC; 2.
Hypochetical protein.
NON TER
SEQÜENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;
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PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99XA4;
01-UNN-2001 (TrEMBLrel. 17, C:
01-UNN-2001 (TrEMBLrel. 17, Li
01-OCT-2003 (TrEMBLrel. 25, Li
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                     Query Match
Best Local Similarity 63.13
Matches 77; Conservative
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SMART; SM00406; IGV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNYMWWVQAPGKGLESVSVTYSGGSSYYA 60
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus (Mouse).
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Musmalia; Etheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MUX., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
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                                                                                                                                                                                                                                                               01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010798; AAH10798.1; -.
InterPro; IPR00710; Ig-like.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_V.
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118 AA; 12872 MW; B4DIAS944B2D5CCA CRC64;
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EMBL; AF035042; AAD56278.1; -.
PIR; S21205; S21205.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR0073596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv. 1.
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01-MAY_2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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TISSUE=Colon;
                                  VIVSS 120
                                                                            140 VTVSS 144
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60 TDSMKGRFTISRDNAKNTVYLHMANLKPEDTAVYYCKALI--SSYDG-SWNDYGGQGTQV 116
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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Q91XE

us-09-805-290a-25.rspt

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QBN5K4;
QBN5K4;
01-OCT-2002 (
01-OCT-2003 (
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X MEDLINE-88277139; PubMed=9614934;
A Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
A Young D.C.;
I "Myosin-reactive autoantibodies in rheumatic carditis and normal
I fetus.";
I Clin. Immunol. Immunopathol. 87:184-192(1998).
R HSPS PO1772; 2F84.
R InterPro; IPRO0710; Ig-like.
R InterPro; IPRO0710; Ig-like.
R InterPro; IPRO0710; Ig-like.
R R NEMBLY SM00406; IG-like.
R SMART; SM00406; IG-like:
R PROSITE: PS50835; IG-like:
I NON_TER
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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TISSUBE-TORBIL;
Strausberg N. S.
Strausberg (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020240; AAH20240.1; -.
PIR; PL0120; PL0120.
PIR; S15590; S15590.
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Interpro; IPR003006; Ig-like.
Interpro; IPR003596; Ig-v.
Pfam; PP00047; Ig's.
SMART; SM0406; IGv.
PROSITE; PS00296; IG_LIKE; S.
PROSITE; PS00299; IG_LIKE; S.
PROSITE; PS00299; IG_MRC; 3.
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133 TMVTVSS 139
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Q9UL90
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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDL------NYWGQGTLVTVS 112
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                                                                                                                                                                                                                                        1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNXYY 60
                                                                                                                                                                                                      1 QVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGTTS-Y 59
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                                                                                                                                                                                                                                                                                                                     60 TDSMKGRFTISRDNAKNTVYLHMINLKPEDTAVYYCKALISSYDGSWNDYGGOGTOVTVS
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01-MAR.2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hymos applems (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                / Match 50.5%; Score 340.5; DB 4; Length 113; Local Similarity 62.0%; Pred. No. 4.7e-26; les 75; Conservative 11; Mismatches 26; Indels 9
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Strausberg R.,
Strausberg R.,
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL, BC021276; AAH21276.1; -.
R PTR, S31205; S21205.
R InterPro; IPR007110; Ig-1ike.
R InterPro; IPR003065; Ig_W.
R Pfant, PF00047; Ig, 4.
R SYART; SM00406; IGV; 1.
R PKOSITE; PS00399; IG_MHC; 2.
Hypothetical protein.
SRQUENCE 573 AA; 62967 MW; PD072344033AC530 CRC64;
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50.5%; Score 340.5; DB 4; Length
Best Local Similarity 59.7%; Pred. No. 3.9e-25;
Matches 80; Conservative 12; Mismatches 37; Indels
113 113
113 AA; 12437 MW; ED57FDD19086D07F CRC64;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    20 EVQLVESGGGGVVRPGGSLRLSCATSGFTFDDSGASWVRQAPGKGLEWVSSINWNGGSTNY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 58.5%; Pred. No. 6.1e-25;
Matches 72; Conservative 17; Mismatches 27; Indels 7;
                                                                                                                                                                                                                                                                                                                                                         50.1%; Score 338; DB 4; Length 499; 54.7%; Pred. No. 5.8e-25; ive 20; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Straubberg N. Straubberg N. Straubberg N. Straubberg N. Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC0156; AAH15656.1; -
InterPro; IPR00710; Ig-1ike.
InterPro; IPR003306; Ig-Mrc.
InterPro; IPR003596; Ig-V.
Pfam; PF00047; ig; 4.
PROSITE; RS00406; IG-IKE; 4.
PROSITE; PS00290; IG-IKE; 4.
                                                                                                          Strausberg R.;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, 5022249; AAH32249.1;
InterPro; IPR003599; Ig.
InterPro; IPR00310; Ig-like.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003596; Ig-MrC.
                                                                                                                                                                                                                          Fram; PF0047; 1g; 4.
SWART; SW00409; 1G; 4.
SWART; SW00409; 1G; 4.
PROSITE; PS50835; 1G_LIKE; 4.
PROSITE; PS08290; 1G_MHC; 1.
BHYPOCHETical protein.
SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O91WP5 PRELIMINARY; PRT; 479 AA.
O91WP5;
01-DBC-2001 (TrEMBLrel. 19, Created)
01-DBC-2003 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical procein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 TTVTVSSASPTSPKVFP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TQVTVSS-EPKTPKPQP 129
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 54.7% nes 75; Conservative
Hypothetical protein.
               Homo sapiens (Human)
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                                                                                  SEQUENCE FROM N.A.
                                                        NCBI_TaxID=9606;
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                                                                                                 rissum=Blood;
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7

Gaps

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2
                                                                                                     60 TDSMKGRFTISRDNAKNTVYLHMANLKPEDTAVYYCKALISSYDGSWNDYGGOGTQVTVS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DYAAPVKGRLTISRDSSKNTLYLRMNSLKTEDTAVYYCTTGITMIIVVITTSSKRTSFEY 120
                                                                                                                                    80 SDIMKGRFIISRDNAKSILYLQMSSLRSEDTAFYYC-----VRGGYFDVWGAGTAVIVS 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSKAMMSWVRQAPGKGLEWVGRIKSKTDGGTT
                         20 EVQLVESGGGLVKPGGSLKVSCAASGLTFSNYAMSWVRQSPEKRLEWVAAINSNGGNTYY
QVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSD-GTTSY
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Myosin-reactive autoantibodies in rheumatic carditis and normal
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49.9%; Score 336.5; DB 4; Length 131;
Best Local Similarity 57.3%; Pred. No. 1.4e-25;
Matches 75; Conservative 14; Mismatches 31; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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EMBL, AF035026; AAD56262.1; -.
PIR, S21205; S21205.
HSSP, PO1010; SFBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR005596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                           131 AA.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 GGOGTQVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                   120 SEP 122
                                                                                                                                                                                                                                                                         SEP 136
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1 OVOLOESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSD-GTTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 GTQVTVSS-EPKTPKPQP 129
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig; 4.
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PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                        118 VSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGTTS-YT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
[1]
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MIX., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
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MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.,
"Myosin-reactive autoantibodies in rheumatic carditis and normal
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 49.8%; Score 335.5; DB 4; Length Best Local Similarity 62.5%; Pred. No. 1.5e-25; Matches 75; Conservative 10; Mismatches 30; Indels
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116 AA; 12434 MW; 0DA0348154DD6061 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035021, AAD56257.1; -
PIR; PLO120; PL0120.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR0073956; Ig_V.
Pfan; PF0047; ig; 1.
SMART; SM00406; IGV.
PROSITE; PS50835; IG_LIKE; 1.
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035043; AAD56279.1; -.
INTEXP. PO1772; 2F84.
INTEXPO. IPRO07110; Ig-like.
IntexPro, IPR003596; Ig_v.
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Q9UL71 RESULT 12 Q9UL71

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60 TDSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGS-----WNDYGGQ 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 EVOLVESGGGLVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGKGLEWVSSISSRSDYIYY 79
                         9
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 49.6%; Score 334.5; DB 4; Length 494; Best Local Similarity 57.2%; Pred. No. 1.3e-24; Matches 79; Conservative 13; Mismatches 31; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 494 AA; 53088 MW; 9AlD7AEB5AE34C0E CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                           Q96K68;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ14473.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 TDSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGSWNDYGGQGTQVTVS 119
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O
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBL_TaxID=10090,
                                                      Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                          Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 64.2%; Pred. No. 2.2e-25;
Matches 77; Conservative 8; Mismatches 31; Indels
                                                                                                                                                                                                                           SEQUENCE FROW N.A.

SEQUENCE FROM N.A.

WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

Young D.C.;
Myosin-reactive immunoglobulin heavy chain variable region
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Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, EC010324, AAH10324.1,
INTERPROF IPRO07100, Ig-11ke.
INTERPROF IPRO035006, Ig-NG.
INTERPROF IPRO03506, Ig-V.
Pfam; PF00047; 1g/4 4.
SMART; SM00406; IGV:
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SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;
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01-0207;
01-DEC-2001 (TEMBLrel. 19, Created)
01-DEC-2001 (TEMBLrel. 19, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
Hypothetical procein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Immunol. Immunopathol. 87:184-192 (1998).
EMBL; AF035023; AAD56259.1; -.
FIR; S21205; S21205.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Ffam; PF00047; ig; 1.
SMARF; SM00406; IGv. 1.
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118 AA; 12843 MW;
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                                                                                                                                                              WCBI_TaxID=9606;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                       OM protein - protein search, using sw model
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October 5, 2004, 07:04:10; Search time 98.1435 Seconds (without alignments) 371.381 Million cell updates/sec US-09-805-290A-25 674 1 QVQLQESGGGLVQAGGSLRL......GGQGTQVTVSSEPKTPKPQP 129 Title: Perfect score: Sequence: Run on:

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

1586107

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\*
1: geneseqp1980s:\*
2: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2001s:\*
7: geneseqp2003bs:\*
7: geneseqp2003bs:\*
8: geneseqp2003bs:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Aael0558 HPL inhib	e105	55 HPL	51 HPL	61 HGL	0556 HPL	Aael0563 HGL inhib	0564 HGL	Aae10557 HPL inhib	99 HGT	Aael0552 HPL inhib	83 Anti	Aae05288 Anti-pota	7 HGL	4 HPL	Aae10565 HGL inhib	Abg30620 Immunoglo	_	Abr62882 Llama ant	Abr62881 Llama ant	Abg30972 Immunoglo	819	887	e105	Abg30618 Immunoglo
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ID	AAEL	AAE1	AAEL	AAE1	AAE1	AAE1	AAE1	AAEI	AAE1	AAE1	AAE10	AAEO	AAE0	AAE10	AAE1	AAE10	ABG3	ABR62	ABR62	ABR62	<b>ABG30</b>	ABR62	ABR62	AAE1	ABG3
DB	4	4,	4	4	4	4	4	4	4	4	4	4	4,	4	4	4	ហ	7	7	7	Ŋ	_	7	4	2
Length	129	129	131	129	129	130	124	129	130	124	130	152	149	130	130	128	131	190	190	190	133	190	190	130	134
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Result No.		N	6	4	Ŋ	9	7	80	σ	10	11		13	14	15					20	21				25

7 ABR62878 7 ABR42878 7 ABR42878 4 AAA505286 4 AAA505286 2 AAX41173 2 AAX41172 2 AAX41165 2 AAX41165 4 AAB10560 4 AAB10560 4 AAB10560 4 AAB10560 7 AAX3819		EGGLIIO88 EEGGLIII 8 EE EGG 801 801 801 801 804 804 804 804 804 804 804 804	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		Llama	Abr62885 Llama ant	Llama			з глата	Mouse		Llama	Aay41165 Llama Vhh	Amin	Aab67779 Amino aci	HGL		Abr62884 Llama ant	_	Aab72413 Llama bi-	Aay41167 Llama Vhh	Aay39819 Llama ant
		4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	644.3 644.3 644.1 64	287	디	$\alpha$	AAE05286	AAE05287	н	AAY41173	ABG30617	AAB67778	AAY41172	AAY41165	AAB67777	AAB67779	AAE10560	AAE10562	ABR62884	AAB07654	AAB72413	AAY41167	AAY39819
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# ALIGNMENTS

RESULT 1 AAE10558 ID AAE	T 1 1558 AAB10558 standard, peptide; 129 AA.
¥ Z	AAE10558;
žĖ:	10-DEC-2001 (first entry)
E K	HPL inhibiting VHH fragment, HPL #22 from llama species.
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2 2 3 3 8	പ്രത്യേഷ ആവ
臣	Loca
FT	Region 3135 // Alabel CDR1 // Alabel Momentarity Asterminist region 1"
FT	COMPLEMENTATION GENERALING LEGION CDR2 COR2
FFF	CDR3 "Complementarity determining region
X Z S	EP1134231-A1.
X G :	19-SEP-2001.
X E	20-FEB-2001; 2001EP-00200703.
X K	14-MAR-2000; 2000EP-00200930.
X & & :	(UNIL.) UNILEVER NV. (UNIL.) UNILEVER PLC.
Y E	Bezemer S, Van De Burg M, De Haard JJW, Tareilus E;
<b>E</b>	WPI; 2001-572718/65.
{	New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
PS A	Example 2; Page 10; 37pp; English.

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           The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #22 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                        DSWKGRFTISRDNAKNTVYLHMMNLKPEDTAVYYCKALISSYDGSWNDYGGGGTQVTVSS 120
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                                                                                                                                                                                             100.0%; Score 674; DB 4; Length 129; 100.0%; Pred. No. 3.7e-55; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPL inhibiting VHH fragment, HPL #13 from llama species.
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98. .109
/label= CDR3
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/label= CDR2
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'label= CDR1
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PLC.
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Best Local Similarity
Matches 129; Conserv
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                                                                                                                                                                  Sequence 129 AA;
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useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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/label= CDR3
/note= "Complementarity determining region 3"
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                                                                                                                            Example 2; Page 9; 37pp; English.
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/label= CDR1
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Best Local Similarity 79.8
Matches 103; Conservative
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/label= (
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                                                               of light chains.
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                                                                                                                       The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHM) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human panoreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #15 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
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                                           New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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/note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                               Length 131;
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   Tareilus E;
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/label= CDR2
/note= "Complementarity determining 98. .109
                                                                                                                                                                                                                                                              75.4%; Score 508; DB 4; 77.1%; Pred. No. 1.2e-39; iive 11; Mismatches 17
   De Haard JJW,
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                                                                                                     Example 2; Page 9; 37pp; English.
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/label= CDR1
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   Van De Burg M,
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                        WPI; 2001-572718/65
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Best Local Similarity
                                                                               of light chains
                                                                                                                                                                                                                                           Sequence 131 AA;
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   Bezemer S,
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #11 from llama (camelid) species
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                                                                                                                                                                            New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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/label= CDR3
/note= "Complementarity determining region 3"
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|Jabel= CDR2
|note= "Complementarity determining region
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77.2%; Pred. No. 5.4e-39;
iive 9; Mismatches 20
                                                                             De Haard JJW,
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/label= CDR1
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Best Local Similarity 77.2
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                                                                                                                                                                                                                                                                   of light chains
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Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 130 AA;
                                                                                                                                                                                                                                         light chains.
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                                                                                                                                                              Bezemer
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L H X O X M M M X E X D X X Y X Y I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 원
                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                         The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #4 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGSWNDYGGQGTQVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
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|Jabel= CDR2
|note= "Complementarity determining region 2"
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                                                                                                                                                                                                                                                                                                                                                           Length 129;
                                                                                                                                                                                                                                                                                                                                                                               22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPL inhibiting VHH fragment, HPL #18 from llama species.
                                                                                                         Tareilus E;
                                                                                                                                                                                                                                                                                                                                                         73.3%; Score 494; DB 4; 75.2%; Pred. No. 2.4e-38;
                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches
                                                                                                        De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE10556 standard; peptide; 130 AA.
                                                                                                                                                                                                       Example 4; Page 13; 37pp; English.
                               20-FEB-2001; 2001EP-00200703.
                                                    14-MAR-2000; 2000EP-00200930
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/label= CDR1
                                                                                                        Bezemer S, Van De Burg M,
                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                       (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
                                                                                                                          WPI; 2001-572718/65.
                                                                                                                                                                                                                                                                                                                                                                 l Similarity
97; Conserv
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           19-SEP-2001
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Best Local (
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Matches
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #18 from llama (camelid) species
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPNYA
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                                   /note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGL inhibiting VHH fragment, HGL #9 from llama species.
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73.8%; Pred. No. 4.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 31. .35
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/label= CDR3
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                                                                                                                                                                                                                                                                                                                                   The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes. Sepcially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #9 from lama (camelid) species
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
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                                                                                                                                                                                                                                                           New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DSVKGRFTISRDNIKNTWYLQMNSLKPEDTGVYYCAG----TGAEGHYWGQGTQVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Gaps
                                        2
                                                                        /note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 124;
          "Complementarity determining region 1"
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                                                                                                                                                                                                                  Tareilus E;
                                        'note= "Complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.5%; Score 488.5; DB 4; 73.6%; Pred. No. 7.6e-38; iive 11; Mismatches 18;
                                                                                                                                                                                                                  De Haard JJW,
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                                                                                                                                         20-FEB-2001; 2001EP-00200703.
                                                              CDR3
                                                                                                                                                             14-MAR-2000; 2000EP-00200930
                            /label= CDR2
label= CDR1
                                                                                                                                                                                                                  Van De Burg M,
                                                  98. .104
/label= CI
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           note=
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Best Local Similarity
Matches 95; Conserv
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                                                                                                                                                                                                                                                                                             light chains
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #10 from llama (camelid) species
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                                                                                                                                                                                                                      'note= "Complementarity determining region 3"
                                                                    "Complementarity determining region 1"
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                                                                                                              /label= CDR2
/note= "Complementarity determining
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74.4%; Pred. No. 8.8e-38;
tive 11; Mismatches 22
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Location/Qualifiers
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                          11. .35
'label= CDR1
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Best Local Similarity 74.43,
The Set Conservative
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/label= C
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(UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
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es 94; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           of light chains
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                               10-DEC-2001
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            AAE10566;
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                                                                                                                     Lama sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #10 from llama (camelid) species
                   Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                     New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALIS-SYDGSWNDYGGQGTQVTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSVKGRFTISRDNDKNTEYLQMNNLKPEDTAVYYCNAQVRVRFSSDYTNYWGQGTQVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGTTSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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H
                                                                                                                     "Complementarity determining region 1"
                                                                                                                                                    'note= "Complementarity determining region 2"
                                                                                                                                                                                    'note≈ "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Indels
HPL inhibiting VHH fragment, HPL #19 from llama species.
                                                                                                                                                                                                                                                                                                                            Tareilus E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.3%; Score 487.5; DB 4.71.5%; Pred. No. 9.9e-38; iive 14; Mismatches 22,
                                                                                                                                                                                                                                                                                                                            De Haard JJW,
                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 10; 37pp; English.
                                                                                                                                                                       CDR3
                                                                                              31. .35
/label= CDR1
                                                                                                                                                                                                                                                   20-FEB-2001; 2001EP-00200703
                                                                                                                              0. .64
label= CDR2
                                                                                                                                                                                                                                                                       14-MAR-2000; 2000EP-00200930
                                                                                                                                                                                                                                                                                                                           Bezemer S, Van De Burg M,
                                                                                                                                                             98. .110
/label= Cl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEPKTPKPOP 130
                                                                                                                      note=
                                                                                                                                                                                                                                                                                           (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC
                                                                                                                                                                                                                                                                                                                                                WPI; 2001-572718/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
93; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                       light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 130 AA;
                                                                                                                                                                                                        EP1134231-A1
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Best Local Si
Matches 93
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AAE10566
ID AAE10
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AAE10566 standard; peptide; 124 AA.

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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #15 from llama (camelid) species
                                                          Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGTTSYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                              "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.7%; Score 483.5; DB 4; Length 72.9%; Pred. No. 2.2e-37; Inve 11; Mismatches 19; Indels
HGL inhibiting VHH fragment, HGL #15 from llama species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tareilus E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De Haard JJW,
                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 14; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-2001; 2001EP-00200703.
                                                                                                                                                                                                                                                                                                                30. .35
/label= CDR1
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/label= CDR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= CDR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 EPKTPKPOP 124
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61 DSVKGRFTISRDNTLNTVYLQMNDLKPEDTAVYYCNADVRPYRTSRYLEVWGQGTLVTVS 120

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #12 from llama (camelid) species
                                                                                                                                              Llama antibody, camélid, anorectic, heavy chain variable domain, VHH; human dietary enzyme inhibitor; medicament, human pancreatic lipase; HPL; food, human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                     31. .35
/label= CDR1
/note= "Complementarity determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                             /note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 130;
                                                                                                                                                                                                                                                                                                                                 /note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                  HPL inhibiting VHH fragment, HPL #12 from llama species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tareilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 71.1%; Score 479.5; DB 4; Local Similarity 73.8%; Pred. No. 5.6e-37; les 96; Conservative 10; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Haard JJW,
                                                                                                                                                                                                                                       Location/Qualifiers
                            AAE10552 standard; peptide; 130 AA
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                                                                                                                                                                                                                                                                                                                                             98. .110
/label= CDR3
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                                                                                                                                                                                                                                                                                                             /label= CDR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van De Burg M,
                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          EP1134231-A1.
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                                                                                      10-DEC-2001
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                                                         AAE10552;
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Region
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Matches
RESULT 11
AAE10552
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The present invention relates to a method for modifying a plant to produce an antibody or an active fragment or derivative, or a protein functional equivalent, in a cellular compartment comprises introducing a functional equence encoding a heavy chain immunoglobulin, where the DNA is linked to promoters and provided with an additional sequence encoding a peptide capable of targeting heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain immunoglobulin or an active fragment or derivative, or a protein that is immunoglobulin or an active fragment or derivative, or a protein that is functionally equivalent for increasing the pathogen resistance in a plant or modulate metabolism in a plant. Under some circumstances it may be desirable to retain the antibody product with the plant rather than extracting and isolating the product. In particular, edible selected antigens may be used in a method of passively immunising an animal, present sequence is an anti-potato SBEII antibody (denoted Clone46) heavy chain variable domain (VH) attached to peptide linkers, myc and hisé tag.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                   Potato; heavy chain immunoglobulin; pathogen resistance;
metabolism modulator; passive immunisation; heavy chain variable domain;
VH; anti-potato SBEII; starch branching enzyme; SBE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGTTSYT
                                                                                                                                                                                                                      Anti-potato SBEII (Clone46) VH region attached with myc and his6 tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 152;
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2e-36;
ches 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.4%; Score 474.5; I
72.7%; Pred. No. 2e-36
:ive 11; Mismatches
                                                                                                                   AAE05283 standard; protein; 152 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Der Logt CPE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-2000; 2000EP-00310997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99EP-00310188
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Best Local Similarity 72./..
hea 96; Conservative
                                                                                                                                                                                      (first entry)
                               SEPKTPKPOP 130
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SEPKTPKPOP
                                                                                                                                                                                                                                                                                                                            Solanum tuberosum
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNIL ) UNILEVER (UNIL ) UNILEVER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                EP1118669-A2
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120
                               121
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119

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DSWKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGS-WNDYGGGGTQVTVS

1 QVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGTTSYT

ਨੇ g ò 2,

Indels

15;

8; Mismatches

76.0%;

98; Conservative

Similarity

Query Match Best Local Si Matches 98

120

62

1 OVOLOESGGIVOAGGSIRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGTTSYT DSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGSMNDYGGQGTQVTVSS

70.3%; Score 474; DB 4; Length 149; 76.0%; Pred. No. 2.2e-36;

DSVKGRFTISRDNAKNTLYLOMNSLKPEDTAVYYCTA----GGS---YWGQGTQVTVAS 114

EPKTPKPQP 129

121

61 63

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EPKTPKPOP 123

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The present invention relates to a method for modifying a plant to produce an antibody or an active fragment or derivative, or a protein functional equivalent, in a cellular compartment comprises introducing a DNA sequence encoding a heavy chain immunoglobulin, where the DNA is linked to promoters and provided with an additional sequence encoding a performance of the performance of the product of peptide capable of targeting heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain immunoglobulin or an active fragment or derivative, or a protein that is immunoglobulin or an active fragment or derivative, or a protein that is functionally equivalent for increasing the pathogen resistance in a plant or to modulate metabolism in a plant. Under some circumstances it may be desirable to retain the antibody product with the plant rather than extracting and isolating the product. In particular, edible selected antigens may be used in a method of passively immunishing an animal, preferably human, against the antigen, e.g., pathogenic organisms. The present sequence is an anti-potato SBEII antibody (denoted Clone68) heavy chain variable domain (VH) attached to peptide linkers, myc and hisé tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a
                                                        117
                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                           Potato; heavy chain immunoglobulin; pathogen resistance;
metabolism modulator; passive immunisation; heavy chain variable domain;
VH; anti-potato SBEII; starch branching enzyme; SBE A.
DSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKA---LISSYDGSWNDYGGQGTQVT
                                                                                                                                                                                                                                                                                                                                                                          Anti-potato SBEII (Clone68) VH region attached with myc and his6 tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Teh Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jobling SA,
                                                                                                                                                                                                                                                            AAE05288 standard; protein; 149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 13; Fig 28; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-2000; 2000EP-00310997.
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                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                 118 VSSEPKTPKPQP 129
                                                                                                                                                                115 VSSEPKTPKPOP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNILEVER PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cellular compartment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-427157/46.
N-PSDB; AAD10059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanum tuberosum.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1118669-A2.
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                                                                                                                                                                                                                                                                                                                                       18-SEP-2001
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                                                                                                                                                                                                                                                                                                 AAE05288;
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HGL inhibiting VHH fragment, HGL #16 from llama species.

(first entry)

10-DEC-2001

AAE10567;

AAE10567 standard; peptide; 130 AA.

AAE10567

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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VIII) derived from an immunosjobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipse (HGL) or human gastric lipse (HGL) which are useful for the cosmetic control of body weight of human beings.
                                                                                                   Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                 98. .110
/label= CDR3
/note= "Complementarity determining region 3"
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                                                                                                                                                                                                                                        "Complementarity determining region
                                                                                                                                                                                                                                                                                   /note= "Complementarity determining region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Haard JJW,
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 14; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-2001; 2001EP-00200703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2000; 2000EP-00200930.
                                                                                                                                                                                                                                                    50. .64
/label= CDR2
                                                                                                                                                                                                                         /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bezemer S, Van De Burg M,
                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC
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                                                                                                                                                                                                                                                                                                                                                              EP1134231-A1
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                                                                                                                                                                 Lama sp.
                                                                                                                                                                                                            Region
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Sequence 149 AA;

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7
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                                                                                                                                                                           114
The present peptide sequence is HGL inhibiting VHH fragment, HGL #16 from llama (camelid) species
                                                                                                                                                                                         61 DSVKGRFTISRDNARGTVYLOMNSLKPEDTAVYYCAAARSLELTPTSY-----DYWGOGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                        9
                                                                                                                                     1 QVQLQESGGGLVQAGGSLRLSCAASGSDFRYNAMAWYRQAFGKQRKLVATITYTYRTNYA 60
                                                                                                                       1 QVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGTTSYT
                                                                                                                                                                           61 DSMKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALIS----SYDGSWNDYGGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally
                                                                                               Gaps
                                                                 Score 469.5; DB 4; Length 130;
Pred. No. 4.8e-36;
9; Mismatches 18; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPL inhibiting VHH fragment, HPL #14 from llama species.
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                                                                                                                                                                                                                                                                                                                          AAE10554 standard; peptide; 130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 9; 37pp; English.
                                                                                                                                                                                                                                                     116 QVTVSSEPKTPKPQP 130
                                                                                                                                                                                                                              OVIVSSEPKTPKPOP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= CDR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-2000; 2000EP-00200930
                                                                 Query Match
Best Local Similarity 71.9%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR1
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                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                          Sequence 130 AA;
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devoid of light chains specific for inhibiting human dietary enzymes. The maribodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especiálly human pancreatic lipase (HPL) or human gastric lipase (HPL) has the useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #14 from lama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                     120
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                                                                                                                                                                                                                                                                                                          1 QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQDGGSTNYA
                                                                                                                                                                                                                                                                                                                                                                                      61 DSVKGRPTISRDNILNTVYLQMNSLKPEDTAVYHCNADVRPYRTSRYLELWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                               61 DSMKGRFTISRDNAKNTVYLHMANLKPEDTAVYYCKALISSYDGS-WNDYGGGGGTQVTVS
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H
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                                                                                                                                                                                                                                            24;
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                                                                                                                                                                                                  69.4%; Score 467.5; DB 4
72.3%; Pred. No. 7.3e-36;
iive 11; Mismatches 24
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                                                                                                                                                                                              Query Match
Best Local Similarity 72.3%
Matches 94, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEPKTPKPQP 129
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                                                                                                                                                                Sequence 130 AA;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

October 5, 2004, 07:36:16; Search time 21.0648 Seconds (without alignments) 593.639 Million cell updates/sec

US-09-805-290A-26
692
1 QVQLQDSGGGLVQAGGSLRL.....WGQGTLVTVFLEPKTPKPQP 130 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

KIES	scription	q heavy chain -	g heavy chain V	q heavy chain -	g heavy chain V	g heavy chain V	heavy	g heavy chain V	g heavy chain p	g heavy chain -	g heavy chain -	g heavy chain V	g heavy chain -	g heavy chain V	g heavy chain -	g heavy chain V	g heavy chain V	g variable regi	g heavy chain V	g heavy	g heavy chain pr	g heavy chain v	g heavy chain V							
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heavy	heavy	heavy	heavy chain	heavy	heavy chain	heavy	heavy	heavy							
S19878	846391	831678	PH1647	S48797	A60943	S31598	AZHUBU	S31104	A30561	S22657	831120	F27888	D27889	526790	831109
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127	114	139	112	128	151	135	115	121	138	140	114	119	119	128	117
œ	48.8	48.7	48.6	48.6	48.6	48.6	48.4	48.4	48.4	48.4	48.3	48.3	48.3	48.3	48.3
48.8	<b>a</b> o													334.5 48.3	

## ALIGNMENTS

RESULT 1 31107 19 heavy chain - human c; Species: Homo sapiens (man) c; Species: Homo sapiens (man) c; Species: Homo sapiens (man) c; Species: Homo sapiens c; Species: Homo sapiens c; Species: Homo sapiens c; Species: Homo sapiens c; Stacession: S31107 R; Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Fur. J. Immunol. 22, 247-251, 1995 A; Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complements restricted utilization of germ-line V(H)3 genes and short diverse third complements. Preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: mRNA A; Residues: 1-119 < RAA> A; Residues: 1-119 < RAA> A; Rossicues: EmBL:X62955 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Reywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology < IMM>	Ouery Match  S2.3%; Score 362; DB 2; Length 119;  Best Local Similarity 64.2%; Pred. No. 5.7e-25;  Matches 77; Conservative 9; Mismatches 30; Indels 4; Gaps 2;  Qy 1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQ-SGGSTNY 59;
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Signification: Signification of Statement (Statement) (Statement)

32;

10; Mismatches

Conservative

Similarity

Best Local Sim. Matches 76; Query Match

임 ò RESULT 3

52.0%;

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Igheavy chain V region (M43) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Stecessian: 136605
C;Accessian: D36605
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene f
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Reseidue: preferential utilization of conserved immunoglobulin heavy chain variable gene f
A;Retus: preferential utilization of conserved immunoglobulin heavy chain variable gene f
A;Reterence number: A36005; MUID:90349571; PMID:2117273
A;Reterence number: A36005
A;Retus: preferences: GB:M34024
A;Residues: 1-119 < CKH3
A;Cross-references: GB:M34024
A;Cross-references: GB:M3403233
A;Gene iGB:IGH0; immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Oc-Jan-1995 #sequence_revision O6-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38489
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S submitted to the EMBL Data Library, June 1993
A;Bescription: Human antibody fragments specific for human blood group antigens from a EA;Accession: S38489
A;Accession: Junany
A;Accessio
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                                                    61 ADSVKGRFTISEDNSKNTLYLOMNSLRAEDTAVYYCAKD-RGF-WSGYKDYWGQGTLVTV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYY-----WNADVRPYRTSRYLEIWGQG 114
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60 ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADVRPYRTSRYLEIWGQGTLVTV
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60.9%; Pred. No. 2.5e-24;
ive 9; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.8%; Pred. No. 1.3e-24;
Matches 76; Conservative 10; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78; Conservative
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Best Local Similarity
Matches 78; Conserve
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1g heavy chain - human

C;Species 102-bec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C;Accession: S31108

C;Accession: S31108

C;Accession: S31108

A;Raaphorst, F.M., Timmens, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman

Bur. J. Immunol. 22, 247-221, 1992

A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem

A;Reference number: S31104; MUID:92111633; PMID:1730252

A;Accession: S31108

A;Accession: S31108

A;Accession: S31108

A;Accession: S31108

A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: EMBL:X62956
A;Oross-references: EMBL:X62956
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Stoperfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999 C;Accession: S48798 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999 R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D. Submitted to the EMBL Data Library, October 1994 A;Reference number: S48797 A;Reference number: S48797 A;Reference number: S48798 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
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                                                                                                                                                                                                                                                                                                                                               60 ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADVRPYRTSRYLEIWGQGTLVTV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-120 <MAH>
A;Cross-references: BMBL:246382; NID:9562324; PIDN:CAA86521.1; PID:91340167
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <1MM>
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                                                                                                                                                                                1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQ-SGGSTNY
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             Score 360; DB 2; Length 140;
Pred. No. 1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 359; DB 2; Deligated No. 1e-24; Tridels
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8; Mismatches

Conservative

Query Match Best Local Similarity Matches 78; Conserv

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1-119 <RAA>

A; Residues:

51.9%;

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10; Mismatches

Query Match Best Local Similarity 65.0<sup>§</sup> Matches 78; Conservative

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C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31114
B;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Br. J. Immunol. 22, 247-251, 1992
A;Raphorst F.M.; Timmers E.; Renter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Br. J. Inmunol. 22, 247-251, 1992
A;Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 02-Uul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Date: 02-Uul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession. 155673
R;Knight, G.B.; Agnello, V.; Bonagura, V.; Barnes, J.L.; Panka, D.J.; Zhang, Q.X.
J. Exp. Med. 178, 1903-1911, 1993
A;Title: Human rheumatoin factor cross-idiotypes. IV. Studies on WA XId-positive IgM with tinct from the 17.109 and G6 XIds.
A;Reference number: 155673; MUID:94065558; PMID:8245772
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology < IMM>
F;15-98/Domain: immunoglobulin homology < IMM>
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                                                                                                1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQ-SGGSTNY
                                                                                                                                                     20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                   60 ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYW-NADVRPYRTSRY--LEIWGQGTL
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              4; Gaps
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 63.3%; Pred. No. 4.4e-24;
Matches 76; Conservative 10; Mismatches 32; Indels
              Indels
              30;
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Pred. No. 4.5e-24;
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A;Molecule type: mRNA
A;Residues: 1-121 <RES>
              12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:120086; OMIM:147020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ig heavy chain - human (fragment)
              77; Conservative
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Best Local Similarity
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              Matches
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R/Kishimoto, T.

R/Kishimoto, T.

A/Reference number: S05270

A/Reference number: S05270

A/References: EMBL:X14584

R/Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

R/Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

R/Kishimoto, T.; Okajima, H.; Okumoto, T.; Paniguchi, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C.Date: 22-Nov-1993 #sequence_revision 1999
C.Date: 23-Jul-1999
C.Da
61 ADSVKGRFIISRDNSKATLYLONNSLRAEDTAVYYC-AKEGPFPASDYYDSSGYYSFDYW 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQ-SGGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mENA
A;Molecule types mENA
A;Molecule types mENA
A;Crose: 1-138 cCUr.
A;Crose-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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/Residues: 1-144 < MIS2>

/Rosidues: 1-144 < MIS2>

/Rosidues: 1-144 < MIS2>

/Rosidues: BMBL:X14584

/Superfamily: immunoglobulin v region; immunoglobulin homology

/Reywords: heterotetramer; immunoglobulin

/Reywords: heterotetramer; immunoglobulin

// 1-19/Domain: signal sequence #status predicted < SIG>

// 1-10/Product: Iq heavy chain (fragment) #status predicted < MAT>

// 1-17/Domain: immunoglobulin homology < LMM>
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Pred. No. 4e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 51.3%; Score 355; DB 2; Best Local Similarity 58.6%; Pred. No. 2.8e-24; Matches 75; Conservative 11; Mismatches 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain precursor - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                S31666
Ig heavy chain V region - human (fragment)
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                                                                                                                                            112 GOGTLVTV 119
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                                                                                                                                                                                                                              120 GOGTLVTV 127
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Best Local Similarity
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Species: Homo sapiens (man)
Cispecies: Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
Cispecies: Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
Cispecies: Signature in the language of the V(H)? Gene famil Airfele: The human cord blood antibody repertoire. Frequent usage of the V(H)? gene famil Airfelerence number: S26786; MUD:92111632; PMID:1730251
Airfelerence number: S26786; MUD:9211632; PMID:1730251
Airfelerence number: S26786; MUD:92111632; PMID:1730251
Airfelerence number: S26786
Airfelerence number: S26786; MUD:92111632; PMID:1730251
Airfelerence number: S26786
Airfelerence number: S2678
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G heavy chain V region - human

G heavy chain V region - human

G species: Homo sapiens (max)

G hacession: $26794

R;Mortari, F.; Nowton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

R;Mortari, F.; Nowton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

R;Mortari, F.; Nowton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene famil A;Reference number: $26786; MUID:92111632; PMID:1730251

A;Reference number: $26786; MUID:92111632; PMID:1730251

A;Reference number: $26794

A;Residues: 1-123 «MOR»

A;Residues: 1-123 «MOR»

A;Coss-references: EMBL:X61011

G;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYMNADVRPYRTSRY-LEIWGQGTLVT 118
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                                                                                                                                                                                                                     61 DSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADVRPYRTSRY-LEIWGQGTLVTV 119
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                                                                                                                                                                                                                                                                62 DSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRQGEGYRYDDYAMDYWGQGTSVTV 121
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                                                                 2 VQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGS-TNYA
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                                                                                                                1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGS-TNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 123;
   Indels
   32;
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59.5%; Pred. No. 1.2e-23;
ive 15; Mismatches 32;
       12; Mismatches
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       74; Conservative
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       Matches
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C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C;Datesion: C36008
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Accession: C36005
A;Accession: C36005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-122 <CAT>
A;Residuence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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Ig heavy chain V region (H35-C6) - mouse
Cispecies: Was musculus (house mouse)
Cipbate: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
CiAccession: E27888
Ricaton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1996
A.Title: Structural and functional implications of a restricted antibody response to in A.Reference number: A91043; MUD:86300658; PMID:2427335
           3
                                                                                                                                                                                                                             ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADVRPYRTSRYL-----EIWG 112
                                                                                                                                                                                                                                                                       61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC-----AKASLYLRFLEWLFDYWG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYY-----WNADVRPYRTSRYLEIWGQ 113
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                                                                                 OVOLODSGGGLVOAGGSLRLSCAASGSIGDIHTMGWYROTPGKQRDVVATIQ-SGGSTNY
                                                                                                                                               1 EVOLLESGGGLVOPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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           Gaps
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           Indels
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           26;
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ilarity 59.5%; Pred. No. 5.3e-24;
Conservative 10; Mismatches 25;
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Pred. No. 8.2e-24;
           10; Mismatches
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61.7%;
           77; Conservative
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-119 <SCF
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Cy Deccies: Homo sapiens (man)

Cy Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

Cy Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

Cy Accession: S1110

Ry Raphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992

Ay Rittle: Restricted utilization of germ-line V(H)3 genes and short diverse third complem Ay Reference number: S31104; MUID:92111633; PMID:1730252

Ay Accession: S3110

Ay Section S3110

Ay Restidues: J-116 < ARA>

Ay Rocession: Sapient acid sequence not shown; translation not shown

Ay Residues: J-116 < ARA>

Ay Rossion Sapient Sequence was submitted to the EMBL Data Library, October 1991

Cy Superfamily: immunoglobulin V region; immunoglobulin homology

Cy Keywords: heterotetramer; immunoglobulin

F; 15-97/Domain: immunoglobulin homology < IMM>
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Ig heavy chain - human
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Gaps . 2 Query Match 50.1%; Score 346.5; DB 2; Length 116; Best Local Similarity 60.5%; Pred. No. 1.3e-23; Matches 72; Conservative 13; Mismatches 29; Indels 5;

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Search completed: October 5, 2004, 08:17:17 Job time : 21.0648 secs

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AC P19151;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
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115 AA;
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(c) 1993 - 2004 Compugen Ltd.
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A Torano A., Putnam F.W.;

Torano A
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10-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
1g heavy chain V-III region BUT.
1g heavy chains (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SMART; SM00406; ig; 1.
PROSITE; PS50835; iG LIKE; 1.
Immunoglobulin V region.
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Gaps

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61 ABSVKGRFIISRDBSKBILYLQMNSLRAEBTAVYYCARDRPLYGBYRAFNYWGQGTLVIV 120
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Capra J.D., Kehoe J.M.;

Capra J.D., Kehoe J.M.;

"Structure of antibodies with shared idiotypy: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins.";

Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).

-:- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryoča, Metazoa, Chordata, Czaniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 55.1%; Pred. No. 1.6e-24;
Matches 65; Conservative 15; Mismatches 37; Indels 1.
                                                                                                                                                                                                                                                                                                                                      DB 1; Length 122;
                                                                                                                                                                                                                                                                                                                               ; Score 318.5; DB 1; Length
; Pred. No. 1.3e-24;
13; Mismatches 39; Indels
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                Pfam; PF00047; ig; 1.
SMART; SM00406; IGv. 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
119 heavy chain V-III region LAY.
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InterPro, IPR007110, Ig-like.
InterPro, IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDDMed=3125551; W. MEDLINE=8144476; PubMed=3125551; Wilson M.R., Middleton D., Warr G.W.; Wilson M.R., Middleton D., Warr G.W.; Immunoglobulin heavy chain variable region gene evolution: structure and family relationships of two genes and a pseudogene in a teleost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The man D.W., Putnam F.W.,

"Amino acid sequence of the variable region of a human mu chain:

"Amino acid sequence of the variable region of a human mu chain:

Docation of a possible JH segment.

Proc. Natl. Acad. Sci. U.S.A. 77:239-3243 (1980).

-! MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF PATIENT WITH MACROGLOBULINEMIA.

-! SIMILARLY: Contains 1 immunoglobulin-like domain.

PIR; A02051; M3HUAM.

HSSP: PO1772; ZEB4.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0005825; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 321; DB 1; Length 116;
Pred. No. 7.1e-25;
9; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK-1,
COMPLEMENTARITY-DETERMINING-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEAVY CHAIN V REGION 5A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9C2279E2DF199B12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570 (1988).
HSSP; P01772; 2FB4.
InterPro; IPR00110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00647; ig; 1.
SMART; SM00406; IGv; 1.
PROGITE; PS50835; IG Like; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
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21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region CAM.
      15-JUL-1999 (Rel. 38, Last annotation update) Ig heavy chain V region 5A precursor. Carassius auratus (Goldfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK-3.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12808 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
116
116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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NON TER
SEQUENCE
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Best Local
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Matches

RESULT 3 HV3G\_HUMAN

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SIGNAL

CHAIN

Gaps

us-09-805-290a-26.rsp

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Chordata, Craniata, Vertebrata, Euteleostomi,
Primates, Catarrhini, Hominidae, Homo.
                                                            SEQUENCE.
MEDLINE=77070269; PubMed=826475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119
   Bukaryota; Metazoa;
              Mammalia; Eutheria;
NCBL TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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MOD RES
DISÜLFID
NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLVESGGDLVQPGRSLRLSCAASGFNFHEYNMHWLRQGPGKGPEWVSTITWNGGSVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             BIOCHEMISTRY 18:4054-4067(1979).
-!- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN
HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
                                                                                         21-JUL-1986 (Rel. 01, Created)
10-UT-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last amoutation update)
1g heavy chain V-III region DOB.
1g heavy chain V-III region E.
1d heavy chain W-III region DOB.

Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                     Steiner L.A., Lopes A.D.;
"The crystallizable human myeloma protein Dob has a hinge-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 120;
                                                                                                                                                                                                                                                           Steiner L.A., Garcia Pardo A., Margolies M.N.;
Amánio ecid sequence of the heavy-chain variable region of
crystallizable human myeloma protein Dob.";
Biochemistry 18:4068-4080(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.7%; Score 316.5; DB 1; Length 55.6%; Pred. No. 2e-24; Live 12; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 AA; 13440 MW; 880DDE307C4B2627 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A90431; G1HUDB.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain V-III region NIE.
Homo sapiens (Human).
                                                                120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P01772, 2PB4.

GO, GO:0005576; C:extracellular; NAS.
GO, GO:0003823; F:antigen binding; NAS.
OG: GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE
                                                                                                                                                                                                                              SEQUENCE.
MEDLINE=80020921; PubMed=114209;
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=80020920; PubMed=114208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                            STANDARD;
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SMART; SM00406; IGv; 1
PROSITE; PS50835; IG L
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Best Local Similarity
To; Conserve
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                                                                                                                                                                                                NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                        CRYSTALLIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HV3I HUMAN
P01770;
                                                                HV3U HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                deletion.
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60 ADSVKGRFTISRDNTLNTVYLOMNDLKPEDTGVYYWNADVRPYRTSRYLEIWGGGTLVTV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQ-SGGSTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                                          MEDLINE=77070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Mile of antibody structure. The primary structure of a monoclonal igg1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the characterization of the protein, the L- and H-chains, the Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

-I. MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HV3E HUMAN STANDARD; PRT; 114 AA.
P01763,
21-JUJ-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region WEA.
Ig heavy chain V-III region WEA.
Bumon sapiens (Human).
Human).
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1012 TaxID=9606;
                                     a
The
Ponsingl H., Hilschmann N.,
"The rule of antibody structure. The primary structure of a
"The rule of antibody structure. The primary structure of a
monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
obymotryptic peptides of the H-chain, alignment of the tryptic
peptides and discussion of the complete structure.",
Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE-83273707; PubMed-6410398;
Goni F., Frangione B.;
"Amino acid sequence of the Fv region of a human monoclonal I protein WEA, with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.4%; Score 314; DB 1; Length 119; 57.5%; Pred. No. 3.6e-24; ive 14; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 AA; 13242 MW; C96935A6E55E165B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003596; Ig_v.
Pfam; PR0047; 1g; 1.
SMART; SM0406; IGv.
PROSTITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMSGTER; PSE0835; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                          64; Conservative
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                                                                                                                               19
117
>117
                                                                                                                                                                                                                    117 1
117 AA;
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                                                                                                                                                                                                                                                                                                                                                Local Similarity
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Best Local Similarity
Matches 64; Conserv
                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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P01774;
                                                                                                                                                                                                                    NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
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SEQÜENCE
                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                            CHAIN
                                                                                                                               SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV3M_HUMAN
                                                                                                                                                                                                                                                                                                                                                                          Matches
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         S F F F F F S
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(7)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGST-NY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVDSGGGLVEPGGSLRLSCSASGFTFSANDWNWVRQAPGKGLEWLSFIGGSGSTIYY 60
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
-!- MISCELLARBGOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3.4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH WALDENSTROM'S MARCROGLOBULINEMIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.3%; Score 313.5; DB 1; Length 114; 56.7%; Pred. No. 3.8e-24; Live 14; Mismatches 29; Indels 9;
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                                                                                                                        -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02046; M3HUWE.
HSSP; P01772; 2FB4.
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114 AA; 12256 MW; D88294FB41BA07B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ilg heavy chain V-III region VH26 precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA
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EMBL, M35415; AAA58755.1; -.
PIR, A02047; H3HU26.
PDB, 1HOU; 23-DEC-99.
Genew, HGANC:5545; IGHVG.
GO:0005575; C:extracellular; NAS.
GO; GO:0005575; C:extracellular; NAS.
GO; GO:0006555; P:immula response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                             GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
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Best Local Similarity 56.74
Matches 68; Conservative
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NCBI_TaxID=9606;
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HV3C HUMAN
   70000084484444444¥FFF8
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MEDLINE=75046755; PubMed=4139708;

Tapra U.D., Kehoed J.M.;

"Structure of antibodies with shared idiotypy: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins.";

Ta nti-gamma globulins.";

Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036 (1974).

--- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

--- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

--- SIMILARITY: Contains 1 immunoglobulin-like domain.

R MSSP, PO1772; PEB4.

R GO; GO:0005957; P:BEB4.

R GO; GO:0005957; P:Immune response; NAS.

R InterPro; IPR007110; 19-like.

R InterPro; IPR007110; 19-like.
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                                                                                                                                                                                                                                                                            1 OVOLODSGGGLVOAGGSLRLSCAASGSIGDIHTWGWYROTPGKORDVVATIO-SGGSTNY
                                                                                                                                                                                                                                                                                                                   20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/FIId=VAR_003966.
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IG HEAVY CHAIN V-III REGION VH26. IG-LIKE.
                                                                                                                                                        DB 1; Length 117;
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                                                                                             CRC64;
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                                                                                             12582 MW; E826733F1A3CB0F1
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                                                                                                                                                    45.2%; Score 312.5; DB 1
67.4%; Pred. No. 4.9e-24;
iive 8; Mismatches 22
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region POM.
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IG-LIKE
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MEDLINE=75059123; PubMed=4803843;
Query Match
Best Local Similarity 53.4...
T0; Conservative
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P01781;
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    ADSVNGRFTISRNDSKNTLYLLANSLQAZBTALYYCARDAGPYVSPTFFAHYGGGTLVT 119
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MEDLINE=83289131; PubMed=6884994;
Schmidt W.E., Unng H.-D., Palm W., Hilschmann N.;
Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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21-UUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region KOL.
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"The primary structure of a monoclonal Igw-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu type), subgroup H III. Architecture of the complete Igw-molecule.";
Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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    Length 126;
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54.8%; Pred. No. 1.9e-23;
iive 11; Mismatches 30;
45.0%; Score 311.5; DB 1;
53.4%; Pred. No. 6.7e-24;
ive 14; Mismatches 28;
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21-JTL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homo sapiens (Human)
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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PIR, E90809, GIMS21.
PDR, IIGC, 03-JUN-95.
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HV16_MOUSE
        SO PRESENTANT SO PRESENTANT PRESE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Immunol. 128:302-307(1982).
-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQ---SGGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Capra J.D., Hopper J.E.;
"Comparative studies on monotypic IgM lambda and IgG kappa from an
                                                                                                                                                                                                                                                                                                                                                                                                       Johnson N., Slankard J., Paul L., Hood L.;
"The complete V domain amino acid sequences of two myeloma inulin-
binding proteins.";
                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
16 heavy chain V-III region BRO.
19 heavy chain V-III region BRO.
10 heavy chain V-III region BRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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Similarity 51.6%; Pred. No. 2.6e-23;
63; Conservative 21; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 AA; 12887 MW; 9B4517648C121C5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; D92811; AVMS82.
HSSP; P01810; 2PBJ.
                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
gheavy chain V-III region W3082.
                                                                                                                                115 AA.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=82099361; PubMed=6798111;
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InterPro; IPR003596; Ig_v.
Pfam; Pr00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LiKE; 1.
Immunoglobulin V region.
                                                                                                                             STANDARD;
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111 LVTV 114
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HV3E HUMAN
                                                                                                       HV33_MOUSE
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
individual patient. III. The complete amino acid sequence of the VH region of the IGW paraprotein."; Immunochemistry 13:995-99(1976).

-!- MISCELLANBOUS; THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM TE SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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                                                                                                                                                                                                                     -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PTR: A02049; M3HUBW.
RSP: P01772; 2FB.
RGO; GO:000557; 2FB.
RGO; GO:000555; P:immune response; NAS.
RGO; GO:0006955; P:immune response; NAS.
RINE-PPO; IPRO03596; Ig-v.
RFam; PF00047; ig; 1.
SMART; SMO0406; IGv. 1.
PROSITE; PSCO815; IG-LIKE; 1.
PROSITE; PSCO815; IG-LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 43.9%; Score 304; DB 1; Length 12 Best Local Similarity 54.2%; Pred. No. 3.5e-23; Matches 65; Conservative 13; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13227 MW; D3F0428F7C2E6410 CRC64;
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Adecugbo K., Milstein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
Nature 265:299-204(1977).
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4
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                                                                                                                                                                                                                                                                                                                                       18 VOLVESGGGLVOPGGSRKLSCAASGFTFSSFGMHWVROAPEKGLEWVAYISSGSSTLHYA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=82099361; PubMed=6798111; Johnson N., Slankard J., Paul L., Hood L.; Johnson N., Slankard J., Paul L., Hood L.; The complete V domain amino acid sequences of two myeloma inulinbinding proteins."; J. Immunol. 128:302-307(1982).

-!- MISCELLANDOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
                                                                                                                                                                                                                                                                                                              2 VOLODSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGST-NYA
                                                                                                                                                                                                                                                                                    9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-071-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-071-1986 (Rel. 42, Last annotation update)
10 heavy chain V-III region J606.

Bukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. MyCNI_TaxID=10090;
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.4%; Pred. No. 4.5e-23;
Matches 70; Conservative 9; Mismatches 34; Indels 9.
                                                                                                   IG HEAVY CHAIN V REGION MOPC 21.
D SEGMENT.
JH4 SEGMENT.
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12810 MW; B67AD6638A121A5F CRC64;
                                                                                                                                                                                                                               15071 MW; 2276A98DBDBF7016 CRC64;
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--- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR, C92811, AVMSO6.
INTERPRO, 1PR007110; IG-like.
InterPro, IPR003596; IG-V.
                                                                                                                                                           HYAD -> DYAH (IN REF. 2)
DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).
           InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
PROST; SNOO406; IGv. 1.
PROSTIF; PS50335; IG LiKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
NON TER 1 1 16 IG HEAVY CHAIN V REDOMAIN 115 119 D SEGMENT.
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BY SIMILARITY.
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
DOMAIN 1 114 IC
InterPro, IPR007110; Ig-like.
InterPro, IPR003596; Ig.v.
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115 1
115 AA;
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Query Match Best Local Similarity

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                                            1 EVKLEESGGGIVQPGGSMKLSCVASGFTFSNYWMWWWQSPEKGLEWVAEIRLKSNNYAT 60
                                                                                 58 NYADSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADVRPYRTSRYLEIWGQGTLV
12; Gaps
 26; Indels
  21; Mismatches
    63; Conservative
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    Matches
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Search completed: October 5, 2004, 08:01:57 Job time: 11.6358 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 5, 2004, 07:34:11; Search time 68.8117 Seconds (without alignments) 596.081 Million cell updates/sec Run on:

Title: Perfect score:

US-09-805-290A-26 692 1 QVQLQDSGGGLVQAGGSLRL.....WGQGTLVTVFLEPXTPKPQP 130 Sequence:

1017041 seqs, 315518202 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

1017041 Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL\_25:\*

1: \$P\_archea:\*
2: \$p\_bacteria:\*
3: \$p\_tungi:\*
4: \$p\_human:\*
5: \$p\_mammal:\*
6: \$p\_mammal:\*
7: \$p\_mbc:\*
8: \$p\_phage:\*
9: \$p\_phage:\*
1: \$p\_vorganelle:\*
9: \$p\_phage:\*
1: \$p\_vorganelle:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1	sapien	sapien	sapien	sapien	sapien	mnscnln	sapien	sapien	sapien	musculu	musculu	musculu	sapien	sapien	sapien	musculu
Description	omod eddee	Q9ul72 homo	Q8n5k4 homo	Q8wuk1 homo	Q9ul90 homo	Q99ka4 mus	Q9ul71 homo	Q9hcc1 homo	Q9ul91 homo	Q920e7 mus	Q91xel mus	Q91207 mus	Q8wu38 homo	99y509 homo	Q9ul88 homo	Q91wp5 mus
ΠD	Q96BB9	Q9UL72	Q8N5K4	Q8WUK1	09UL90	Q99KA4	Q9UL71	Q9HCC1	Q9UL91	Q920E7	Q91XE1	091207	Q8WU38	Q9Y509	Q9UL88	Q91WP5
DB	4	4	4	4	4	11	4	4	4	11	11	11	4	4	4	11
% Query Match Length DB	597	118	499	613	113	487	121	112	118	119	480	486	573	147	131	479
% Query Match	51.7	50.5	50.1	48.6	48.4	48.3	48.0	47.9	47.2	47.1	46.8	46.8	46.8	46.2	45.8	45.8
Score	358	349.5	346.5	336.5	335	334.5	332	331.5	326.5	326	324	324	324	319.5	317	317
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Q9ul84 homo sapien Q80zi7 mus musculu Q96k68 homo sapien Q8n4y9 homo sapien Q9ul93 homo sapien	9 mus 4 mus 5 mus homo	Ugulbe nome saplen Qgqyfe mus musculu Q725W1 home sapien Qgnowe oryctolagus C8veac mus musculu	0 4 4 4 4 4	Q91495 Anno Saplen Q91x92 mus musculu Q77mt6 mus musculu Q91173 homo saplen Q91195 homo saplen Q9195 mus musculu Q8469 mus musculu	Q8vcx7 mus musculu Q96qs0 homo sapien Q96qs6 homo sapien Q99ng4 mus musculu
Q9UL84 Q80ZI7 Q96K68 Q8N4Y9 Q9UL93	Q8R3V9 Q9R1A4 Q91Z05 Q8NCL6	Q9ULB6 Q9QYF0 Q7Z5W1 Q9N0W6 Q8VRA0	09N0W4 Q7TMK4 Q7Z351 Q9UL87	Q9UGP3 Q91X92 Q7TMT6 Q9UL73 Q8UDC95	Q8VCX7 Q96QS0 Q96GA6 Q99NG4
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## ALIGNMENTS

																		3;	59	79	116	139
B9 PRELIMINARY; PRT; 597 AA. B9:	01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	l protein.	etazoa; Chordata;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;		SEQUENCE FROM N.A. TISSUE=B-cell;		Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.	5760; AAH15 TREESTI		interFro; IPR03596; Iq v.	PF00047; ig; 5.	400406; IG	PS50835;	ITE; PS00290; IG_MHC; 3.	ical proti 597 AA		arch 1517%; Score 358; DB 4; Length 597; cal Similarity 63.4%; Pred. No. 1.9e-25; 78; Conservative 10; Mismatches 31; Indels 4; Gaps	1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQ-SGGSTNY 59	20 EVQLLESGGGILVQPGGSLRLSCAASGFSFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYY 79	60 ADSVKGRFTISRDNTLNIVYLOMNDLKPEDTGVYYMNADVRPYRTS-RYLEIWGGGTL 116	80 ADSVKGRFTISRDNSRDTLYLONNSLRAEDTAVYYCAKDPRGYSASGNYTREDYWGQGTL 139
RESULT 1 296BB9 ID 096BB9	0100	Hypot	Eukaı	Mamma	Ξ	TISSI	Strai	Subm	EMBL	Intel	Inte	Pfam	SMART;	PROS.	PROSITE;	Hypothet	) )	Query Match Best Local Matches 7				
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-98277139, PubMed=9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 50.5%; Score 349.5; DB 4; Length 118; Best Local Similarity 61.7%; Pred. No. 1.5e-25; Matches 74; Conservative 11; Mismatches 30; Indels 5;
                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last seg
01-OCT-2003 (TrEMBLrel. 25, Last ann
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140 VTV 142
117 VTV 119
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NON TER
SEQUENCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                          Length 499;
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BC020240; AAH20240.1;
R PIR; PL0120; PL0120.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003596; Ig-V.
R PRAMER; PR00471; Ig-S.
R PROSTE; PS003596; Ig-V.
R PROSTE; PS00359; IG-V.
R PROSTE; PS00359; IG-V.
R PROSTE; PS00359; IG-LIKE; S.
R PROSTE; PS00359; IG-LIKE; S.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 4.
SMART; SM00409; IG; 4.
SMART; SM00407; IGc1; 2.
SMART; SM00407; IGv; 1.
PROSITE; PS00209; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;
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SEQUENCE 613 AA, 67296 MW, 60C7F5950671E315 CRC64;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                      Query Match 50.1%; Score 346.5; DB 4; Best Local Similarity 54.0%; Pred. No. 1.9e-24; Matches 74; Conservative 18; Mismatches 38;
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|140 TTVTVSSASPTSPKVFP 156
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134 MVTV 137
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487 AA; 52554 MW; 7DC8E96DB333077B CRC64;
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ID Q9HCC
AC Q9HCC
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukaryota, Weltazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
MY X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.4%; Score 335; DB 4; Length 113; 60.8%; Pred. No. 3.5e-24; Live 9; Mismatches 28; Indels
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Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BEOO478 5. AAH04786.1;
HSSP; PO1810, 2FBJ.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003056; Ig-W.
InterPro; IPR003056; Ig-W.
Ffam; PF00047; ig; 4.
SWART; SW00466; IG-W.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MIC; 2.
                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus.",
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMEL. AF035024; AAD56260.1; -.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Ffan, PF00047; ig: 1.
SMART; SM00406; IGv: 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                              113 AA.
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nes 73; Conservative
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Matches
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Q9UL90
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60 ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADV--RPYRTSRYLEIWGQGTLV 117
                                                                                                                                                                                                                                                                                 80 PDNVKGRFTISRDNAKNNLYLQMSHLKASEDTAMYYCARDMGGSPYGGYSRFDYWGQGTT1 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ADSVKGRPTISRDNSKNSLYLQMNSLRAEDTALYYC---AKGKVTTIYDRPDIWGQGTMV 117
                                                                                                                                1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTWGWYRQTPGKQRDVVATIQSGGS-TNY 59
                                                                                                                                                                  20 EVQLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVATISDGGSVTYY 79
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MEDLINE-98277139; PubMed=9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
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            48.3%; Score 334.5; DB 11; Length 487; 56.8%; Pred. No. 2.5e-23; ive 14; Mismatches 37; Indels 3;
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48.0%; Score 332; DB 4; Length 121;
Best Local Similarity 59.0%; Pred. No. 7.3e-24;
Matches 72; Conservative 15; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QUL71;
01-WAY-2000 (TEMBirel. 13, Created)
01-WAY-2000 (TEMBirel. 13, Last sequence update)
01-CCT-2003 (TEMBirel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
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EMBL, AF035043, AAD56279.1; -.
HSSP, 2FB4.
InterPro, IPR007110; Ig-like.
InterPro, IPR003596; Ig-v.
Pfam. PF00047; ig, 1.
SMART; SM00406; IGv.
NON TER.
121 121
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Query Match
Best Local Similarity 56.8%
warches 71; Conservative
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01-DEC-2001
01-DEC-2001
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SEQUENCE
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Q91XE1
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                                                                                                                                                                                                                                                                                                                                                      61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYY-----CARRYALDYWGQGTLV 112
                                                                              Gaps
                                                                                                                                                                                                                                                                               9; Gaps
                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                         DB 4; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                              09UL91;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT--2003 (TrEMBLrel. 25, Last amnotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                       Query Match 47.9%; Score 331.5; DB 4; Length Best Local Similarity 59.7%; Pred. No. 7.4e-24; Matches 71; Conservative 13; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 118
118 Aa; 12843 MW; D0633949F2AC149D CRC64;
                                                                                                                                                                                                                         112 112
112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;
01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035023; AAD56259.1; -.
PIR, S21205, S21206.
InterPro, IPR007110; Ig-like.
InterPro, IPR003596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                      118 AA
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SMART; SM00406; IGv; 1.
PROSITE; PS50838; IG_LIKE; 1.
NON_TER 1 1 1 1 NON_TER 118 As; 12843 MW;
                    Single chain Fv (Fragment).
Homo sapiens (Human)
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                                                               NCBI_TaxID=9606;
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NON TER
SEQUENCE
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Q9UL91
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                                                                                                                                             61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGD----SSEAFDIWGQGTMVT 115
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                                  61 PDSVKGRFTISRDNAKOTLYLQMSSLKSEDTAMYYC-----ARHGDYDVGFAYWGQGTL
1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGST-NY
                                                                                                                 60 ADSVKGRFTISRDNTLNTVYLOMNDLKPEDTGVYYW-NADVRPYRTSRYLEIWGQGTLVT
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Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
In Mammalian Cells.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR109421.1;
EMBL, AR109437; AR109421.1;
InterPro: IPR00310; Ig-like.
InterPro: IPR003596; Ig-v.
Fam. PR0047; ig; 1.
SWART; SM00406; IGv; 1.
PROSITE, PSS0835; IG_LIKE; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Buks musculus (Mouse).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
pterin-mimicking anti-idiotope heavy chain variable region
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Mus musculus (Mouse)
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116 LVTVFLE 122
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01-NOV-1999 (
01-NOV-1999 (
01-OCT-2003 (
VH3 protein (
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Q9Y509
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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46.8%; Score 324; DB 11; Length 486;
Best Local Similarity 52.8%; Pred. No. 2.5e-22;
Matches 67; Conservative 17; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            46.8%; Score 324; DB 11; Length 480; 55.8%; Pred. No. 2.4e-22;
                                                                       Strausberg R.;
Strausberg R.;
Submitted (JuL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC010798, AAH10798.1; -
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003065; Ig-v.
InterPro; IPR003596; Ig-v.
Ffam; PF00047; Jg, 4.
SMARI; SM0406; IGv; 1.
PROSITE; PS50835; IG-IIKE; 4.
PROSITE; PS09395; IG-IIKE; 4.
PROSITE; PS0939; IG-IIKE; 4.
Mypothetical protein.
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Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC10124; AAH1034.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00306; Ig_WHC.
InterPro; IPR00356; Ig_V.
Fram; PF00047; Ig; 4.
Fram; PF00047; Ig; 4.
FROSITE; PS00835; IG_IKE; 4.
FROSITE; PS00290; IG_MHC, 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Indels
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches
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les 72; Conservative
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                        SEQUENCE FROM N.A.
TISSUE=Colon;
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60 ADSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADVRPYRTSRY-----LEIWGQ 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
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MEDLINE=56071149; PubMed=7475288;
Gao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
Lichtenstein A.K., Berenson J.R.,
"A CD10-positive subset of malignant cells is identified in multiple
myeloma using PCR with patient-specific immunoglobulin gene primers.";
Leukemia 9:1948-1953(1995).
EMBL; S80860; AAD14339.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQ-SGGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
OBWU38
OBWU38
OBWU38
OBWU38
OLYAR-2002 (TYENBIrel. 20, Created)
OLYAR-2002 (TYENBIrel. 20, Last sequence update)
OLYAR-2003 (TYENBIREL. 25, Last annotation update)
OLOCT-2003 (TYENBIREL. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.8%; Score 324; DB 4; Length 573; 52.9%; Pred. No. 3.1e-22; ative 15; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Butel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021276; AAH21276.1; -.
PIR; S21205, S21205.
                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR0030596; Ig_V.
Phoris PR0047; ig; 4.
SWART; SW00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS0290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 GILVIVELEP-KTPKPOP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grivivssaprkapovep 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 12, (TrEMBLrel. 12, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 52.>.
The 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                      61 AGSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYYCAKDGNYFDSVGYYYAGIDYWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 NYADSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADV------RPYRTSRYL 108
                                                                                                                                                                                                                                                                              1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTN-Y 59
                                                                                                                                                                                                                                                                                                               1 OVHLVESGGGVVOPGKSLRLSCEASGFTFSTYGMSWVRQAPGKGLDWVALISYDGSTQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQS---GGST 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSKAMMSWVRQAPGKGLEWVGRIKSKTDGGTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.8%; Score 317; DB 4; Length 131;
55.0%; Pred. No. 2.16-22;
Live 12; Mismatches 33; Indels 14; Gaps
                                                                                                                                                                                                                                              Gaps
HSSP; P01772; 2FB4.

G0; G0:0005887; C:integral to plasma membrane; NAS.

G0; G0:0016489; P:immunoglobulin receptor activity; NAS.

G0; G0:0016066; P:cellular defense response (sensu Vertebrata); NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig-v.

Pfam, PF00047; ig: 1.

PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         foung D.C.;  \text{Myosin-reactive autoantibodies in } rheumatic \text{ carditis and normal } \\ \text{Myosin-reactive autoantibodies} 
                                                                                                                                                                                                                                             5,
                                                                                                                                                                                                           DB 4; Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9UL88 PRELIMINARY, PRT, 131 AA.
Q9UL88,
Q1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                          46.2%; Score 319.5; DB 4; Length 57.3%; Pred. No. 1.4e-22; Live 10; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER 131 131
NON TER 131 131
SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;
                                                                                                                                                                         147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fetus.,

fetus.,

Clin. Immunol. Immunopathol. 87:184-192(1998).

EMBL, AF035026; AAD56262.1; -.

PIR, S21205; S21205.

HSSP; P01810; 2FBJ.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.

Ffam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PSS0835; IG_LIKE; 1.
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Best Local Similarity 55.00
Best Local Similarity 55.00
                                                                                                                                                                                                                            Best Local Similarity 57.33
Matches 71; Conservative
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Oy 109 EIWGGGTLVTV 119
| | | | | | | | | | | |
| Db 119 EYWGGGTLVTV 129
| Search completed: October 5, 2004, 08:13:49
Job time: 69.8117 secs
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                    - protein search, using sw model
              Copyright
                                                                    OM protein
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5, 2004, 07:04:10 ; Search time 98.9043 Seconds (without alignments) 371.381 Million cell updates/sec October Run on:

US-09-805-290A-26 692 1 QVQLQDSGGGLVQAGGSLRL.....WGQGTLVTVFLEPKTPKPQP 130 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A Geneseq 29Jan04:\*

1: geneseq11980s:\*

2: geneseq1990s:\*

4: geneseq22001s:\*

5: geneseq2203s:\*

6: geneseq2203as:\*

7: geneseq2203bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

### STIMMARTES

	uo	HPL inhib	HPL inhib		HPL inhib	HPL inhib			HGL inhib	Anti-pota	Immunoglo	HGL inhib	HPL inhib		HGL inhib			HGL inhib	HPL inhib	Llama ant	Llama ant		Llama HCV	Llama HCV	Llama ant	Amino aci
	Description	6		Aae10554	Aae10555 ]	Aae10557	Aae10556	Aae10553	Aae10563	Aae05283	Abg30620		Aae10558			Aae10561	Aae10565	Aae10564	Aae10551	Aay39819	Abr62883	Abr62882	Aae05286	Aae05287	Abr62881	Aab67778
SUMMAKIES	σı	AAE10559	AAE10552	AAE10554	AAE10555	AAE10557	AAE10556	AAE10553	. AAE10563	AAE05283	ABG30620	AAE10566	AAE10558	AAE05288	AAE10567	AAE10561	AAE10565	AAE10564	AAE10551	AAY39819	ABR62883	ABR62882	AAE05286	AAE05287	ABR62881	AAB67778
	DB	4	4	4	4	4	4	4	4,	41	'n	4	4	4	4	4	4	4	4	~	<b>r</b>	7	4	4	7	4
	Length	130		130	131	130	130	129	124	152	131	124	129	149	130	129	128	129	CI	Н	a.	σ	377	œ	190	119
*	Query	100.0	95.6	σ,	ω.	72.5	2	68.3	67.9	67.9	67.8	66.3	64.5	63.9			63.6			61.1		8.09			60.4	60.3
	Score	692	641	617	505.5	502	500	472.5	470	7	469.5	459	446.5	442.5	442	441.5	440	437.5	427.5	422.5	422	421	419.5	6	418	417
	Result No.	-	7	m	4	ഹ	v	. 1	8	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25

Example 2; Page 10; 37pp; English.

	2.0	_	8 Llama	Aay41172 Llama Vhh		Abg30618 Immunoglo	Aay41165 Llama Vhh	Aab67779 Amino aci			Immr		7 Mouse	Llama	Aay41173 Llama Vhh		7 Llama	Aay41169 Llama Vhh
AAB67777	AAY41167	ABR62880	ABR62878	AAY41172	AAY28615	ABG30618	AAY41165	AAB67779	AAE10562	AAE05282	ABG30972	AAE10560	ABG30617	ABR62885	AAY41173	AAY39816	AAY39817	AAY41169
41	۰ ۲۷	7	۲-	N	N	Ŋ	N	4	4	4	2	4	S	7	7	7	7	7
1119	204	190	198	211	124	134	225	119	124	153	133	130	127	194	205	111	125	206
60.3	60.2	60.1	60.09	59.8	59.6	59.5	59.3	58.8	58.8	58.7	58.2	57.8	57.7	57.7	57.6	57.2	56.6	56.5
417	416.5	416	415	413.5	412.5	412	410.5	407	407	406.5	402.5	400	399.5	399	398.5	396	392	391
26	78	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // 35
//abel= CDR1
//note= "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79. .64
/label= CDR2
/note= "Complementarity determining region 2"
98. .110
/note= "Complementarity determining region 3"
/note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                        HPL inhibiting VHH fragment, HPL #30 from llama species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                               AAE10559 standard; peptide; 130 AA
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                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                             10-DEC-2001
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                                                                                                                                      AAE10559;
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Region
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RESULT 1
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         The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary anzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #30 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                       DSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADVRPYRTSRYLEIWGQGTLVTVF 120
                                                                                                                                                                                                                                                                                                                                          DSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADVRPYRTSRYLEIWGQGTLVTVF 120
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                                                                                                                                                                                                                                                                                         1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA 60
                                                                                                                                                                                                                                                           OVOLODSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA
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                                                                                                                                                                                              Query Match
100.0%; Score 692; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.3e-57;
Matches 130; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPL inhibiting VHH fragment, HPL #12 from llama species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE10552 standard; peptide; 130 AA.
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/label= CDR1
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label= CDR2
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/label= CDR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               121 LEPKTPKPOP 130
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                                                                                                                                                                    Sequence 130 AA;
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                                                                                                         chain variable domain (MHE) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #12 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DSVKGRFTISRDNTLATVYLQMADLKPEDTAVY2CNADVRPYRTSRYLEVWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
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useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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                                                                                               The patent discloses antibodies or their fragments comprising a heavy
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/label= CDR3
/note= "Complementarity determining region 3"
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                                                                                                                                                                                                                                                                                           Length 130;
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note= "Complementarity determining region
                                                                                                                                                                                                                                                                                         Query Match 92.6%; Score 641; DB 4; Length 13
Best Local Similarity 93.1%; Pred. No. 4.8e-52;
Matches 121; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPL inhibiting VHH fragment, HPL #14 from llama species.
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                                                                Example 2; Page 9; 37pp; English
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label= CDR1
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(UNIL ) UNILEVER
                                                                                                                                                                                                                                                            Sequence 130 AA;
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human dietary er
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14-MAR-2000; 2000EP-00200930
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                                                       Bezemer S,
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                                                                                                                     The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #14 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                61 DSVKGRFTISRDNILNTVYLQMNSLKPEDTAVYHCNADVRPYRTSRYLELWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; tood; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                 DSVKGRFTISRDNTLNTVYLQMNDLKPEDIGVYYWNADVRPYRISRYLEIWGQGTLVTVF 120
                                            New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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                                                                                                                                                                                                                                                                                                                           1 QVQLQESGGGLVQAGGSLRLSCAASGSIGSIHTMGWYRQTPGTERDVVATIQDGGSTNYA 60
                                                                                                                                                                                                                                                                                                      1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA
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                                                                                                                                                                                                                                                          89.2%; Score 617; DB 4; Length 130; 90.0%; Pred. No. 8.3e-50; ive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPL inhibiting VHH fragment, HPL #15 from llama species.
  Tareilus
 De Haard JJW,
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                                                                                                  Example 2; Page 9; 37pp; English.
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/label= CDR3
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/label= CDR1
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 Van De Burg M,
                                                                                                                                                                                                                                                                   Best_Local Similarity 90.0
Matches 117, Conservative
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                       WPI; 2001-572718/65.
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                                                                             of light chains
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                                                                                                                 New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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74.8%; Pred. No. 2.2e-39;
live 11; Mismatches 21
   De Haard JJW,
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/label= CDR3
/note= "Comple
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/label= CDR1
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Best Local Similarity 74.8%
Matches 98; Conservative
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/label= C
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   Van De Burg
                                                                WPI; 2001-572718/65.
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of light chains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                     New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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                                                                                                                                                                                                                                                                                                                                                                    72.5%; Score 502; DB 4; Length 13
74.6%; Pred. No. 4.5e-39;
ive 8; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPL inhibiting VHH fragment, HPL #18 from llama species.
                                                                                                           Tareilus
                                                                                                           De Haard JJW,
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                                                                                                                                                                                                             Example 2; Page 10; 37pp; English.
                               20-FEB-2001; 2001EP-00200703
                                                      14-MAR-2000; 2000EP-00200930
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/label= CDR2
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label= CDR1
                                                                                                         Bezemer S, Van De Burg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 74.6
nes 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LEPKTPKPOP 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                          UNIL ) UNILEVER NV.
                                                                                                                                WPI; 2001-572718/65
                                                                                                                                                                                                                                                                                                                                               Sequence 130 AA;
                                                                                                                                                                                       of light chains
          19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                 Н
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
AAE10556
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LILLLLXSXXAXXBXLLLLLLX
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #18 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADVRPYRTSRYLEIWGQGTLVTVF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 OVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQDSGGGLVQAGGSLRLSCAASGTIGDIYTMAWHRQAPGKERELVASATESGSPNYA
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98. .110
/label= CDR3
/note= "Complementarity determining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tareilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 500; DB 4;
Pred. No. 7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 10; 37pp; English.
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                                                                                                                                                                                                                                                                     20-FEB-2001; 2001EP-00200703.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bezemer S, Van De Burg M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 72.3
Best Local Similarity 75.4
Matches 98; Conservative
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PLC.
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Lama sp.
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AAE05283
ID AAE0
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AC AAEC
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DT 18-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody; camelid; anorectic; heavy chain variable domain; VHH; dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADVRPYRISRYLEIWGQGTLVTVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DSAKGRFTISKDNAKONTVYLQMNSLKPEDTAVYYCNALITRWDKS-VNDYWGQGTQVTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGGGLVQAGGSLRLSCAASGTILSIIYMDWYRQTPGKQRELVGRITAAGGSTNYA 60
                                                                                                                                                                                                                                                                            New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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                                             2
                                                       98. .109
/label= CDR3
/note= "Complementarity determining region 3"
            "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGL inhibiting VHH fragment, HGL #9 from llama species.
                                                                                                                                                                                                                                  Tareilus E;
                       50. .64
/label= CDR2
/note= "Complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 68.3%; Score 472.5; DB 4; Best Local Similarity 73.1%; Pred. No. 2.6e-36; Matches 95; Conservative 9; Mismatches 25;
                                                                                                                                                                                                                                    De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE10563 standard; peptide; 124 AA.
                                                                                                                                                                                                                                                                                                                                        Example 2; Page 9; 37pp; English.
                                                                                                                                                                          14-MAR-2000; 2000EP-00200930
                                                                                                                                                    20-FEB-2001; 2001EP-00200703
                                                                                                                                                                                                                                    Van De Burg M,
  label=
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(UNIL ) UNILEVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 129 AA;
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                                                                                                       EP1134231-A1
                                                                                                                             19-SEP-2001
                                                                                                                                                                                                                                    Bezemer S,
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human
food;
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #9 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DSVKGRFTISRDNTLNTVYLOMNDLKPEDTGVYYWNADVRPYRTSRYLEIWGOGTLVTVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DSVKGRFTISRDNIKNTMYLQMNSLKPEDTGVYYCAG-----TGAEGHYWGQGTQVTVS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGGGLVQAGGSLRLSCAASGS1GSLYVMSWYRQAPGKQREPVAALMGSGSTTYA
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                                                                            "Complementarity determining region 1"
                                                                                                                                                            region 2"
                                                                                                                                                                                                                                            region 3"
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                                                                                                       50. 64
/label= CDR2
/note= "Complementarity determining
98. 104
/label= CDR3
/note= "Complementarity determining
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Jocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 13; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-2000; 2000EP-00200930.
                                1. .35
label= CDR1
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                                                                                     note≕
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                                                                                                                                                                                                                                                                                                         EP1134231-A1
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Matches 9
  Key
Region
                                                                                                             Region
                                                                                                                                                                                            Region
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Heavy chain variable domain; antibody; protein array; aging; VHH; immunoglobulin; sticky phage-antibody; micro-panning; immune library;

proteomic; mouse.

WO200248193-A2.

20-JUN-2002

Immunoglobulin G specifc heavy chain variable domain antibody #3.

(first entry)

21-OCT-2002

ABG30620;

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Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
                     Potato, heavy chain immunoglobulin; pathogen resistance; metabolism modulator; passive immunisation; heavy chain variable domain; WH; anti-potato SBEII; starch branching enzyme; SBE A.
Anti-potato SBEII (Clone46) VH region attached with myc and his6 tag.
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                                                                                                                                                                                                                      Jobling SA,
                                                                                                                                                                                                                                                                                                                            Example 1; Fig 12; 81pp; English.
                                                                                                                                                                                                                       Frenken LGJ, Van Der Logt CPE,
                                                                                                                                               38-DEC-2000; 2000EP-00310997;
                                                                                                                                                                    99EP-00310188.
                                                                                                                                                                                       (UNIL ) UNILEVER PLC. (UNIL ) UNILEVER NV.
                                                                                                                                                                                                                                          WPI; 2001-427157/46.
N-PSDB; AAD10054.
                                                               Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 152 AA;
                                                                                                       EP1118669-A2.
                                                                      Unidentified.
Chimeric.
                                                                                                                                                                    17-DEC-1999;
                                                                                                                           25-JUL-2001,
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Novel protein array useful for detecting the presence of individual proteins in sample, comprises heavy-chain variable domain antibodies antibody fragments obtainable from Camelidae.

De Haard JJW, Hermans P, Landa I, Verrips CT;

WPI; 2002-583487/62.

(UNIL ) UNILEVER PLC. (UNIL ) HINDUSTAN LEVER LTD.

(UNIL ) UNILEVER NV.

03-DEC-2001; 2001WO-EP014471. 13-DEC-2000; 2000EP-00311142.

The present invention relates to a method for modifying a plant to produce an antibody or an active fragment or derivative, or a protein functional equivalent, in a cellular compartment comprises introducing a DNA sequence encoding a heavy chain immunoglobulin, where the DNA is linked to promoters and provided with an additional sequence encoding a peptide capable of targeting heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain immunoglobulin or an active fragment or derivative, or a protein that is functionally equivalent for increasing the pathogen resistance in a plant or to modulate metabolism in a plant. Under some circumstances it may be desirable to retain the antibody product with the plant rather than extraoring and isolating the pathod. In particular, edible selected antigens may be used in a method of passively immunising an animal, preferably human, against the antigen, e.g., pathogenic organisms. The preferably human, against the antigen, e.g., pathogenic organisms. The preferable domain (VH) attached to peptide linkers, myc and hise tag. The potato SBEII is a starch branching enzyme also designated SBE A

1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA 67.9%; Score 470; DB 4; Length 152; 72.4%; Pred. No. 5.3e-36; ive 5; Mismatches 20; Indels Local Similarity 72.4 nes 97; Conservative Query Match Best Loca Matches

DSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNAD----VRPYRTSRYLEIWGQGTL 116 61 DSVXGRFTISRDNAKNTVYLQMSSLKPEDTAVYYCAAGNLLVKRPY------WGQGTL 112 9 1 QVQLQESGGGLVQAGGSLRLSCVASGNTFSIIAMAWYRQAPGKQREVVASINSIGSTNYA 117 VTVFLEPKTPKPQP 130 61 ઠે g 8

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The invention describes a protein array (I) comprising a number of heavychain variable domain antibodies or antibody fragments, obtainable from chain variable domain antibodies or antibody fragments, obtainable from camelidae. The method is useful for removing abundant proteins from an extract or sample which do not provide useful information on the condition of a cell or tissue in the extract or sample to be condition of a cell or tissue in the extract or sample to be proteins in a sample, comparing the distribution of proteins in different cell types, and identification of proteins that may be of importance in determining the altered properties of cells in disease, aging or other conditions. Using a heavy-chain variable domain derived from an immunoglobulin that is naturally devoid of light chains (VHH) in (I) provides a number of advantages, such as an improvement of sensitivity/resolution in the order of 10-100 times, and detection of post-translationally modified proteins. The invention also describes a centhod (II) that enables the simultaneous processing of large numbers of panning condition. This feature combines in corporated phage-ELISA for continuation of a limited number of selections. In (II), due to the fact that many different conditions can be tested, varying amounts of input-phages can be used simultaneously in order to decrease the enrichment of sticky phage. Continuels, moder to decrease the enrichment of sticky phage. The fine frames needed for the generation of large panels of antibodies in short time frames needed for the generation of arrays (proteomics). This sequence represents an immunoglobulin (Igd) heavy chain variable domain continued.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 3; 80pp; English
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1 QVOLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA 60
                                                   1;
67.8%; Score 469.5; DB 5; Length 131; 71.0%; Pred. No. 5e-36; ive 10; Mismatches 27; Indels 1;
Query Match 67.8
Best Local Similarity 71.0
Matches 93; Conservative
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Gaps

ABG30620 standard; protein; 131 AA.

RESULT 10 ABG30620 ID ABG3

113 VTVSSEPKTPKPOP 126

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69.2%;

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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #15 from llama (camelid) species
                                                                                                                                                                                                                                                                                                               antibody; camelid; anorectic; heavy chain variable domain; VHH; dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; human gastric lipase; HGL; cosmetic control; body weight.
                            119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
9
                                            61 DSVKGRFTISRDNAKNTVYLQMNSLKPEDTGVYYCNAETVRATTGRFITDLWGQGTTVTV
QVQLQESGGGLVQPGGSLRLSCAASKSIFGFGAVGWHRQAPGKQRELVARITYDSGTNYA
                              DSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYVWNADVRPYRTSRYL-E1WGQGTLVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98. 104
/label= CDR3
/note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10. 64
1abel= CDR2
Inotes "Complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                  HGL inhibiting VHH fragment, HGL #15 from llama species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tareilus E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                             AAE10566 standard; peptide; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 14; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2000; 2000EP-00200930.
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                                                                                                                                                                                                                                                                                                                                                                                                                           30. .35
/label= CDR1
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                                                                                                                                                                                                                                                       (first entry)
                                                                                       120 FLEPKTPKPOP 130
                                                                                                                   121 SSEPKTPKPÓP 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 124 AA;
                                                                                                                                                                                                                                                                                                                  Llama antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1134231-A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-SEP-2001
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                              61
                                                                                                                                                                                                                           AAE10566;
                                                                                                                                                                                                                                                                                                                                                                             Lama sp
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Region
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food;
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Length 124;

4 DB

Score 459;

66.3%;

Query Match

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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipses (HBL) which are useful for the cosmetic control of body weight of human baings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #22 from
            ۲;
                                                                                                                                                                                                                                                                                                                                                                                     Llama antibody, camelid, anorectic, heavy chain variable domain, VHH;
human dietary enzyme inhibitor; medicament; human pancreatic lipase, HPL;
food, human gastric lipase, HGL; cosmetic control; body weight.
                                                                                                  DSVKGRFTISRDNTLNTVYLOMNDLKPEDTGVYYWNADVRPYRTSRYLEIWGOGTLVTVF 120
                                                                                                                              61 DSVKGRFTISRDNEKNTMYLQMNSLTPEDTGVYYCAG-----TGAEGHYWGQGTQVTVS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                         9
                                                                      9
                                                           1 QVQLQESGGGLVQAGGSLRLSCAASGSIGSMYVMSWYRQAPGKEREPIAALMGSGSTTYA
                                   VOLODSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA
            6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98. .109
/label= CDR3
/note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region 2"
            Indels
                                                                                                                                                                                                                                                                                                                                                           HPL inhibiting VHH fragment, HPL #22 from llama species.
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/label= CDR2
/note= "Complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tareilus
Pred. No. 4.4e-35;
3; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                       AAE10558 standard, peptide, 129 AA
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    .35
    label= CDR1

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                                                                                                                                                                                                                                                                                                                                  10-DEC-2001 (first entry)
Best Local Similarity 69.2
Matches 90; Conservative
                                                                                                                                                                 130
                                                                                                                                                                                            115 SEPKTPKPOP 124
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PLC.
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(UNIL ) UNILEVER
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Region
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114 SEPKTPKPOP 123
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                                                                                                                                                                   Best Local Similarity
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                                                                                                                     Sequence 149 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method for modifying a plant to produce an antibody or an active fragment or derivative, or a protein functional equivalent, in a cellular compartment comprises introducing a DNA sequence encoding a heavy chain immunoglobulin, where the DNA is peptide capable of targeting heavy chain immunoglobulin to a cellular compartment. The method is used for producing a heavy chain immunoglobulin to a cellular immunoglobulin or an active fragment or derivative, or a protein that is functionally equivalent for increasing the pathogen resistence in a plant or to modulate metabolism in a plant. Under some circumstences it may be desirable to retain the antibody product with the plant rather than
                                                                                                                                                                                                 61 DSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADVRPYRTSRYLEIWGQGTLVTVF 120
                                                                                                                                                                                                                     61 DSWKGRFTISRDNAKNTVYLHMNNLKPEDTAVYYCKALISSYDGS-WNDYGGQGTQVTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying a plant to produce an antibody useful for increasing pathogen resistance or to modulate metabolism comprises introducing a DNA sequence encoding a heavy chain immunoglobulin linked to a peptide that targets a cellular compartment.
                                                                                                                                                       1 QVQLQESGGGLVQAGGSLRLSCAASGSIRSISIMTWYRQAPGKERELVARMSSDGTISYT 60
                                                                                                                                1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potato, heavy chain immunoglobulin; pathogen resistance; metabolism modulator; passive immunisation; heavy chain variable domain; WH; anti-potato SBEII; starch branching enzyme; SBE A.
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-potato SBEII (Clone68) VH region attached with myc and his6 tag
                                                                    Length 129;
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Teh Y;
                                                    64.5%; Score 446.5; DB 4;
69.2%; Pred. No. 6.8e-34;
... Micmatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jobling SA,
                                                                                                                                                                                                                                                                                                                                                                                   AAE05288 standard; protein; 149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; Fig 28; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-2000; 2000EP-00310997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99EP-00310188,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                             Query Match
Best Local Similarity 69.2
Matches 90; Conservative
                                                                                                                                                                                                                                                                                        120 SEPKTPKPQP 129
llama (camelid) species
                                                                                                                                                                                                                                                                  121 LEPKTPKPOP 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Solanum tuberosum,
Unidentified,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAD10059
                                   Sequence 129 AA
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                                                                                                                                                                                                                                                                                                                                                  RESULT 13
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extracting and isolating the product. In particular, edible selected antigens may be used in a method of passively immunising an animal, preferably human, against the antigen, e.g., pathogenic organisms. The present sequence is an anti-potato SEBII antibody (denoted Clone68) heavy chain variable domain (VH) attrached to peptide linkers, myc and his6 tag. The potato SEBII is a starch branching enzyme also designated SEE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Llama antibody, camelid, anorectic, heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                          09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 DSVKGRFTISRDNAKNTLYLOMNSLKPEDTAVYYCTAGG-----SYWGQGTQVTVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DSVKGRPTISRDNTLNTVYLQMNDLKPEDTGVYYWNADVRPYRTSRYLEIWGQGTLVTVP
                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA
                                                                                                                                                                                                                                                                                                                                                                                                                            3 QVQLQESGGGLVQAGGSLRLSCAASGSIFRRPHMGWFRQAFGGERELVALISAGGRTWYA
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                 Length 149;
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/label= CDR3
/note= "Complementarity determining region 3"
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| Tabel = CDR1
| Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGL inhibiting VHH fragment, HGL #16 from llama species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            亩
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                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                              ch
1 Similarity 69.2%; Pred. No. 1.9e-33;
90; Conservative 8; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE10567 standard; peptide; 130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-2001; 2001EP-00200703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130
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Tue Oct

4; Page 14; 37pp; English.

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                                 The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #16 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYYWNADVRPYRTSRYLEIWGQGTLVTVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSVKGRFTISRDNARGTVYLQMNSLKPEDTAVYYCAAARSLELTPTSYDYWGQGTQVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                              63.9%; Score 442; DB 4; Length 130; 70.8%; Pred: No. 1.8e-33; Live 4; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                 Query Match 63.9
Best Local Similarity 70.8
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEPKTPKPOP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEPKTPKPOP 130
                                                                                                                                                                                                                                                                          Sequence 130 AA;
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HGL inhibiting VHH fragment, HGL #4 from llama (camelid) species

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Example 4; Page 13; 37pp; English

Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight. HGL inhibiting VHH fragment, HGL #4 from llama species. AAE10561 standard; peptide; 129 AA (first entry) 10-DEC-2001 AAE10561;

RESULT 15

/note= "Complementarity determining region 1"

Location/Qualifiers

g

Гата

Key Region

31. .35 /label= CDR1

/note= "Complementarity determining region

98. .109 /label= CDR3

Region

EP1134231-A1

19-SEP-2001

50. .64 /label= CDR2

Region

/note= "Complementarity determining region 3"

Tareilus E;

De Haard JJW,

Van De Burg M,

Bezemer S,

WPI; 2001-572718/65

14-MAR-2000; 2000EP-00200930

(UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.

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61 DSVKGRFTISRDNTLNTVYLQMNDLKPEDTGVYY -- WNADVRPYRTSRYLEIWGQGTLVT 118
                                                                                                                                                                                                                                                                                                     DSVKCRPTIARENAKNTVYLQMSSLKPEDTAVYYCKGRGGLTQYSEHDY---WGQGTQVT 117
                                                                                                                                                                                                                                             1 QVQLQDSGGGLVQAGGSLRLSCAASGSIGDIHTMGWYRQTPGKQRDVVATIQSGGSTNYA 60
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د
                                                                                                                                                                                                     Length 129;
                                                                                                                                                                                                     63.8%; Score 441.5; DB 4;
67.4%; Pred. No. 2e-33;
live 10; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                           5, 2004, 08:00:14
                                                                                                                                                                                                                            89; Conservative
                                                                                                                                                                                                                                                                                                                                      119 VFLEPKTPKPQP 130
                                                                                                                                                                                                                                                                                                                                                          118 VSSEPKTPKPÓP 129
                                                                                                                                                                                                                                                                                                                                                                                           Search completed: October
Job time : 99.9043 secs
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                  Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                 61
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Sold Bioth (Usy

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us-09-805-290a-8.rpr

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

October 5, 2004, 07:36:16; Search time 2.10648 Seconds (without alignments) 593.639 Million cell updates/sec

US-09-805-290A-8 68 1 DVRPYRTSRYLEV 13 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1. Dir1:\*
2. Dir2:\*
3: Dir3:\*
4: Dir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ption	hypothetical prote	in (E	III	einase III	protease III precu	4	ctas	agaE protein [impo	hypothetical prote	_	9.15 prote	30S ribosomal prot	hypothetical prote	$\circ$	hypothetical prote	probable transport	probable transport	T)	probable membrane	hypothetical prote		orin-8	protein F18014.23	hypothetical prote	hypothetical prote	hypothetical prote	ε	i hy	translation elonga
ID	T47356	SNECPI	F91088	H85933	AC0865	E84828	AD3042	H98243	T15202	T00447	A86274	B82559	T00335	T24300	T08250	G90705	B85556	G64790	AB0573	G91067	H85911	T10798	G86327	H72721	T00446	T16910	AG0015	~	4384
DB	1	H	N	N	~	7	Ŋ	N	N	~1	~	~3	~	7	0	7	7	7	7	0	~	0	7	~	N	N	Ŋ	Н	7
Length	303	962	962	962	962	775	442	442	594	258	526	569	1441	103	286	415	415	415	415	437	441	599	84	168	260	269	278	310	376
% Query Match	61.8	Η.	61.8	ä	ä	60.3	58.8	58.8	58.8	57.4	57.4	57.4	57.4	55.9	54.4	54,4	54.4	54.4	54.4	54.4	54.4	4.	52.9	ď	ď.	52.9	ά.	ď.	ď
Score	42	42	42	42	42	41	40	40	40	39	39	39	39	38	37	37	37	37	37	37	37	37	36			36			
Result No.	-	8	m	41	ഗ	9	7	<b>.</b>	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

	propable isocitrat	hypothetical prote	hypothetical prote	ribosomal protein	30S ribosomal prot	RNA-directed RNA p	RNA-directed RNA p	RNA-directed RNA p	Fas-binding protei	probable heterochr	RND multidrug effl	probable dna-direc	ataxia telangiecta	hypothetical prote	_	
	A/2658	T48966	E84465	B82141	C83250	P2IVBS	P2IVBC	P2IVBW	T03847	T37916	H83071	T40607	A43100	C84898	C81220	G81990
(	7	7	7	7	0	-	Н	-	N	~	~	~	-	7	0	N
	435	448	536	556	559	725	726	726	740	960	1043	1405	1708	787	113	113
6	52.3	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.2	51.5	51.5
. (	36	36	36	36	36	36	36	36	36	36	36	36	36	35.5	35	35
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

	RESULT 1
	T47356
	hypothetical protein F18P9.140 - Arabidopsis thaliana
	C;Species: Arabidopsis thaliana (mouse-ear cress)
	C;Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text_change 20-Apr-2000
	C,Accession: T47356
	R,Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; N
	Mayer, K.F.X.
	submitted to the Protein Sequence Database, April 2000
	A; Reference number: 224458
	A; Accession: T47356
	A;Status: preliminary
	A; Molecule type: DNA
	A;Residues: 1-303 <nya></nya>
	A; Cross-references: EMBL: AL138654
	A;Experimental source: cultivar Columbia; BAC clone F18F9
	C;Genetics:
	A;Map position: 3
	A;Introns: 47/3; 103/3; 140/2; 182/1; 210/2; 241/3
	A;Note: F18F9.140
	Query Match 61.8%; Score 42; DB 2; Length 303;
-	
	Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
	Qy 1 DVRPYRTSRYLEV 13

# |:|||:|| 10 DIRPYKTSWRIQV 22 엄

RESULT 2 SNECPI pitrilysin (EC 3.4.24.55) precursor [validated] - Escherichia coli (strain K-12) pitrilysin (EC 3.4.24.55) precursor proteinase III NyAlternate names: endopeptidase Pi, proteinase III C;Species: Escherichia coli C;Species: Bscherichia coli C;Accessial-Mar-1993 #Sequence revision 31-oct-1997 #text_change 27-oct-2003 C;Accession: F65064; A29093; A25765; B25532	R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col., R. Rose, D.U.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Title: The A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: F65064	A)Status: nucleic acid sequence not shown, translation not shown A,Molecule type: DNA A,Residues: 1-962 < BLAT> A,Residues: 1-962 < BLAT> A,Cross-references: GBRAE000365, GB:U00096, NID:g2367163, PIDN:AAC75860.1, PID:g2367164; A,Experimental source: strain K-12, substrain M01655 A,Experimental source: strain K-12, substrain M01655	Kiclaverie-marking, F.; Diaz-loires, M.K.; Aushher, S.K. 8-185-195, 1987 A;Title: Analysis of the regulatory region of the protease III (ptr) gene of Escherichia A;Reference number: A29093; MUID:88005781; PMID:3308636
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A;Status: preliminary
A;Molecule type: DWA
A;Molecule type: L925 <STO>
A;Cross-references: GB:AE005174; NID:g12517303; PIDN:AAG57932.1; GSPDB:GN00145; UWGP:Z413
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable WD-40 repeat protein [imported] - Arabidopsis thaliana [c.Species: Arabidopsis thaliana (mouse-ear cress) [c.Species: Arabidopsis thaliana (mouse-ear cress) [c.Species: Arabidopsis thaliana (mouse-ear cress) [c.Species: O.Z-Feb-2001] [c.Spacession: E84828 [c.Spacession: E84828] [c.Spacession: E84828] [c.Spacession: E84828] [c.Spacession: E84828] [c.Spacession: E84828] [c.Spacession: E94828] [c.Spacess
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A;Note: this species has also been called Salmonella typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09:Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Oct-2003
C;Accession: Ac0865
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica servor A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease III precursor (pitrilysin) [imported] - Salmonella enterica subsp. enterica serc
C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Oct-2003
C;Accession: H85933
F;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grobeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Fitler: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-962 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02819.1; PID:g16504073; GSPDB:GN00176 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 16;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 2; Length 962;
Pred. No. 16;
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C,Superfamily: insulin-degrading enzyme (IDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: ptr
C,Superfamily: insulin-degrading enzyme (IDE)
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ilarity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 61.8%;
Local Similarity 80.0%;
les 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: AC0865
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Matches
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C;Species: Escherichia coli
C;Species: Ba-Jul-201 #sequence_revision 18-Jul-2001 #text_change 27-Oct-2003
C;Accession: F91088
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. agaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gence A;Accession: F91088
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Description: endopeptidase degrades small peptides [validated, MUID:92237263]
A, Pathway: protein degradation
A, Pathway: protein degradation
C, Superfamily: insulin-degrading enzyme (IDE)
C, Superfamily: insulin-degrading enzyme (IDE)
C, Keywords: hydrolase; metalloproteinase; monomer; periplasmic space; protein degradatic
F;1-23/Domain: signal sequence #status predicted <SIG>
F;2-4-962/Product: pitrilysin #status experimental <AMT>
F;88,92/Binding site: zinc (His) #status experimental
F;91/Active site: Glu #status experimental
                                       A; Molecule type: DNA
A; Residues: 1-276, 'HYBGLR', 283,'W', 285-296 < CLA>
A; Residues: 1-276, 'HYBGLR', 283,'W', 285-296 < CLA>
A; Cross-references: GB:MI7095; NID:g147390; PIDN:AAA24436.1; PID:g147391
A; Experimental source: strain K12
A; Note: part of this sequence, including the amino end of the mature protein, was confir
R; Finch, P.W.; Wilson, R.E.; Brown, K.; Hickson, I.D.; Emmerson, P.T.
Nucleic Acids Res. 14, 7695-7703, 1986
A; Title: Complete nucleotide sequence of the Escherichia coli ptr gene encoding protease
A; Reference number: A25765; MUID:87040734; PMID:3534791
                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A25765
A;Molecule type: DNA
A;Residues: 1-962 <R1N
A;Cross-references: GB:XX06227; NID:g42560; PIDN:CAA29576.1; PID:g42561
B;Becker, A.B.; Roth, R.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 3835-3839, 1992
A;Title: An unusual active site identified in a family of zinc metalloendopeptidases. A;Reference number: A38854; MUID:92237263; PMID:1570301
A;Contents: annotation; active site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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A;Residues: 1-962 <HAY>
A;Ressireferences: GB:BA000007; PIDN:BAB37101.1; PID:g13363150; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 2; Length 962.
Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.88;
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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A,Map position: 61
C,Function:
        A; Accession: A29093
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A;Status: preliminary A;Molecule type: DNA A;Residues: 1-775 <STO>

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cross-references: EMBL:AC004260, NID:g3176694, PID:g3540203; GSPDB:GN00059; ATSP:T14N5.
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A;Experimental source: strain Bristol N2; clone F12B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: T00447
R;Federspiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Araujo, i Vysotskaia, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z14152
A;Accession: T00447
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                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15202
R;Pauley, A; Maggi, L.
R;Dauley, A; Maggi, L.
A;Description: The sequence of C. elegans cosmid F12B6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T14N5.4 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: (1-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 22-0ct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 594;
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A;Map position: 1
A;Introns: 45/2; 146/3; 211/3; 316/1; 367/3; 407/3; 552/2
                                                                                                                                                                  hypothetical protein F12B6.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-594 <PAU>
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Pred. No. 23;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-258 <FED>
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Best Local Similarity 61.5%;
Matches 8; Conservative 5
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     421 DPRPYRYSRFFD 432
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PWRTSRYMQ 207
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A; Introns: 38/3; 106/1
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I R;Wood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rigodoner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Hitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oxidoreductase Atu3952 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD3042
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A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-442 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89474.1; PID:g15159342; GSPDB:GN00170
A;Cross-references: GB:AE002093; NID:g4586061; PIDN:AAD25679.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agaE protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon) C;Species: Agrobacterium tumefaciens C;Date: 22-Oct.-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002 C;Accession: H98243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 2; Length 442; Pred. No. 17; 3; Indels 2; Mismatches 3; Indels
                                                                                                                                                                  Length 775;
                                                                                                                                                                                                                          Indels
                                                                                                                                                               Score 41; DB 2;
Pred. No. 20;
                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                               60.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative 7
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A,Map position: linear chromosome
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429 DLRPYPNSCYLE 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 DPRPYRYSRFFD 432
                                                                                                                                                            Query Match 60.3
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                             1 DVRPYRTSRYLE 12
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                                                                            A,Gene: At2940360
A,Map position: 2
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57.4%; 87.5%;

Query Match
Best Local Similarity 87.5
Matches 7, Conservative

A; Map position: 1

RESULT 12

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Nypotherical protein H0411 [imported] - Halobacterium sp. (strain NRC-1) plasmid pNRC100 N/Alternate names: hypothetical protein H1942 C.Species: Halobacterium sp. (species: Halobacterium sp. C.Species: Halobacterium sp. C.Species: 11-Unn-1999 #sequence_revision 11-Jun-1999 #text_change 03-Nov-2000 C.Species: 11-Unn-1999 #sequence_revision 11-Jun-1999 #text_change 03-Nov-2000 C.Species: 11-Oun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Nov-2000 C.Species: 13-Mail, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.; I Genome Res. 8, 1131-1141, 1998 dynamic replicon in a halophilic Archaeon: megaplasmid or mish. Reference number: Z16408; WUID:99063795; PMID:9847077 A.Reference number: Lanslated from GB/EMBL/DDBJ A.Residues: 1-286 cNGW> A.Residues: 1-286 cNGW>
hypothetical protein KIAA0564 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00339
B;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. DNA Res. 5, 31-39, 1998
A;Nitle: prediction of the coding sequences of unidentified human genes. IX. The complete A;Recession: T00335
A;Retans: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1441 -NAG>
A;Residues: 1-1441 -NAG>
A;Cross_references: EMBL:AB011136; NID:g3043651; PIDN:BAA25490.1; PID:g3043652
A;Experimental source: brain; clone HH1811
C;Genetics:
A;Note: KIAA0564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitochondrial [similarity] - Caenorhabditis elegans
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A)Experimental source: clone T01E8
C;Genetics:
A;Gene: CESP:T01E8.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ribosomal protein S14 T01E8.6, mitochondrial [similarity] - Caenorhabditis e
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: AF016485; NID: 92822278; PID: 92822311; HALOSP: H0411
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Pred. No. 87;
2; Mismatches 3; Indels
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A;Introns: 20/3
C;Superfamily: Escherichia coli ribosomal protein S14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C)Accession: T24300
R;McMurray, A.
Submitted to the EMBL Data Library, March 1995
A;Reference number: Z19871
A;Accession: T24300
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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Pred. No. 9;
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61.5%;
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Local Similarity 61.5.
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Best Local Similarity 60.0.
Best Conservative
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A; Residues: 1-103 <WIL>
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A/Cross-references: GB:AE004052; GB:AE003849; NID:g9107617; PIDN:AAP85237.1; GSPDB:GN001
A/Experimental source: strain 9a5c
R/Simpson, A.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
Briones, M.R.S.; Bueno, W.R.P.; Camargo, A.A.; Ferreira, A.G.S.;
Submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Madeira, A.M.B.; Matsukuma, A.Y.; Menck, C.F.M.; Miracoa, B.C.; Miyaki, C.Y.;
F.G.; Numes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.C.; Sancelli, R.Y.; Sancelli, R.Y.; Sancelli, R.Y.; Sancelli, R.Y.; Sancelli, R.Y.; Tsuhako, M.H.; Vallada, H.; Van Sllva, F.R.; da Silva, A.M.; Silva Jr., V.R.; A.R.; A.R.
                      Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200.
Nature 408, 816-820, 200.
Nature 408, 816-820, 200.
Nature 408, 816-820, 200.
Nature 5, Mairi, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, S. Razo, M.; Rowley, T.; Rowley, D.; Sakano, H.
Nature 5, S.L.; Sowley, T.; Rowley, D.; Sakano, H.
Nature 6, N.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
Nature 5, Square 6, and analysis of chromosome 1 of the plant Arabidopsis.
Nature 6, Mairie 7, Muid. 13016, 191, PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Accession: B82559
R,anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent R,anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent A)Title: A,Title: A,Title: Mulp. 20365717; PMID: 10910347
A,Reference number: A82515; MUID: 20365717; PMID: 10910347
A,Note: for a complete list of authors see reference number A59328 below
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary
A,Molecule type: DNA
A,Rebidues: 1-526 <STO>
A,Cross-references: GB:AE005172; NID:g5080782; PIDN:AAD39292.1; GSPDB:GN00141
C,Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 34;
0; Mismatches 4; Indels
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Accession: B82559

57.4%; 66.7%;

Local Similarity 66.7 nes 8; Conservative

Matches

Query Match

Contents: annotation

Gene: XF2438

Genetics

1 DVRPYRTSRYLE 12 149 DVRPVRDPAYLE

160

RESULT 13 TO0335

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A; Experimental source: strain NRC-1
A;Genetics: COP1
A;Genetics: COP1
A;Genetics: COP1
A;Genetics: COP1
A;Genetics: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-286 -CDAS>
A;Cencics: L286 -CDAS>
A;Cencics: COP1
A;Genetics: COP1
A;Genetics: COP1
A;Genetics: COP2
C;Genetics: COP2
A;Genetics: COP3
A;Genetics: C
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Search completed: October 5, 2004, 08:16:48 Job time : 7.10648 secs

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Quevez escherichia P05458 escherichia P05458 escherichia Q82418 ealmonella Q82403 shigella fil Q24391 caenorhabdi Q24391 caenorhabdi Q2429 drosophila Q8442 bifidobacte P11138 providencia p11138 providencia b1138 influenza b P113871 influenza b P13871 influenza b Q84b2 influenza b Q8vibz rattus norv 03641 influenza b Q8vibz rattus norv 03641 mus musculu Q91003 schizosacch Q10103 schizosacch Q1311 homo sapien Q62388 mus musculu Q92pb rhizobium m P81003 aedes aegyp O50164 borrelia bu P19029 feline immu p19029 feline immu
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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EMBL; AE005510; AAG57932.1;

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sapien pox vir

mycobacteri

Q9xb14 Q50642 P14384 Q9j5b1

DHAA MYCBO DHAA MYCTU CBPM HUMAN V111\_FOWPV

us-09-805-290a-8.rsp

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MEDLINE=2238624; PubMed=12471157;

MEDLINE=22386234; PubMed=12471157;

MEDLINE=2386234; PubMed=12471157;

MEDLINE=2386234; PubMed=12471157;

MEDLINE=2386234; PubMed=12471157;

MANHAW G.F., Burland V., Plunkett G. III, Redford P., Roesch P.,

MANHAW G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

T. Extensive mosaic structure revealed by the complete genome sequence

T. Contact Compation of Sci. U.S.A. 99:17020-17024(2002).

T. Contact Modepeptidase that degrades small peptides of less than

T. K.Da, Such as glucagon and insulin (By similarity).

T. Contact M. Contact M. Scheller M. Scheller M. Also acts on cother substrates of Mw less than 7 kDa such as insulin and
                            PIR; F91088; F91088.
InterPro; IPR001431; Peptidase M16.
InterPro; IPR007863; Peptidase M16.
Pfam; PF00675; Peptidase M16; I.
Pfam; PF05193; Peptidase M16; I.
Pfam; PF05193; Peptidase M6 C; 2.
Pfam; PF05193; Peptidase M6 C; 2.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-001-2003 (Rel. 42, Created)
10-00T-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Protease III precursor (EC 3.4.24.55) (Pitrilysin) (Protease pi).
PRAA OR PTR OR C3415.
Escherichia coli 06.
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--- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
--- SUBUNIT: Monomer (By similarity).
--- SUBCELLULAR LOCATION: Periglasmic (By similarity).
--- SIMILARITY: Belongs to peptidase family M16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 1; Length 962;
Pred. No. 6.2;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                   24 962 PROTEASE III.
88 88 ZINC (BY SIMILARITY).
91 91 BY SIMILARITY.
92 92 ZINC (BY SIMILARITY).
169 169 ZINC (BY SIMILARITY).
962 AA, 107808 MW, 30785644GEF0E452 CRC64;
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InterPro; IPR007863; Peptidase M16_C.
Pfam; PF00675; Peptidase M16; I.
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      EMBL; AP002563; BAB37101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.8%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
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Best Local Similarity
Matches 8; Conserv
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QBCVS2;
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ACT SITE
METAL
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SEQUENCE
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PTRA_ECOL6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN-KI2 / MG1655;

STAIN-KI2 / MG1655;

STAIN-KI2 / MG1655;

Blattner F.R. / Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

Mau B., Shao Y.;

"The complete genome sequence of Escherichia coli K-12.";

Science 277:1453-1474(1997).
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Pfam, PF05193; Peptidase_M16_C; 2.
PROSTTE; PS00143; INSTLINASE; 1.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protease III precursor (EC 3.4.24.55) (Pitrilysin) (Protease pi)
PTRA OR PTR OR B2821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=87040734; PubMed=3534791;
Finch P.W., Wilson R.E., Brown K., Hickson I.D., Emmerson P.T.;
"Complete nucleotide sequence of the Escherichia coli ptr gene
encoding protease III.";
Nucleic Acids Res. 14:7695-7703(1986).
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Pred. No. 6.2;
1; Mismatches 1; Indels
                                                                                                                                                 1 23 BY SIMILARITY.
84 962 PROTEABE III.
88 8 ENC (BY SIMILARITY).
91 91 BY SIMILARITY.
92 92 ZINC (BY SIMILARITY).
169 169 ZINC (BY SIMILARITY).
169 169 ZINC (BY SIMILARITY).
962 AA, 107891 MM, DEDDZCAA9AADF8D CRC64;
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MEDLINE-92237263; PubMed=1570301;
Becker A.B., Roth R.A.;
"An unusual active site identified in a family of zinc metalloendopptidases.";
Proc. Natl. Acad. Sci. U.S.A. 89:3835-3839(1992).
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Nature 413:848-852(2001)
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SEQUENCE FROM N.A.
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SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ZINC.
H->R: LOSS OF ACTIVITY AND OF ZN-BINDING.
E->Q: LOSS OF ACTIVITY.
H->R: LOSS OF ACTIVITY AND OF ZN-BINDING.
E->Q: 20% LOSS OF ACTIVITY AND OF ZN-BINDING.
E->Q: LOSS OF ACTIVITY AND OF ZN-BINDING.
E->Q: NO LOSS OF ACTIVITY.
THYVEA -> HYHSLERW (IN REF. 4).
[6]
MUTACENESIS, AND ACTIVE SITE.
MUDINE=93277449; PubMed=8099278;
Becker A.B., Roth R.A.;
"Identification of glutamate-169 as the third zing-binding residue in proteinase III, a member of the family of insulin-degrading
                                                                                                                                                                           Biochem. J. 292:137-142(1993).
-!- FUNCTION: Endopeptidase that degrades small peptides of less than
-!- Aba, such as glucagon and insulin.
-!- CATALYTIC ACTIVITY: Preferential cleavage of 16-Tyr-|-Leu-17 and
25-Phe-|-Tyr-26 bonds of oxidized insulin B chain. Also acts on other substrates of Mw less than 7 kDa such as insulin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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InterPro; IPR001431; Peptidase M16.
InterPro; IPR007863; Peptidase M16.
Pfam; PF00675; Peptidase M16. 1.
Pfam; PF00193; Peptidase M16. 1.
PR03ITE; PS00143; INSUINASE; PR05ITE; P
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                                                                                                                                                                                                                                                                                                                                    glucagon.
-!- COFACTOR: Binds 1 zinc ion per subunit.
-!- SUBGINT: Monomer.
-!- SUBCELLULAR LOCATION: Periplasmic.
-!- SIMILARITY: Belongs to peptidase family M16.
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1; Mismatches
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EMBL; U29581; AAB40468.1;
EMBL; AE000365; AAC7580.1; -.
EMBL; X06227; CAA29576.1;
EMBL; M17095; AAA24436.1; -.
PIR, F65064; SAECPI.
MEROPES; M.6.001; -.
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Best Local Similarity 80..
Best Local 8; Conservative
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METAL
ACT SITE
METAL
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MUTAGEN
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MUTAGEN
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
SEROURINE=Y2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ". Bacteriol. 185:2330-2337(2003).

-!- FUNCTION: Endopeptidase that degrades small peptides of less than 7 kDa, such as glucagon and insulin (By similarity).

-!- CATALYTIC ACTIVITY: Preferential cleavage of 16-Tyr-|-Leu-17 and 25-Phe-1-Tyr-26 bonds of oxidized insulin B chain. Also acts on other substrates of Mw less than 7 kDa such as insulin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00675; Peptidase_MI6; I. Perior PF00675; Peptidase_MI6; I. Prositrs; PS00143; INSULINASE; FALSE NEG.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
                                                         Salmonëlla typhi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=601;
10-OCT-2003 (Rel. 42, Last annotation update)
Protease III precursor (EC 3.4.24.55) (Pitrilysin) (Protease pi)
PTRA OR, PTR OR STY3133 OR T2903.
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-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
-!- SUMLARITY: Belongs to peptidase family M16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.8%; Score 42; DB 1; Length 962;
80.0%; Pred. No. 6.2;
tive 1; Mismatches 1; Indels
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PROTEASE II.

ZINC (BY SIMILARITY).

BY SIMILARITY.

ZINC (BY SIMILARITY).

ZINC (BY SIMILARITY).

MW, 5745C2C77F7F5832 CRC64;
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                                                                                                                                                                               STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 169 ZI.
962 AA; 107524 MW;
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METAL
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SEQUENCE
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Matches
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4 PYRTSRYLEV 13

962 AA

STANDARD;

PTRA SALTI Q8Z418; 10-OCT-2003 10-OCT-2003

RESULT 4 PTRA SALTI (Rel. 42, Created) (Rel. 42, Last sequence update)

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                                                                                                                                                                                                                                                                                                                                                         McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulyaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 413:852-856(2001).

-!- FUNCTION: Endopeptidase that degrades small peptides of less than 7 kDa, such as glucagon and insulin (By similarity).

-!- CATALYTIC ACTIVITY: Preferential cleavage of 16-Tyr-|-Leu-17 and 25-Phe-|-Tyr-26 bonds of oxidized insulin B chain. Also acts on other substrates of Mw less than 7 kDa such as insulin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00675; Peptidase M16; 1.
Pfam; PF05193; Peptidase M16, 2.
PR051TE; PS00143; INSULNASE; 1.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal; Complete proteome.
                                                                                                                               10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Protease III precursor (EC 3.4.24.55) (Pitrilysin) (Protease pi).
PTRA OR PTR OR STM2991.
Salmonella typhimurium.
                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucagon.
--- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
--- SUBNIT: Monomer (By similarity).
--- SUBCELLULAR LOCATION: Periplasmic (By similarity).
--- SIMILARITY: Belongs to peptidase family M16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 1; Length 962;
Pred. No. 6.2;
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ZINC (BY SIMILARITY).
1, 322AD6E87B873952 CRC64;
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ZINC (BY SIMILARITY).
BY SIMILARITY.
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InterPro, IPR001431; Peptidase_M16.
InterPro, IPR007863; Peptidase_M16_C.
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-LIT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed=11677609;
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                                                                                                                                                                                                                                               Enterobacteriaceae; Salmonella NCBI TaxID=602;
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80.0%;
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962
88
91
92
169
107486 N
                                                                                                       STANDARD;
||||: ||||
124 PYRTAFYLEV 133
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91
92
169
169
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Best Local Similarity
Matches 8; Conserv
                                                                                                       SALTY
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METĀL
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SEQUENCE
                                                                                                       PTRA SA
QBZMB5;
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                                                                                       PTRA_SALTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infect. Immun. 71:2775-2786 (2003).
-!- FUNCTION: Endopeptidase that degrades small peptides of less than 7 kDa, such as glucagon and insulin (By similarity).
-!- CATALYTIC ACTIVITY: Preferential cleavage of 16-Tyr-| Jeu-17 and 25-Phe-|-Tyr-26 bonds of oxidized insulin B chain. Also acts on other substrates of Mw less than 7 kDa such as insulin and
                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                            STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang G., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE015297; AAN44319.1; -.
EMBL; AE015297; AAN44319.1; -.
EMBL; AE016987; AAP18144.1; -.
InterPro; IPRO01431; Peptidase_M16.
InterPro; IPR00983; Peptidase_M16_C.
Pfam; PF00675; Peptidase_M16; \overline{1}.
Pfam; PF00513; Peptidase_M16, \overline{1}.
PROSITE; PS00143; INSULINSES.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
                                                                                                                                              Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Shigella.
                                                    10-0CT-2003 (Rel. 42, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
Protease III precursor (EC 34.24.55) (Pitrilysin) (Protease pi).
PIRA OR PIR OR SF2832 OR S3029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=2457T, ArCC 700930 / Serotype 2a;
MEDLINE=22590774; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Meu B., Perna M.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.,
Incomplete genomic sequence and comparative genomics of Shigella
flexneris excetype 2a strain 24577";
Infect. Immun. 71:2775-2786(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEASE III.
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
MW; 662041A5DCA07254 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
-!- SIMILARITY: Belongs to peptidase family M16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
962 AA
PRT;
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962 PRG
88 ZIN
91 BY
92 ZIN
169 ZIN
169 ZIN
                                    (Rel. 42, Created)
    STANDARD;
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92
169
169 1
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                      Shigella flexneri
                                                                                                                                                                                             NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glucagon.
                                      10-OCT-2003
    SHIFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
METAL
ACT SITE
METAL
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SEQUENCE
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Gaps

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1; Indels

1; Mismatches

8; Conservative

124 PYRTAFYLEV 133

4 PYRTSRYLEV 13

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                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21016719; PubMed=11130712; Rederspiel N.A., Kaul S., MEDLINE-21016719; PubMed=11130712; Rederspiel N.A., Kaul S., MEDLINE-21016719; PubMed=11130712; Rederspiel N.A., Kaul S., Merchologia A., Ecker J.R., Palm C.J., Promer C.L., Brooks S.Y., White O., Alonso J., Conway A.B., Cheasy T.H., Dewar K., Chung M.K., Conn.L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Dunn P., Etgu P., Feldblyum T.V., Feng B., Fujii C.Y., A Gill J.B., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Arman J., Conway A.R., Creasy T.H., Dewar K., A Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Miltscher J., Miranda M., Nguyen M., Nachaman W.C., Osborne B.I., A Lin S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W., E. Marbidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identification As purative fucosyltransferase, and rissue specificity. MEDLINE=216608393; PubMed=11743104; Sarria R., Wagner T.-A., O'Neill M.A., Faik A., Wilkerson C.G., Keegstra K., Raikhel N.V.; Characterization of a family of Arabidopsis genes related to xyloglucan fucosyltransferase1."; Plant Physiol. 127:1595-1606(2001).
-!- FUNCTION: May be involved in cell wall biosynthesis. May act as a fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 37.
-!- CAUTION: Ref.1 (AAF79408) sequence differs from that shown due to erroneous gene model prediction.
                                                                  Gaps
                                                                                                                                                                                                                                                                         99XIB1, 99LMR2;
28-FEB-2003 [Rel. 41, Created)
28-FEB-2003 [Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Probable fucosyltransferase 7 (EC 2.4.1.-) (Argury).
FUT7 OR ATIG14070 OR F7A19.15 OF F16A14.19 OR F16A14.28.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II, Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- PATHWAY: Glycosylation.
-:- SUBCELTULAR LOCATION: Type II membrane protein. Membrane-bound form in trans cisternae of Golgi (By similarity).
-:- TISSUE SPECIFICITY: Expressed in roots, leaves, stems and
                                                                  ö
                    Score 42; DB 1; Length 962;
Pred. No. 6.2;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                526 AA.
                         61.8%;
80.0%;
Ouery Match
Best Local Similarity 80...
8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                  124 PYRTAFYLEV 133
                                                                                                           4 PYRTSRYLEV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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0
                                                                                                               CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-!- SIMILARITY: Belongs to the S14P family of ribosomal proteins.
                                                                                                                                                               26 526 LUMENAL, CATALYTIC (POTENTIAL).
211 211 N-LINKED (GLCNAC. .) (POTENTIAL) 215 N-LINKED (GLCNAC. .) (POTENTIAL) 363 N-LINKED (GLCNAC. .) (POTENTIAL) 526 AA, 60537 MW, 8F3B447551025FCD CRC64;
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0
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0
EMBL; AC007576; AAD39292.1; -.
EMBL; AC068197; AAF79408.1; ALT_SEQ.
PIR, AB6274; A86274.
InterPro; IPR00939; XG_FTase.
Pfam; PF03254; XG_FTase; 1.
Transferase; Glycosyltransferase; Transmembrane; Glycoprotein; Gignal-anchor; Golgi stack; Cell wall.
DOMAIN
TRANSMEM 5 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE F)
                                                                                                                                                                                                                                                                Score 39; DB 1; Length 526;
Pred. No. 12;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McMurray A.A.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIGURE 1. CE32923.
InterPro, IPR001209, Ribosomal S14.
InterPro, IPR001209, Ribosomal S14.
PROSITE; PS00527, RIBOSOWAL S14; I.
PROSITE; PS00527, RIBOSOWAL S14; FALSE_NEG.
STBOSOMAL Proceein; Mitochondrion.
SEQUENCE 199 AA; 23414 MW; 2CC0021A618EFF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sentocation update)
Putative mitochondrial 40S ribosomal protein S14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 60.0%; Pred. No. 6.4; 6; Conservative 3; Mismatches 1
                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                  Match 57.4%;
Local Similarity 87.5%;
les 7; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z48809; CAA88746.2; -. PIR; T24300; T24300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                                                                                    4 PYRTSRYL 11
                                                                                                                                                                                                                                                                                                                                                                  79 PYRTSEYL 86
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
RT14_CAEEL
ID FR14_CAEEL
P49391;
REB-199
                                                                                                                                                                  DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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Matches
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172 IKPYRLSRHL 181

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RATANT=SERGREBY;

RATANT=SERGREBY;

RATANT=SERGREBY;

RAGARN=SERGREBY;

RAGARN=SERGREBY;

RAGARN FOLLSCHORER S.E., Holt R.A., Ganle R.F.,

RAGARN M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RAGARN M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RAGARN M.C., Lewis S.E., Farchards S., Ashburmer M., Henderson S.N.,

Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D.,

RAGARN M.M. Baeu M., Barendal M.D., Rayaktaroglu L., Basaldy E.M.,

Ballew R.M., Benos P.V., Berman B.P., Bandarin D., Ballahakov S.,

RAGARN M.M. Benos P.V., Berman B.P., Bandarin D., Bollahakov S.,

RAGARN M.M. Benos P.V., Berman B.P., Bandarin D., Bollahakov S.,

RAGA BUTLIS K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RAGA BUTLIS K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RAGA BADLOS B., Doldher A., Domac Z., Mays A.D., Dew I., Dietz S.M.,

Boutin K.J., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,

RAGA BADLOS B., Doldher A., Howland T.J., Wei M.-H., Lbegwam C.,

RAGA BADLOS B., Houston K.A., Howland T.J., Wei M.-H., Lbegwam C.,

RAGA RAMM M.L., Harvey D.A., Heiman T.J., Wei M.-H., Lbegwam C.,

RAGA Kimmel B.E., Kodira C.D., Kardt C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattei B., McIntosh T.C., Morris J., Moshrefi A.,

RAHARINO G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Rallos D.R., Nelson K.A., Mixon K., Duray D.M., Parly D., Mallon D.L.,

Radiazolo M., Pittenan G.S., Pan S., Pollard J., Wang X.,

Rainer K.M., Remingron K.A., Worled S., Wang X., Shulb S., Rainer K., Techer S., Wang X.,

Rainer K., Remingron K., Saunders R.D.C., Scheeler F., Shen H.,

Rainer S.M., Woodage T., Sarpen G.M., Weissenbach J.,

Wang Z.-Y., Wassarman D.A., Weinstock M., Weissenbach J.,

Rainer K., Shorer E.W., Worley M., Mulling M., Zhang M., Zhang G., Zhan K.,

Walling S.M., Woodage T., Stapel G.M., Weissenbach J.,

Rainer K., Shorer E.W., Worley C., Chronison S., Pan S., Coller F.,

Rainer K., Shorer E.W., Worley C., Shorer S.,

Rainer S.M., Woodage T., Worley C
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95324813; PubMed=7601355;
Clark H.P., Brentrup D., Schnedtz K., Bieber A., Goodman C., Noll M.;
"Dachsous encodes a member of the cadherin superfamily that controls
imaginal disc morphogenesis in Drosophila.";
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL
                                                                                                                                     Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noll M , Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                  Q24292; Q9VPS4;
28-FB8-2003 (Rel. 41, Created)
E-FB8-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
PRT; 3503 AA.
                                                                                                           Dachsous protein precursor (Adherin).
DS OR CG17941.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes Dev. 9:1530-1542(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287:2185-2195(2000).
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                rissum=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS.
  DROME
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No. 17 yease; Figh 100 years a membrane; ISS.

R G0; G0:0005887; C:integral to plasma membrane; ISS.

R G0; G0:0005887; C:integral to plasma membrane; ISS.

R G0; G0:0008014; F:calcium-dependent cell adhesion molecule ac. .; ISS.

R G0; G0:0008283; P:calcium-dependent cell-cell adhesion; ISS.

R G0; G0:0008283; P:cell proliferation; IMP.

R G0; G0:000904; P:cellular morphogenesis during differentiation; IMP.

R G0; G0:0008137; P:cequator specification; IMP.

R G0; G0:0018149; P:establishment of epithelial rell polarity; IMP.

R G0; G0:0018149; P:protein-protein cross-linking; IPI.

R InterPro; IPR00125; Cadherin.

R Ffam; PR00128; cadherin. C_term.

R PRINTS; PR00205; CADHERIN.

R PRNTNS; PR00121; CA; 25.
                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                    Misra S., Crosby, M.A., Mungail C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P., Battencourt B.R., Celniker S.B., de Grey A.D.N.J., Drysdale R.A., Hartis N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                  GRENOME BIOL. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00232; CADHERIN_1; 20.
PROSITE; PS50288; CADHERIN_2; 27.
CELL adhesion; Glycoproclein; Transmembrane; Calcium; Calcium-binding; Repeat; Signal; Developmental protein.
                                                                                                                                                                                                               -!- SUBCELLUIAR LOCATION: Type I membrane protein (Potential).
-!- TISSUB SPECIFICITY: Expressed in embryonic ectoderm. In larvae,
expression is restricted to imaginal disks and brain.
-!- DEVELOPMENTAL STAGE: Expressed throughout embryogenesis where it
is first detected during gastrulation. Also expressed in larvae
                                                                                                                                       Annotation of the Drosophila melanogaster euchromatic genome: a
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EXTRACELLULAR (POTENTIAL)
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CADHERIN 6.
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CADHERIN 8.
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           MEDLINE=22426069; PubMed=12537572;
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FlyBase; FBgn0000497; ds.
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SPECIES-E.coli, STRAIN-KI2 / MG1655;
Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
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SPECIESEE.Coll; STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
OSHIMA T., Aiba H., Baba T., Pujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Kimura S., Kitagawa M., Makino K., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
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SEQUENCE E. COli, STRAIN-K12 / MG1655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Ralley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao.Y.;
"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRDG_ECOLI STANDARD; PRT; 415 AA.

PR3455; P77602;
01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 32, Last annotation update)
10-OCT-2003 (Rel. 31, Created)
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Pred. No. 1.4e+02;
1; Mismatches 3; Indels
CADHERIN 17.
CADHERIN 18.
CADHERIN 20.
CADHERIN 21.
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V -> I (IN REF. 1).
K -> S (IN REF. 1).
K -> S (IN REF. 1).
K -> A (IN REF. 1).
K -> B (IN REF. 1).
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Best Local Similarity 60.0
Matches 6; Conservative
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SPECIES-S.flexneri; STRAIN-2457T / ATCC 700930 / Serotype 2a;

MEDINE-2590274; PubMed=12704152;

Med J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

RA Wei J., Goldberg M.B., Eurland V., Venkatesan M.M., Deng W.,

RA Wei J., Goldberg M.B., Eurland V., Venkatesan M.M., Deng W.,

RA Golwartz D.C., Blattner F.R.;

Complete ganome sequence and comparative genomics of Shigella

ST Infect. Immun. 71:275-2786(2003):

Infect. Immun. 71:275-2786(2003):

Infect. Immun. 71:2775-2786(2003):

Infect. Immun. 71:2775-2786(2003):

Comparation protein (Potential).

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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang Y., Zang X., Zhang Y., Zhang Y., Zhang Y., Zhang J., Xang G., Wu H., Qu D., Dong J.,
Suu L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
Yu J.;
                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-77 FROM N.A.
SEQUENCE OF 1-77 FROM N.A.
MEDIINE=55113294; Pubmed=7813889;
Michael N.P., Brehm J.K., Anlezark G.M., Minton N.P.;
Michael N.P.;
Michael N.P.;
FEMS Microbiol. Lett. 124:195-202(1994).
Yano M., Horiuchi T.;
14 718-kb DNA sequence of the Bscherichia coli K-12 genome
corresponding to the 12 7-28.0 min region on the linkage map.";
DNA Res: 3:137-155(1996).
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EMBL; U82598; AAB40775.1; -
EMBL; U07000; BAA5257.1; -
EMBL; U07060; BAA5257.1; -
EMBL; U07860; AAC43265.1; -
EMBL; AE015680; AAA43265.1; -
EMBL; AE015680; AAA42134.1; ALT_INIT.
EMBL; AE015690; AAP16008.1; -
EMBL; AE015690; AAP16008.1; -
EMBL; AE015690; AAP16008.1; -
EMBL; AE015690; AAP16008.1; -
EMBL; AE015690; AB0160.1; -
EMBL; AE015690; AE01
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SEQUENCE OF 1-12 FROM N.A.
SPECIES=E.Coli; STRAIN=K12 / C600;
Zenno S., Koike H., Tanokura M., Saigo K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
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Matches 6; Conserv
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SEQUENCE FROM N.A.
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MEDLINE=2229977; PubMed=12381787;
SCHELI M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.; Berser M., Berser B.,
Pridmore R.D., Arigoni F.; Berser M.,
The genome sequence of Bifidobacterium longum reflects its adaptation
to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S. 99:4422-14427(2002).
-: CATMLYIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
diphosphate + L-arginyl-tRNA(Arg).
-: SUBGNATT: Monomer (By similantry).
-: SUBGRILUAR LOCATION: Cytoplasmic.
-: SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                          15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
ARGS OR B11272.
Bifidobacterium longum.
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PROSITE; PS00178; AA TRNA LICASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
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Bifidobacteriaceae; Bifidobacterium.
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620 AA; 67206 MW; F51C3C0C8CD9AB06 CRC64;
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HAWAP; MF 00123; -; 1.
InterPro; IPR001278; Arg_tRNA-synt_lc.
InterPro; IPR00148; N.
InterPro; IPR001419; RNA-synt_ld_C.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR001412; tRNA-synt_l.
Pfam; PF03485; N-Arg; IL.
Pfam; PF03485; N-Arg; I.
Pfam; PF00750; tRNA-synt_ld; I.
Pfam; PF00750; tRNA-synt_ld; I.
Pfam; PF001038; TRNASYNTHARG.
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Matches 6, Conservative
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Q8G4V2;
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                                                                                                                                                                                                                                                                                              MEDLINE=86013618; PubMed=3862932;
MEDLINE=86013618; PubMed=3862932;
Schnier J., Faist G.
Schnier J., Faist G.
Comparative studies on the structural gene for the ribosomal protein
S1 in ten bacterial species.";
Mol. Gen. Genet. 200:476-481(1985).
-!- FUNCTION: BINDS MRNA, THUS FACILITATING RECOGNITION OF THE
INITIATION POINT. IT IS NEEDED TO TRANSLATE MENA WITH A SHORT
SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
-!- SIMILARITY: Belongs to the S1P family of ribosomal proteins.
-!- SIMILARITY: Contains 5 S1 motif domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                    Providencia sp.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Providencia.
NCBL_TaxID=589;
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01-JUJ-1999 (Rel. 11, Created)
01-JUJ-1999 (Rel. 11, Last sequence update)
12-FBB-2003 (Rel. 11, Last sequence update)
RNA-directed RNA polymerase subunit P2 (EC 2.7.7.48) (Polymerase acidic protein) (PA).
Influenca B virus (strain B/Singapore/222/79).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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Pred. No. 31;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9052424346D2E904 CRC64;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           725 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X02828; CAA26596.1; -.. HSSP, POSS5; LSCO.
HISCPPO: IPRO08994; Nucleic_acid_OB.
InterPro: IPRO08099; Nucleic_acid_OB.
InterPro: IPRO08099; S1.
Pfam; PPO0575; S1; S.
PRINTS; PRO0681; RIBOSOMALS1.
SMART; SM00316; S1; 4.
SMART; SM00316; S1; 4.
Ribosomal protein; Repeat; RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S1 MOTIF 1.
S1 MOTIF 2.
S1 MOTIF 3.
S1 MOTIF 4.
                                                                                              30S ribosomal protein S1 (Fragment).
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVRPYRTSRYLE 12
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259 3
346 3
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52.9%; Score 36; DB 1; Length 726; 46.2%; Pred. No. 62; tive 4; Mismatches 3; Indels

1 DVRPYRTSRYLEV 13

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Pfam; PF00603; Flu PA; 1.
Transferase; RNA-directed RNA polymerase.
SEQUENÇE 726 AA; 83181 MW; CAFDIA4388034F26 CRC64;
                                                    Query Match
Best Local Similarity 40...
6; Conservative
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                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - RNA)(N).
- SUBUNIT: Influenza RNA polymerase is composed of three subunits:
P1 (or PB1), P2 (or PA), and P3 (or PB2).
- SIMILARITY: Belongs to the influenza viruses polymerase PA family.
                                                                                                        {RNA}(N).
--- SUBUNIT: Influenza RNA polymerase is composed of three subunits:
P1 (or PB1), P2 (or PA), and P3 (or PB2).
---- SIMILARITY: Belongs to the influenza viruses polymerase PA family.
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 163:429-443(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence comparison of wild-type and cold-adapted B/Ann Arbor/1/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0AN-1990 (Rel. 13, Created)
01-0AN-1990 (Rel. 13, Last sequence update)
01-0AN-1990 (Rel. 41, Last annotation update)
28-PEB-2003 (Rel. 41, Last annotation update)
acidic protein) (PA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Influenca B virus (strain B/Ann Arbor/1/66 [cold-adapted]). Viruses; ssRNA negative-strand viruses; orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Length 725;
Pred. No. 62;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=88179548; PubMed=3354202;
Deborde D.C., Donabedian A.M., Herlocher M.L., Naeve C.W.,
                                                                                                                                                                                                                                                                                                                      EMBL; M16711; AAA43776.1; -.
PIR; A27814; P21VBS.
InterPro; IPR01009; RNA_pol_P2.
Pfan, PF00603; Plu_PA. 1.
Transferase; RNA-directed RNA polymerase.
SEQUENCE 725 AA; 83088 MW; 8237757EF40C0FBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               726 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
          MEDLINE=87265462; PubMed=3604058;
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DLFDYKTKRFIEV 121
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Best Local Similarity 46.4.
Best Local Similarity 66.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=11522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Influenzavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maassab H.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INBAC
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RRP2_INBAC
IND_RRP3_INBAC
DT 01-JAN-
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EMBL, M20171; AAA43765.1; -. PIR, E28604; P2IVBC. InterPro; IPR001009; RNA\_pol\_P2

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence comparison of wild-type and cold-adapted B/Ann Arbor/1/66 influenza virus genes."; virology_163:429-443(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                             01-0AN-1990 (Rel. 13, Created)
01-0AN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RNA-directed RNA polymerase subunit P2 (EC 2.7.7.48) (Polymerase acidic protein) (PA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88179548; PubMed=3354202;
Deborde D.C., Donabedian A.M., Herlocher M.L., Naeve C.W.,
Maassab H.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 726;
                                                                                                                                                                                                                                                                                                                                  Influenza B virus (strain B/Ann Arbor/1/66 [wild-type]).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; F28604; P21VBW.
InterPro; IPR01009; RNA_pol_P2.
Pfam: PF00603; Flu_PA; 1.
Transferase: RNA-directed RNA polymerase.
SEQUENCE 726 AA; 83166 MW; C9D85DA44844019E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.9%; Score 36; DB 1;
46.2%; Pred. No. 62;
vative 4; Mismatches
                                                                                                                                           726 AA.
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109 DLFDYKTKRFIEV 121
109 DLFDYKTKRFIEV 121
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                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: October
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=11523;
                                                                                                                                                                                                                                                                                                                                                                                                   Influenzavirus B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA (N)
                                                                                                                RRP2 INBAD
ID RRP2 INBAD
AC P13874;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: October 5, 2004, 07:34:11; Search time 6.88117 Seconds

(without alignments)

596.081 Million cell updates/sec

Title: US-09-805-290A-8
Perfect score: 68
Sequence: 1 DVRPYRTSRYLEV 13

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

SPTREMBL\_25:\*

2: sp\_archea:\*
2: sp\_barceria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_mnc:\*
7: sp\_mnc:\*
8: sp\_organelle:\*
9: sp\_phage:\*
10: sp\_phage:\*
11: sp\_rodent:\*
12: sp\_virus:\*
13: sp\_vertebrate:\*
14: sp\_unclassified:\*
15: sp\_mins:\*
16: sp\_bacteriap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

SUMMARIES

ion	arabidopsis	arabidopsis	rattus norv	arabidopsis	arabidopsis	agrobacteri	caenorhabdi	streptococc	ciona intes	nonomuraea	Q25368 loligo opal	arabidopsis	pseudomonas	methanopyru	mus musculu	
Description	Q9m1k7	Q91tul	035390		Q81aq8		001792 c	Q52001 s	P91590 C	Q7wz84 n	Q25368 l	080652	Q884i1	Q8tgz6	6u0080	
ΠD	Q9M1K7	Q9LTU1	035390	6XIS6O	QBLAQ8	QSUBY6	001792	Q52001	P91590	Q7WZ84	025368	080652	Q884I1	QBTGZ6	OBCON9	
	101	10	11	10	10	16	Ŋ	7	S	7	Ŋ	70	16	17	11	
% Query Match Length DB	303	581	451	775	272	442	509	654	766	196	217	258	276	323	462	
% Query Match	61.8	61.8	60.3	60.3	58.8	58.8	58.8	58.8	58.8	57.4	57.4	57.4	57.4	57.4	57.4	
Score	4.2	42	41	41	40	40	40	40.	40	39	39	39	39	88	39	
Result No.	     	2	m	4	Ŋ	Q	7	œ	σι	10	11	12	13	14	15	

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> 1 DVRPYRTSRYLEV 13 |:|||:|| ::| 10 DIRPYKTSWRIQV 22

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OBPBP5 xanthomonas QBpK77 xanthomonas QPpaq7 xylella fas QPq113 influenza b QB4sf5 oryza sativ O60310 homo sapien	Q7uw68 rhodopirell Q84am7 streptomyce Q81re0 oryza sativ Q9yyl drosopila	Q81vml bacillus an Q81vml bacillus ce Q71x5 bacillus ce Q7wgg8 bordetella O7w420 bordetella		Q8pf48 xanthomonas O65983 halobacteri Q8b5n1 wisteria ve Q83fn0 tropheryma Q8xr52 salmonella Q8xr54 escherichia Q8K84 escherichia Q86807 salmonella	Q8X9/2 escherichia
Q8P8P5 Q8PK77 Q9PAQ7 Q9QLJ3 Q84SF5 O60310	Q7UW68 Q84AM7 Q8LRE0 Q9VJY1	Q81VM1 Q81VM1 Q811Z5 Q7WGG8	092RU9 0974N2 07VY02 07W995 08W6J4	Q8PF48 O54583 Q8B5N1 Q83FN0 Q8ZR52 Q8XBX4 Q8KX34	Q8X972
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# ALIGNMENTS

TI  OPANIK7  DEPLIMINARY; PRT; 303 AA.  OPANIK7  OPANIK7

| ||:: | |||: 415 DYRPHKPSLYLEI 427

RESULT 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakamura Y.; "Sequence "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC
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STRAIN=Spraque-Dawley;
MEDLINE=98030622; PubMed=9361017;
MEDLINE=98030622; PubMed=9361017;
Spiro M.J., Bhoyroo, V.D., Spiro R.G.;
"Molecular cloning and expression of rat liver endo-alpha-mannosidase,
an N-linked oligosaccharide processing enzyme.";
J. Biol. Chem. 272:29356-29363(1997).
EMBL; AF023657; AB86925.1; ...
SEQUENCE 451 AA; 51671 MW; 5A987EFD07585066 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                     Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S., Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 10; Length 581;
Pred. No. 28;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64867 MW; SBCB4DB5B0E006DC CRC64;
                                                                                01-OCT-2000 (TrEMBLEE]. 15, Last sequence update)
01-OCT-2003 (TrEMBLEE]. 25, Last annotation update)
Replication protein Al-like
Arabidopsis thaliana (Mouse-ear cress).
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Last annotation update)
                       581 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Cones.";
| Clones.";
| DNA Res. 7:131-135(2000).
| EMBL; AB024034; BAB02796.1; -...
| InterPro; IPR0039371; DUF223.
| R InterPro; IPR003994; Nucleic_acid_OB.
| R Pfam; PF02721; DUF223; 1...
| Promirence 581 AA; 64867 MW; 58CB4DB5
                                                                  Created)
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                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Columbia;
MEDLINE=20277480; PubMed=10819329;
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Best Local Similarity 61.5%;
Matches 8; Conservative
                                                             01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         035390;
01-7AN-1998 (TrEMBLrel. 05,
01-7AN-1998 (TrEMBLrel. 05,
01-NOV-1998 (TrEMBLrel. 08,
Endo-alpha-D-mannosidase.
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                       PRELIMINARY;
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                STRAIN=Columbia;
                                                                                                                                                                                                                                                NCBI TaxID=3702;
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                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledoms; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 775;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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PIN; B84828; E84828.
PIN; B84828; E84828.
PIN B84828; E84828.
PIN B84828; E84828.
PROUGHO; WD40; 4.
SMART; SM00320; WD40; 4.
PROSITE; PS50082; WD_REPEATS 1; 1.
PROSITE; PS50082; WD_REPEATS 2; 1.
PROSITE; PS5024; WD_REPEATS 2; 1.
SREPEAT: MD repeat.
SEQUENCE 775 AA; 88051 MW; CBFC6F54B528F4EA CRC64;
                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Putative WD-40 repeat protein.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.3%; Score 41; DB 10;
66.7%; Pred. No. 58;
775 AA.
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PRT;
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MEDLINE=20083487; PubMed=10617197;
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 402:761-768(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DVRPYRTSRYLE 12
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STRAIN=cv. Columbia;
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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OSLAOS;
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Q9SIY9
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Q8LAQ8
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Gaps

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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                              Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Pauley A., Maggi L.;
"The sequence of C. elegans cosmid F12B6.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                     442 AA; 48309 MW; B074DB4BCFFBB62D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                              Score 40; DB 16;
Pred. No. 49;
2; Mismatches 3
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MEDLINE=99069613; PubMed=9851916;
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001792,
001792,
01-JUL-1997 (TTEMBLrel. 04, Cr
01-DEC-2001 (TTEMBLrel. 19, La
01-CCT-2003 (TTEMBLrel. 25, La
Hypothetical protein.
F12B6.3.
Caenorhabditis elegans.
                                                                                                                 58.8%;
    InterPro, IPR000205; NAD_BS.
Pfam; PF01266; DAO; 1.
Complete proteome.
SEQUENCE 442 AA; 48309 MM
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                                                                                                                                                            Conservative
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"Direct Submission.";
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Best Local Similarity
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Best Local Similarity
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MEDLINE=21608550; PubMed=11743193;

MOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

A Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

A Kutyarin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

A Gang S., Yoo H., Tao Y., Biddle P., Jung M., Fersepan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

A Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

A Roster E.W.,

The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Gurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houndel K., Gordon J., Vaudin M., Lartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Cielo C., Slater S.,
Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
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ATU3952 OR AGR L_1801.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium.
WCBL_TaxID=176299;
Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome
annotation.";
                                                                                                                   58.8%; Score 40; DB 10; Length 272; 46.2%; Pred. No. 30; tive 4; Mismatches 3; Indels
                                                                                                                 SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 AA
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 294 2323-2328 (2001).
EMBL, AE009326; AAL44754.1; -.
EMBL, AE008288; AAK89474.1; -.
PIR, AD3042; AD3042.
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97 DTHPHRMSRYIQL 109
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 46.2
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVRPYRTSRYLEV 13
                                                  annotation.";
Genome Biol. 0:0-0(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Therefore the EMBL/GenBank/DDBJ databases.

Louditted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

Louditted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

Louditted (NOV-2001) to THE LIGAND-GATED TONIC CHANNEL FAMILY.

EMBL; AF003138; AAK21371.2; ---

RBL; AF003138; AAK21371.2; ---

RO, GO:0005231; Cintegral to membrane, IEA.

RO, GO:0005230; Frextracellular ligand-arid ion channel activity; IEA.

RO, GO:0005230; Frextracellular ligand-arid ion channel activity; IEA.

RO, GO:0005230; Frextracellular IEA.

RO, GO:0005230; Frextramsport; IEA.

RO, GO:0007288; P:Navachic transmission; IEA.

RO, GO:0007289; P:Navachic transmission; IEA.

RO, GO:0007289; Neur_channel.

RITERPRO, IPRO06202; Neur_channel.

RITERPRO, IPRO06202; Neur_channel.

REAM: PF02931; Neur_channel.

REAM: PF02932; Neur_channel.

RRINTS; PR00252; NRICNGTANNEL.

RRINTS; PR00254; RRICNGTANNEL.

RRINTS; RROMASE BROOFCTEIN: IONIC Channel;

ROSERVARADLIC membrane; Transmembrane.

ROSERVARADLIC membrane; Transmembrane.
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EMBL; Y10212; CAA71263.1; -. HSSP; P00488; 1GGU.
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Best Local Similarity 77.0.
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137 DVRPHEGARWLE 148
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732 EVRPYRSSR 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ciona intestinalis.
Estaryotai Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,
Phlebobranchia, Cionidae, Ciona.
MCBI_TaxID=7719;
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                                                                                                                                                                                                          SPECIES=Streptococcus sp.; STRAIN=PVA1702; PLASMID=pIP501; MDDLINE=95362640; PubMed=7635806; MDDLINE=95362640; PubMed=7635806; Mang A., Macrina F.L.; "Streptococcal plasmid pIP501 has a functional oriT site."; "Streptococcal plasmid pip501 has a functional oriT site."; "S Bacteriol. 177:4199-4206(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.8%; Score 40; DB 2; Length 654; 60.0%; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                        Streptococcus sp., and Entertococcus faecalis). Entercococcus faecals (Streptococcus Plaemid pres). Plaemid pres), and Plaemid press. Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cariello L.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76493 MW; C3EE5B8BB4468600 CRC64;
                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         Plasmid 46:170-187(2001).

EMBL; 139769; AAA99466.1; -.

EMBL; X92945; CAC29179.1; -.

GO; GO:0046821; C:extrachromesomal DNA; IEA.

GO; GO:005291; P:unidirectional conjugațion; IEA.

InterPro; IPR005053; MobA, MobL.

Pfan; PF03389; MobA_MobL; 1.
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SPECIES=E.faecalis; STRAIN=RE25; PLASMID=pRE25;
PubMed=11735367;
                                                                      654 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        766 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
 204 DLSRYRTSRHTEV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|::|||||:
418 KPFQTSRYLD 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RPYRTSRYLE 12
                                                                                                                                                                                         Streptococcus.
NCBI_TaxID=1306, 1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       654 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transglutiminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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P91590;
                                                                      052001
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P91590
                                                RESULT 8
                                                            052001
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TISSUB=Lens; WEDUMED=8587103; WEDUMED=96139039; PubMed=8587103; Tomarev S.I., Chung S., Piatigorsky J.; Tomarev S.I., Chung S., Piatigorsky J.; "Glutathione S.transferase and S-crystallins of cephalopods: evolution from active enzyme to lens-refractive proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 39727;
Sosion M., Stinchi S., Beltrametti F., Lazzarini A., Donadio S.;
Sosion M., Stinchi S., Beltrametti F., Lazzarini A., Donadio S.;
Harbe gene cluster for the biosynthesis of the glycopeptide antibiotic A40926 by Nonomuraea sp.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, AJS61198; CAD91202.1;
BMBL, AJS61198; CAD91202.1;
SACYltransferase; Carboxypeptidase; Glycosyltransferase; Monooxygenase.
SEQUENCE 196 AA; 22157 WW; 003AA44D19127982 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Loligio opalescens (California market squid).
Bukaryota, Metazoa, Mollisca, Cephalopoda, Coleoidea, Neocoleoidea, Decapodiformes, Loliginidae, Loligo.
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Streptosporangineae, Streptosporangiaceae, Nonomuraea.
NCBI_TaxID=93944;
                                                                                                                                                                                                                                                                                                                                       58.8%; Score 40; DB 5; Length 766; 77.8%; Pred. No. 88; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 57.4%; Score 39; DB 2; Length 196; Best Local Similarity 58.3%; Pred. No. 32; Matches 7; Conservative 3; Mismatches 2; Indels
InterPro; IPR001102; GlutransfG.
InterPro; IPR001102; GlutransfG.
InterPro; IPR008958; Transglute_C.
InterPro; IPR008931; Transglute_C.
Pfam; PF00927; Transglutamin_C; I.
Pfam; PF00868; Transglutamin_N; I.
Pfam; PF01841; Transglute_core; I.
SEQUENCE 766 AA; 87194 MW; 7F90D921D87FDD1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Gaps

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080652

RESULT 12

080652

Matches

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Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M., Doddon R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S., Berinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T., White O., Fraser C., Collmer A.; "Complete sequence of Pseudomonas syringae."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases. TIGR; PSPTO2112; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                             GO; GO:003934; F:GTP cyclohydrolase I activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0019058; P:hiosynthesis; IEA.
InterPro; IPR001474; GTP cyclohydrol.
Pfam; PF01277; GTP cyclohydrol.
Pfam; PF01277; GTP cyclohydrol; I.
Hydrolase; Complete protecome.
SEQUENCE 276 AA; 30751 MW; 693A2CCACBETD9D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.4%; Score 39; DB 16;
46.2%; Pred. No. 46;
ative 4; Mismatches 3;
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PROSITE, PS01153, NOL1 NOP2 SUN, 1.
Methyltransferase, Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DVRPYRTSRYLEV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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les 7; Conserv
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ID Q8C0N9
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Matches
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.

NCBI_TaxID=3702,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=cv. Columbia,
Federspiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,
Au M., Araujo R., Buehler E., Dewar K., Feng J., Kim C., Li Y.,
Oji O., Osborne B.I., Shinn P., Sun H., Toriumi M., Vysotskaia V.S.
Yu G., Ecker J., Theologis A., Davis R.W.,
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                        Length 217;
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AC004260; AAC34353.1; -...
PIR; T00447; T00447.
InterPro; IPR006502; DUF plant_1615.
FIGRPAMS; TIGRO1615; A thal 3542; 1.
SEQUENCE 258 AA; 29578 MW; FBC341434DFA6380 CRC64;
                                                                                                                                                                                                                                                      26113 MW; 66D4D97D9B3B6F8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last seguence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                        57.4%; Score 39; DB 5;
50.0%; Pred. No. 36;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                              InterPro; IPR004045; GST Nterm.
InterPro; IPR004045; GST Nterm.
InterPro; IPR00403083; S Crystallin.
Pfam; PP002798; GST N; 1.
PRINTS; PR01269; SCRYSTALLIN.
J. Mol. Evol. 41:1048-1056(1995)
EMBL; U19300; AAA97551.1; -.
HSSP; P46088; 2GSQ.
                                                                             InterPro; IPR004046; GST_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, 01-JUN-2003 (TrEMBLrel. 24, T14N5, 4 protein.
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125 DLNPYMQTRYME 136
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         1 DVRPYRTSRYLE 12
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| PWRTSRYMQ 207
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                                                                                                                                                                                                                     PRINTS; PR01269; SC
SEQUENCE 217 AA;
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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EXECUTION OF THE STATE OF THE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 AA; 36336 MW; 32AC13F1B5646A98 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
tRNA/rRNA cytosine-C5-methylase.
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RESULT 13

REACCO CONTRACTOR

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                                                                                                                                                                                                                             STRAIN=CSTBL/6J; TISSUE=Testis;
STRAIN=CSTBL/6J; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AR03041; BAC26051; -.
MGD; MGI:2444484; 49327031022Rik.
SEQUENCE 462 AA; 53199 MW; SEA81B9C5075E684 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Q8CON9;
01-MRR-2003 (TrEMBLrel. 23, Created)
01-MRR-2003 (TrEMBLrel. 23, Last sequence update)
01-MRR-2003 (TrEMBLrel. 24, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Endo-alpha-D-mannosidase homolog.
Endo-alpha-D-mannosidase homolog.
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 57.4%; Score 39; DB 11; Length 462; Best Local Similarity 53.8%; Pred. No. 80; Matches 7; Conservative 3; Mismatches 3; Indels
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Search completed: October 5, 2004, 08:13:11 Job time: 11.8812 secs

| ||:: | |||: 426 DYRPHKPSLYLEL 438 1 DVRPYRTSRYLEV 13

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model OM protein - protein search, October 5, 2004, 07:04:10 ; Search time 9.89043 Seconds (without alignments) 371.381 Million cell updates/sec Run on:

US-09-805-290A-8 68 Title: Perfect score:

1 DVRPYRTSRYLEV 13 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\* Database

1: geneseqp1980s:\* 2: geneseqp1990s:\* 3: geneseqp2000s:\*

geneseqp2001s;\*
geneseqp2002s;\*
geneseqp2003as;\*
geneseqp2003bs;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	0540 Aael0540 Llame	0552 APL inhib	542 Aae10542	0559 Aae10559 HPL in	541 Aae10541 Llama	554 Aae10554	0543 Aael0543 Llama spe	962 Abu27962 Protei	234 Abu45234	202 Abu32202	7	766	330 Aay73330	56 Aag06656	55 Aag06655	54 Aag06654	529 Aag31529	528 Aag31528	527 Aag31527	0986 Abb90986	563 Abu33563	9907 Abg99907 Human nov	885 Aau 75885	7763 Aau57763	
)	A	AAE1	AAE1	AAE10	AAE1	AAE10	AAE10	AAE105	ABU27	ABU45	ABU32	AAB4509	ADES4	AAY73	AAG066			AAG31	•	AAG31	ABB9	ABU33	ABG99	AAU75	AAUS	
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æ	Query Match	100.0	100.0				92.6									58.8					57.4	57.4	57.4		55.9	
	Score	69	68	67	67	65	65	64	42	42	42	41	41	40	40	40	40	39	39	39	39	39	39	39	38	•
	Result No.	i	7	ო	4	S	9	7	œ	መ	10	11	12	13	14	15	16						22			

Abp75655 Human sec Adc89474 Ribosomal	_	١٥.	Abul7607 Protein	Abu22918 Protein	Aae26420 Human tra	Abb66499 Drosophil	Aaw87540 Peptide	Abg24628 Novel hum	Aau62932 Propioni	Prop	Aab18798 Fartial	Adc94988 E. faeciu	Adc01045 Enterohae	Aaw87531 An antitu	Abm67347 Photorhab	m	Abp66018 Bifidobac	Abg03838 Novel hum
ABP75655 ADC89474	ABB70887	ABU18705	ABU17607	ABU22918	AAE26420	ABB66499	AAW87540	ABG24628	AAU62932	ABM59451	AAB18798	ADC94988	ADC01045	AAW87531	ABM67347	ABG24803	ABP66018	ABG03838
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55.9	'n	55.9	'n	55.9	'n.	55.9	54.4	54.4	54.4	54.4	54.4	54,4	54.4	54.4	54.4	54.4	54.4	54.4
3 3 3 8 8 8 8 8	38	38		38		38	37	37	37	37	37	37	37	37	37	37	37	37
26 27	28	29	30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 AAE10540

AAE10540 standard; peptide; 13 AA.

AAE10540;

(first entry) 10-DEC-2001 Llama species antibody VHH CDR3 #9.

Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HCL; cosmetic control; body weight; complementarity determining region 3; CDR3. 

Lama sp.

EP1134231-A1.

20-FEB-2001; 2001EP-00200703.

14-MAR-2000; 2000EP-00200930.

(UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.

De Haard JJW, Bezemer S, Van De Burg M,

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Tareilus

WPI; 2,001-572718/65.

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Disclosure; Page 17; 37pp; English.

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human discary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region

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Gaps

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Indels

Length 130;

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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region
                                                                                                                                                                                                                                                                                                                                                                                        Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human panoreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
100.0%; Score 68; DB 4; Le
100.0%; Pred. No. 8.3e-05;
iive 0; Mismatches 0;
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Pred. No. 9.9e-06;
1; Mismatches 0;
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                                                                                                                                                                                                                               AAE10542 standard; peptide; 13 AA.
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Best Local Similarity 92.3%;
Matches 12; Conservative
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                                                                                                                            98 DVRPYRTSRYLEV 110
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                                                                                    1 DVRPYRTSRYLEV 13
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    Query Match
Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
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/label= CDR1
/note= "Complementarity determining region
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                                                                  Length 13;
                                                                                                            0; Indels
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                                                                  DB 4; L
6.4e-06;
                                                                ch 100.0%; Score 68; DB 1 Similarity 100.0%; Pred. No. 6.4 13; Conservative 0; Mismatches
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/label= CDR2
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/label= Cl
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                                                                    Query Match
Best Local Similarity
Matches 13; Conserv
                            Sequence 13 AA;
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Lama sp. Key Region

AAE10552 RESULT

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Gaps

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AAE10559 ID AAE10559 standard; peptide; 130 AA. XX

RESULT 4

Sequence 130 AA;

Length 13;

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Region

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Llama species antibody VHH CDR3 #10.
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Best Local Similarity
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                                                                              Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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Pred. No. 0.00013;
1; Mismatches 0; Indels
                                                     HPL inhibiting VHH fragment, HPL #30 from llama species.
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                                                                                                                                                                     Location/Qualifiers
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/label= CDR1
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/label= CDR3
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PLC.
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Best Local Similarity
Matches 12; Conserv
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                          10-DEC-2001
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RESULT 5 AAE10541

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Llama antibody; camelid, anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tareilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 17; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE10554 standard; peptide; 130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-2001; 2001EP-00200703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4-MAR-2000; 2000EP-00200930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31. .35
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00372851.
06-MAR-2002; 2002US-0362699P.
                          20-FEB-2001; 2001EP-00200703.
                                                        14-MAR-2000; 2000EP-00200930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2002; 2002WO-US009107
                                                                                                                            Σ̈́
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
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                                                                                                                            Bezemer S, Van De Burg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVRPYRTSRYLE
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                                                                                  NV.
PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacter cloacae.
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Trawick JD,
                                                                                                                                                        WPI; 2001-572718/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-029926/02
                                                                                (UNIL ) UNILEVER (UNIL ) UNILEVER
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200277183-A2.
19-SEP-2001
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
ABU27962
  à
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                                                                                                                                                                                                                                                                                                                                                                                                            The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human panoreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #14 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HFL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.
                                                                                                                                                                                                                                                                                                            New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                             -
50. .64
/label= CDR2
/note= "Complementarity determining region
                                                                      'note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 4; Length 130; Pred. No. 0.00031;
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                                                                                                                                                                                                                                                        Tareilus
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                                                                                                                                                                                                                                                        De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
/label= Val, Leu, Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Llama species antibody VHH CDR3 #12.
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                                                                                                                                                         20-FEB-2001; 2001EP-00200703.
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                                           98. .110
/label= CDR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                         Van De Burg
                                                                                                                                                                                                              (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
                                                                                                                                                                                                                                                                                  WPI; 2001-572718/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 130 AA;
                                                                                                                                                                                                                                                                                                                                                          of light chains
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                                                                                                  EP1134231-A1
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                                                                                                                             19-SEP-2001
                                                                                                                                                                                                                                                         Bezemer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE10543;
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     Region
                                            Region
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region
                                                                                                                                        New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense, prokaryotic essential gene, cell proliferation; drug design.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
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Forsyth RA,
Tareilus E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #13489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
Yamamoto R,
De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU27962 standard; protein; 727 AA.
                                                                                                                                                                                                                                                                                                                            Claim 4; Page 29; 37pp; English.
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Carr GJ,
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The invention relates to an isolated mucleic acid comprising any one of the G213 antisense sequences given in the specification where expression of the mucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid of a permoter operably linked to the mucleic acid. (2) a host cell containing the vector; (3) an isolated collypeptide whose expression is inhibited by the antisense mucleic acid. (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid. (4) an antibody capable of specifically binding the polypeptide or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, or that inhibits cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway or required for proliferation. Or that inhibits cellular proliferation of an operance of the test compound that inhibits proliferation of an organism acid acreaming an antibiciotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or organism acids of a compound that inhibits proliferation of an organism. The article of a compound that inhibits the proliferation of an organism. The article of a compound that inhibits the confidence or proliferation in cells other than S. aureus, S. typhimurlum, K. pneumoniae or p. aeruginosa. The present sequence is encoded by one of the tranget prokaryotic essential genes. Note: The sequence data for this process. The present did not form which acid proliferation in cells other than S. aureus, S. typhimurlan, and the control decomes and acid are useful for patient did not form with an article and proliferation in cells other than S. aureus, S. typhimurlan, and the control decomes and acid acid acid acid ac
                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by Prokaryotic essential gene #30761.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.8%; Score 42; DB
80.0%; Pred. No. 47;
:ive 1; Mismatches
                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 55886; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU45234 standard; protein; 944 AA.
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06-SEP-2001; 2001US-00948993.
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Best Local Similarity 80...
8, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella paratyphi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200277183-A2.
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ABU45234
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Length 727; 1; Indels

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The invention relates to an isolated nucleic acid comprising any one of the fill antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid cocding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding to polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cranisense nucleic acid; (4) an antibody capable of specifically binding to proliferation or the activity of agene In an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway compound to a proliferation or that inhibits proliferation of an activity against a collection of an enably which he test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a scrivity; (11) a culture comprising strains in which the set compound that inhibits proliferation of the strains is present in a culture or collection of corpanism acts; (9) manufacturing an antibiotic; (10) profiling a compound; activity; (11) a culture comprising strains in which the strains is present in a culture or collection of the proliferation of an organism. The antisense nucleic acids required for proliferation in cells can be defined or for proliferation in cells can be defined or for screening for homologous nucleic acids required for proliferation in cells contained by neoliferation or form pare of the present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patined for patent format directly from wire the present sequence in electronic format directly from the present sequence is encoded by one of the pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                       Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 944;
                                                                                                                              Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein encoded by Prokaryotic essential gene #17729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 6;
Pred. No. 63;
1; Mismatches 1
                                                                                                                              Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 73158; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU32202 standard; protein; 961 AA.
                                                                                                                                Malone C,
Carr GJ,
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.8%;
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                                                                                      (BLIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 PYRTAFYLEV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 PYRTSRYLEV 13
                                                                                                                              Zamudio C,
Trawick JD,
                                                                                                                                                                                             WPI; 2003-029926/02.
N-PSDB; ACA49104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 944 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU32202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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  XXXXXXXXXXXXXXXX
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AAB45097 standard; protein; 142 AA.

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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                               Claim 25; SEQ ID NO 60126; 1766pp; English.
                                                                                                                              Malone C,
Carr GJ,
                                                                        06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-034292RP.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                               21-MAR-2002; 2002WO-US009107;
                                                                21-MAR-2001; 2001US-00815242.
                                                                                                               (BLIT-) ELITRA PHARM INC.
Klebsiella pneumoniae
                                                                                                                              Zamudio C,
Trawick JD,
                                                                                                                                                      WPI; 2003-029926/02.
N-PSDB; ACA36072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 961 AA;
                WO200277183-A2
                                                                                                                              Wang L,
Wall D,
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Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

the 6113 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway cequired for proliferation or the the inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation or the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is oversxpressed; (12) determining the extent to be which the server compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene or which the server compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which activity; (12) determining the extent the compound that inhibits or a strent or the server or an extent or an extent or a server or a determined to a compound or a server or a determined to a compound or an extent or a server or a determined to a compound or an extent or a server or a determined to a compound or a compound or a compound or an extent or a server or a determined to a compound or a compound or an extent or a server or a determined to a compound or a compound or an extent or a server or a ser drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at the wipo.int/pub/published\_pot\_sequences to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for ceilular proliferation to isolate candidate molecules for rational

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                          Gaps
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61.8%; Score 42; DB 6; Length 961;
80.0%; Pred. No. 64;
.ive 1; Mismatches 1; Indels
                         1; Indels
                          1;
                          8; Conservative
         Best Local Similarity
Matches 8; Conserv
 Query Match
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124 PYRTAFYLEV 133
4 PYRTSRYLEV 13
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AAB45097

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This invention describes novel isolated nucleic acid molecules (I)
encoding a human secreted proteins (II) which have immunosuppressive,
antistribritic, antirhenuatic, antiproliferative, cytostatic, cardinate,
vasotropic, cerebroprotective, nootropic, neuroprotective, antibacterial,
virucide, fungicide, ophthalmological and vulnerary activity and can be
used for gene therapy. (I) and (II) are used to prevent, treat or
c used for gene therapy. (I) and (II) are used to prevent,
c used aptabological condition in e.g. humans, mice, rabbits, goats,
horses, cats, dogs, chickens or sheep. (I) and (II) are also used in
diagnosing a pathological condition or susceptibility to a pathological
condition. The artibodies to (II) can also be used in alleviating
symptoms associated with the disorders and in diagnostic immunoassays
e.g. radioimmunoassays or enzyme linked immunosorben assays (ELSA).
Disorders which are diagnosed or treated include autoimmune disease e.g.
rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the
breast or liver, cardiovascular disorders e.g. cardio arteated
corpusation disorders e.g. Alzheimer's disease, infections caused by bacteria,
viruses and fungi and coular disorders e.g. corneal infection. The
polypeptides can also be used to aid wound healing and epithelial cell
proliferation, to prevent skin aging due to subburn to maintain organs
to regenerate tissues and in chemotaxis. The polypeptides can also be
to regenerate tissues and in chemotaxis. The polypeptides can also be
to regenerate tissues and in chemotaxis. The polypeptides can also be
                                                                                                                                                                                antiproliferative, cytostatic, cardiant, vasotropic, cerebroprotective, noctropic, neuroprotective, antibacterial; virucide, fungicide, ophthalmological; vulnerary, gene therapy, treatment, autoimmune disease, hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder, nervous system disorder; infection, skin aging; wound healing; epithelial cell proliferation; transplantation.
                                                                                                                                                                Secreted protein; human; immunosuppressive; antiarthritic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                      Human secreted protein encoded by gene 31 homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 404-405; 418pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000WO-US007723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JAN-2000; 2000US-0174852P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0126506P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
'has 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-611704/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 142 AA;
                                                                                                                                                                                                                                                                                                                                                                           WO200058357-A1.
                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          capabilities
                                                                                12-FEB-2001
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                                     AAB45097
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| ||:: | |||: DYRPHKPSLYLEI 427

415

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1 DVRPYRTSRYLEV 13

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ADE54766 standard; protein; 451 AA.
                                                             WPI; 2003-268312/26.
                                                         Woolf C, D'urso D,
                         Rattus norvegicus
                                                                GENBANK; AAB86925
                              WO2003016475-A2.
                                  27-FEB-2003
      ADE54766;
ADE54766
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The invention discloses a composition comprising two or more isolated rat or human polymucleotides or a polymucleotide which represents a fragment, and earlyative or allelic variation of the mucleic acid sequence. Also claimed are a vector comprising the movel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a decreases the expression of the polymucleotide sequence that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the composition, a method for identifying a pharmaceutical composition, a cutivity in an animal of one or more of the regulates the security in an animal of one or more of the regulates the cutivity is useful for preparing a medicament for treating condulates its activity is useful for preparing a medicament for treating polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating consideration, which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed consideration, but was obtained in electronic form directly from WIPO at Etp. who. int/pub/published_pot_equences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                    Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Costigan M;
                                                                                            Rat Protein AAB86925, SEQ ID NO 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 451 AA;
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0; Gaps

60.3%; Score 41; DB 7; Length 451; 53.8%; Pred. No. 43; 1. Indels 1; Mismatches 3; Indels

Query Match 60.3 Best Local Similarity 53.9 Matches 7; Conservative

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AAY73325-Y73389 are human transcriptional regulator molecule (HTRM)

protein sequences. The HTRM protein and nucleotide sequences are useful

for preventing or treating disorders associated with decreased expression

or activity of HTRM which include cell proliferative disorders such as

leukaemia; immune disorders such as AIDS, Addison's disease, diabetes

melitus, rheumatoid arthritis, multiple sclerosis, systemic lupus

crythematosus, and myasthenia gravis; infections and trauma. Antagonists

of the HTRM polypeptides are useful for treating or preventing disorders

sosciated with increased expression or activity of HTRMs. HTRM

polypeptides, their immunogenic fragments or oligopeptides are useful for

screening libraries of compounds in drug screening techniques.

Company of Company of HTRM are useful for blocking the transcription

of mRNA and regulating gene function by modulating the activity of HTRM.

Vectors expressing HTRM or agonists can also be used to prevent or treat

disorder associated with decreased HTRM expression. Antibodies which

specifically bind HTRM and polymucleotides encoding HTRM are useful for

disorder associated with decreased HTRM. Nucleotide sequences

of massays that detect the expression of HTRM. Nucleotide sequence

croding HTRM may be useful to generate hybridization probes useful in

mapping the naturally occurring genomic sequence and to detect

differences in gene sequences among normal, carrier and affected

individuals. Using diagnostic assays, cancer can be detected prior to the

appearance of clinical symptoms and therby progression of cancer can be

companied. The sequence are supplemented by progression of cancer can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptides useful for diagnosis, prevention and treatment of cancer and immune disorders.
                                                                                                                                                                                             arteriosclerosis; AIDS
                                                                                                                                                                                         HTRM; human transcriptional regulatory molecule; arteriosclerosis; AIDS arteriosclerosis; cirrhosis; cancer; leukaemia; diabetes mellitus; Addison's disease; multiple sclerosis; rheumatoid arthritis; infection; trauma; myasthenia gravis; adenocarcinoma; immune disorder; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT;
Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prevented by aggressive treatment or preventive measures
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Baughn MR, Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 92-93; 193pp; English
                                      AAY73330 standard; protein; 250 AA.
                                                                                                                                                       HTRM clone 397663 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0094254P.
98US-0095827P.
98US-0102745P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patterson C,
                                                                                                                   24-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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N-PSDB; AAZ52415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1998;
07-AUG-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                          WO9957144-A2
                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillman JL,
Gerstin EH,
                                                                                                                                                                                                                                                                                                                                                                                11-NOV-1999
                                                                          AAY73330;
RESULT 13
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9905-01391199

9905-0139452P

9905-0139454P

9905-0139454P

9905-0139458P

9905-014033P

9905-014033P

9905-014237P

9905-014237P

9905-014237P

9905-014233P

9905-014233P

9905-0144885

9905-0144334P

9905-0144334P
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9905-0145088P-
9905-0145089P-
9905-0145192P-
9905-0145192P-
9905-0145218P-
9905-0145218P-
9905-0145218P-
9905-0145918P-
9905-0147302P-
9905-0147302P-
9905-0147303P-
9905-0147303P-
9905-0147303P-
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23 - JUN - 19
24 - JUN - 19
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                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                              Gaps
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    Score 40; DB 3; Length 250;
Pred. No. 34;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 3507.
                                                                                                                                                                                                                    AAG06656 standard; protein; 252 AA.
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99US-0123180P.
99US-012528P.
99US-0126264P.
99US-0126264P.
99US-0127462P.
99US-0127462P.
99US-0128234P.
99US-0130891P.
99US-0130891P.
99US-0132484P.
99US-0132484B.
99US-0132484B.
99US-0132484B.
99US-0132484B.
99US-0132484B.
99US-0132487P.
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99US-0132487P.
99US-013421P.
99US-013421P.
99US-0134221P.
99US-0134221P.
99US-0134221P.
99US-0134221P.
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990S-0137502P.
990S-0137724P.
990S-0138094P.
990S-0138540P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-2000; 2000EP-00301439
Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                    17-OCT-2000 (first entry)
                                                                                2 VRPYRTSRYLEV 13
                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
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                                                                                                                                                                                                                                                                AAG06656;
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28-MAY-19
01-JUN-19
                                                                                                                                                                             RESULT 14
AAG06656
ID AAG06
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DTHPHRMSRYIQL 89

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 3506.
                                            AAG06655 standard; protein; 272 AA.
                                                                                                                                                                                                                                                                                                                                                                     990S-0131449P

990S-0132480P

990S-0132486P

990S-0132486P

990S-0132486P

990S-0132486P

990S-0132486P

990S-0132863P

990S-0134218P

990S-0134218P

990S-0134218P

990S-0134221P

990S-0134221P

990S-0134221P

990S-0134221P

990S-0134221P

990S-0134221P

990S-0134221P

990S-0134221P

990S-0135621P

990S-0135621P

990S-0136621P

990S-0136621P

990S-0136621P

990S-0136621P

990S-013762P

990S-013762P
                                                                                                                                                                                                                                   990S-0121825P.
990S-0123180P.
990S-0125788P.
990S-012626P.
990S-0126264P.
990S-0126284P.
990S-0128234P.
990S-0128234P.
990S-0130876P.
990S-0130876P.
                                                                                                                                                                                                                   25-FEB-2000; 2000EP-00301439
                                                                                 17-OCT-2000 (first entry)
                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                      28 - APR - 1999;
30 - APR - 1999;
04 - MAY - 1999;
05 - MAY - 1999;
06 - MAY - 1999;
06 - MAY - 1999;
11 - MAY - 1999;
14 - MAY - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAX-1999;
14-MAX-1999;
14-MAX-1999;
19-MAY-1999;
20-MAX-1999;
21-MAX-1999;
24-MAY-1999;
                                                                                                                                                                               EP1033405-A2
                                                                                                                                                                                                 06-SEP-2000
                                                               AAG06655;
                    RESULT. 15 TARAGO 6655
                                             Score 40; DB 3; Length 252;
Pred. No. 34;
4; Mismatches 3; Indels
990S-0148171P.
990S-0148119P.
990S-0148819P.
990S-0148848P.
990S-0149175P.
990S-0149175P.
990S-0149172P.
990S-0149172P.
990S-0149172P.
990S-015133P.
990S-015933P.
990S-01698P.
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990S-01698P.
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46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 58.8
Best Local Similarity 46.2
Matches 6; Conservative
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Gaps ..

DVRPYRTSRYLEV 13

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RR 18-JUN-1999; 99US-013945EP
RR 22-JUN-1999; 99US-013945EP
RR 10-JUL-1999; 99US-013945EP
RR 10-JUL-1999; 99US-014132EP
RR 10-JUL-1999; 99US-014132EP
RR 10-JUL-1999; 99US-014132EP
RR 10-JUL-1999; 99US-014132EP
RR 22-JUL-1999; 99US-014133EP
RR 22-
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PR 18-AUC-1999 9918-0149723 P
PR 20-AUC-1999 9918-0149723 P
PR 20-AUC-1999 9918-0149723 P
PR 20-AUC-1999 9918-0149723 P
PR 21-AUC-1999 9918-0149723 P
PR 21-AUC-1999 9918-0149919 P
PR 21-AUC-1999 9918-0151066 P
PR 21-AUC-1999 9918-0151066 P
PR 21-AUC-1999 9918-015103 P
PR 21-AUC-1999 9918-015103 P
PR 21-AUC-1999 9918-015246 P
PR 21-AUC-1999 9918-015249 P
PR 21-AUC-1999 9918-015440 P
P
P 21-AUC-1999 9918-01540 P
P
P 21-AUC-1999 9918-01540 P
P
P 21-AU
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1 DVRPYRTSRYLEV 13 | | | | | | | :: 97 DTHPHRMSRYIQL 109

Query Match 58.8%; Score 40; DB 3; Length 272; Best Local Similarity 46.2%; Pred. No. 38; Matches 6; Conservative 4; Mismatches 3; Indels

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tes/sec
                                                                                                                                      5. 2004. 07:36:16 ; Search time 2.10648 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                              OM protein - protein search, using sw model
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						(without alignments) 593.639 Million cell updat	aligi Aillic	ments on cel	E F	pdat
ritle:	US-09-805-290A-9	5-29	- WO 6	0						
Sequence:	1 DVRPYRTSRYLEL 13	TSRY	TEL	13						

283366 Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	40 re	hypothetical prote	hypothetical prote	oxidoreductase Atu	agaE protein [impo	hypothetical prote	hypothetical prote	19.15 prot	30S ribosomal prot	) (BC	Η.	III	protease III precu	pro	a 1	NO NO			(J)		Ω		ine ac	ole tran	ıble transp	rote	able memb	ein-tyrosi	i.
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Score	41	40	40	40	40	39	39	39	39	39	39	39	39	38	38	37	37	37	37	36.5	36	36	36	36	36	36	36	36	36
Result No.		7	m	4	ഹ	9	7	æ	თ	10	11	12	13	14	15	16	17	18	19	20	21	N	23	24	25	56	27	28	29

probable isocitrat	hypothetical prote	ribosomal protein	30S ribosomal prot	alpha-mannosidase	probable dna-direc	hypothetical prote	breast/ovarian can	intrinsic factor-B	protein F18014.23	nuclear matrix pro	conserved hypothet	_	diol dehydrase (di	hypothetical prote	hypothetical prote
	2 E84465	2 B82141	2 C83250		2 T40607			2 T09456	2 G86327	2 JU0239	2 E95298	2 AC1219	2 AF1572	2 \$05560	2 T16910
						1441								186	269
52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	51.5	51.5	51.5	51.5	51.5	51.5	51.5
	36		36	36	36	36	36	36	35	35	35	35		35	
7. 30.	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1  B48128  B48128  probable WD-40 repeat protein [imported] - Arabidopsis thaliana c;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 0.2-Feb-2001 G;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Accession: E84828 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.; Town, C.D.; Fujii, C.Y.; N. M; Koo, H,; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, U.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A4420; MUID:20083487; PMID:10617197 A;Accession: E84828 A;Acuse: preliminary A;Molecule type: DNA A;Residues: 1-775 <570> A;Cross-references: GB:AE002093; NID:94586061; PIDN:AAD25679.1; GSPDB:GN00139 C;Genetics: A;Gene: At2940360	A, Map position: 2  Query Match Best Local Similarity 66.7%; Pred. No. 21; Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  Qy 1 DVRPYRESYLE 12  Db 429 DLRPYPNSCYLE 440
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RESULT 2	
hypothetical protein EC83511 [imported] - Escherichia coli (strain O157:H7, subst	sqns
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001	
C.Accession: 69106/ D.M. C. Mariahi W. Virobana V. Tehii V. Vokovama K. Hi	

train RIN

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G91067
A;Astus: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-437 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36934.1; PID:g13362982; GSPDB:GN00154
A;Esperimental source: strain O157:H7; substrain RIMD 0509952
C;Genetics:
A;Genetics:

Score 40; DB 2; Length 437; Pred. No. 18; 58.8%; Query Match Best Local Similarity

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Conservative

.; 8

Matches

317 DVRSERTNSYIEL 329

1 DVRPYRTSRYLEL 13

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C;Species: Arābidopsis thaliana (mouse-eār cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47356
R;Nyakatura, G; Fartmann, B; Dauner, D; Sterr, W; Holland, R; Weichselgartner, M; N
Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: H98243
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; WUID:21608551; PMID:11743194
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CiDate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
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Pred. No. 18;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 258;
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A;Experimental source: cultivar Columbia; BAC clone F18P9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F18P9.140 - Arabidopsis thaliana
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16;
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Pred. No.
                                                                                                                                                                                                                                                                                                       A, Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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199 PWRTSRYMQ 207
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                                                                                                                                                                                                                   A; Residues: 1-442 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-303 <NYA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: ATSP:T14N5.4
A;Map position: 1
A;Introns: 38/3; 106/1
                                                                                                                                                      A,Accession: H98243
A,Status: preliminary
A,Molecule type: DNA
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Z3943 [imported] - Escherichia coli (strain O157:H7, substrain BDL3 (5.)specises: Escherichia coli (5.)specises: Escherichia coli (5.)specises: Escherichia coli (5.)specises: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 (5.)specision: H8S911 (6.) Bulnatet III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Nature 409, 529-533, 2001 (7.) Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Nature 409, 529-533, 2001 (7.) A.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-441 <STO>
A;Cross-references: GB:AE005174; NID:g12517076; PIDN:AAG57756.1; GSPDB:GN00145; UWGP:Z39
A;Experimental source: strain O157:H7, substrain EDL933
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      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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agaE protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
      ;
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Pred. No. 18;
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
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      3,
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Pred. No. 18;
2; Mismatches
      Mismatches
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Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative

A; Gene: Z3943

A, Status: preliminary A, Molecule type: DNA

321 DVRSERTNSYIEL 333

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1 DVRPYRTSRYLEL 13

58.8%;

Query Match
Best Local Similarity 58.3
Matches 7; Conservative

DPRPYRYSRFFD 432

1 DVRPYRTSRYLE 12

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A; Map position: linear chromosome

Gene: Atu3952

Genetics:

Status: preliminary Molecule type: DNA Residues: 1-442 <KUR>

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Silveira A.L.; Za

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putrily (EC 3.4.24.55) precursor [validated] - Escherichia coli (strain K-12) putrily (Species: Escherichia coli (strain K-12) N'Alternate names: endopoptidase Pi; proteinase III (Species: Escherichia coli (C)Becles: Escherichia coli (C)Becles: Escherichia coli (C)Bace: 31-Mar.1993 #sequence revision 31-Oct-1997 #text_change 27-Oct-2003 C; Accession: F65064; A29093; A25765; B25532 C; Accession: F65064; A29093; A25765; B10ch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col A,; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Reference number: A64720; MUD:97426617; PMID:9278503 A; Reference number: A64720; MUD:97426617; PMID:9278503 A; Reference number: A64720; MUD:97426617; PMID:9278503 A; Reference number: A64720; MUD:97426617; PMID:92367163; PIDN:AAC75860.1; PID:92367164; A; Residues: 1-962 *BLAT> A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ajmolecule type: DNA
AjResidues: 1-276, 'HTHSLR', 283,'W', 285-286 «CLA»
Ajresidues: 1-276, 'HTHSLR', 283,'W', 285-286 «CLA»
Ajcross-references: GB:M17095, NID:g147390, PIDN:AAA24436.1; PID:g147391
AjExperimental source: strain K12
AjNote: part of this sequence, including the amino end of the mature protein, was confirm
RjFinch, P. W.; Wilson, R.B.; Brown, K.; Hickson, I.D.; Emmerson, P.T.
Nucleic Acids Res. 14, 7665-7703, 1986
AjTitle: Complete nuclectide sequence of the Escherichia coli ptr gene encoding protease
AjReference number: A25765
AjNolecule type: DNA
AjReference number: A25765
AjMolecule type: DNA
AjReference sides K6627; NID:g42560; PIDN:CAA29576.1; PID:g42561
RjBecker, A.B.; Roth, R.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 3835-3839, 1992
AjTitle: An unusual active site identified in a family of zinc metalloendopeptidases.
AjContents: annotation; active site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Description: endopeptidase degrades small peptides [validated, MUID:92237263]
A,Pathway: protein degradation
C,Superfamily: insulin-degrading enzyme (IDE)
C,Superfamily: insulin-degrading enzyme (IDE)
C,Reywords: hydrolase; metallogroteinase; monomer; periplasmic space; protein degradation
F;1-23/Domain: signal sequence #status predicted <SIG>
F;1-25/Product: plrillysin #status experimental <MAT>
F;88,92/Binding site: zinc (His) #status experimental
F;91/Active site: Glu #status experimental
               Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da
Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore,
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                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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61;
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36;
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Pred. No.
                                                                                                                                                                                                                                                                                                                 Score 39;
Pred. No.
                                                                                                                                                                                                                                             ribosomal
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                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
M.; Tsuhako, M.H.; Vallada, H.; AReference number: A59328
A;Contents: 'annotation C;Genetics'
                                                                                                                                                      Cycentics:
AyGene: XF2438
CySuperfamily: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 DVRPVRDPAYLE 160
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Best Local Similarity
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A,Map position: 61
C,Function:
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C;Species: Arabidopsis thaliana (Mouse-ear cress)
C;Species: Arabidopsis thaliana (Mouse-ear cress)
C;Accession: A86274
C;Accession: A86274
C;Accession: A86274
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansure 408, 816-820, 2000
Ayathors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.Athors: Salzberg, S.L.; Sakano, H.
Ayathors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
Ayathors: Asser, C.M.; Venter, J.C.; Davis, R.W.
Ayathors: Assert Asser, C.M.; Venter, J.C.; Davis, R.W.
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: B82559
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUD:2036,5717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82559
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A,Residues: 1-526 <STO>
A;Cross-references: GB:AE005172; NID:g5080782; PIDN:AAD39292.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30S ribosomal protein S1 XF2438 [imported] - Xylella fastidiosa (strain 9a5c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                          Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                      Indels
                                                                                                                                  2;
   A;Introns: 47/3; 103/3; 140/2; 182/1; 210/2; 241/3
A;Note: F18P9.140
                                                                                                                          Score 39; DB 2
Pred. No. 19;
2; Mismatches
                                                                                                                          Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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DIRPYKTS 17
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Best Local Similarity
7, Conserve
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Conservative

7;

Matches

124 PYRTAFYLEV 133

В

4 PYRTSRYLEL 13

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C;Accession: AC0865
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, A.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove. A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cjaccession: H96974

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bannett, G.N.; Konin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribosomal protein S14 T01E8.6, mitochondrial [similarity] - Caenorhabditis elegans
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A;Cross-references: GB:AL513382; PIDN:CAD02819.1; PID:g16504073; GSPDB:GN00176
C;Genetics:
A;Gene: STY3133
C;Superfamily: insulin-degrading enzyme (IDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-2870 «KUR»
A;Cross-references: GB:AE001437; PIDN:AAK78587.1; PID:g15023480; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z48809; PIDN:CAA88746.1; GSPDB:GN00020; CESP:T01E8.6
A;Experimental source: clone T01E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-May-2002
C;Accession: T24300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cyclic beta 1-2 glucan synthetase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 962;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-103 < WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, March 1995
A;Reference number: Z19871
A;Accession: T24300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.4%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 70.v-
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76 IKPYRLSRHL
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A, Status: preliminary
A, Molecule type: DNA
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A;Map position: 2
A;Introns: 20/3
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                                                                                                                                                                                                                                                      proteinase III [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) C; Species: Escherichia coli C; Species: Escherichia coli C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Oct-2003 C; Accession: F91088 C; Hayashi, F.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Ruhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res: 8, 11-22, 2001 A; Reference number: A99629; MuID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-962 <STO>
A;Cross-references: GB:AE005174; NID:g12517303; PIDN:AAG57932.1; GSPDB:GN00145; UWGP:Z41
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.J.; Mayhew
K.; Apodaca,
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A; Residues: 1-962 <HAX-
A; Residues: 1-962 <HAX-
A; Cross-references: GB:BA000007; PIDN:BAB37101.1; PID:g13363150; GSPDB:GN00154
A; Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Oct-2003
C;Accession: H85933
F;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, I
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, I
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Oct-2003
               Gaps
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Pred. No. 61;
2; Mismatches 1; Indels
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               Indels
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                  1;
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Pred. No. 61;
2; Mismatches
                  Mismatches
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Superfamily: insulin-degrading enzyme (IDE)

Genetics: Gene: ECs3678

Status: preliminary

57.4%; ilarity 70.0%; Conservative

Query Match Best Local Similarity Matches 7; Conserv

124 PYRTAFYLEV 133

4 PYRTSRYLEL 13

8 유 Superfamily: insulin-degrading enzyme (IDE)

Genetics:

Status: preliminary Molecule type: DNA

Accession: H85933

57.4%;

Query Match
Best Local Similarity 70..
Triconservative

124 PYRTAFYLEV 133

g

ò

RESULT 13 AC0865

4 PYRTSRYLEL 13

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0; Gaps

C;Genetics: A;Gene: CAC0609

Query Match 55.9%; Score 38; DB 2; Length 2870; Best Local Similarity 77.8%; Pred. No. 2.8e+02; Matches 7; Conservative 1; Mismatches 1; Indels 5 YRTSRYLEL 13

||: ||||| 2594 YRSGRYLEL 2602

Search completed: October 5, 2004, 08:16:50 Job time: 4.10648 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

October 5, 2004, 07:29:35; Search time 1.16358 Seconds (without alignments) 581.749 Million cell updates/sec

US-09-805-290A-9 68 1 DVRPYRTSRYLEL 13 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	arabidopsi		Q8cvs2 escherichia		Q8z418 salmonella	Q8zmb5 salmonella			caenoi								rattus				bacte	Q9hjl8 thermoplasm		O13016 gallus gall	P18031 homo sapien	рошо	fow1		디	P02349 escherichia	buchnera	borrelia	
SUMMARIES		FUT7 ARATH	PTRA_ECO57	PTRA ECOL6	PTRA ECOLI	PTRA SALTI	PTRA_SALTY	PTRA SHIFL	DEFC AEDAE	RT14_CAEEL	MALQ_PYRKO	DS DROME	SYR BIFLO	RS1 PROSP	METK PSEAE	YBDG_ECOLI	PTN1_MOUSE	PTN1_RAT	M2B1 FELCA	RPC1_SCHPO	BRC1_HUMAN	Y14F_BPT4	FLPA_THEAC	BET4_YEAST	PTN1_CHICK	PIN1 HUMAN	CBPM_HUMAN	V111_FOWPV	FUT8 ARATH	GS1 NEUCR	RS1 ECOLI	RS1_BUCBP	LUXS BORBU	
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	gth	526	962	962	962	962	962	962	66	199	653	3503	620	378	396	415	432	432	1007	1405	1863	210	230	290	434	435	443	444	200	532	557	566	157	
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097d80 P11666	Q9xb14 Q50642	20020 2006066 2007966	025991 Q97167	P81132 Q9x2i8	P45840
DAP2_CLOAB YGGB_ECOLI	DHAA MYCBO DHAA MYCTU	YB1 CHICK TRME HELPJ	TRME_HELPY UXAB_CLOAB	PER2_VOLCA SYE2_THEMA	SYR_MYCLE
пп	44,				-
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ν. 4. τυ	336	u m 4 0 0 0	4 4 2 2	4 4 6 4	45

# ALIGNMENTS

LT 1 ARATH FUT7 ARA	. 41, Creat . 41, Last	28-FEB-2003 (Rel. 41, Last annotation update) Probable fucosyltransferase 7 (BC 2.4.1.) (AtFUT7).	FUL/ OK AIICH40/0 OK F/ALF.13 OK F10A14.19 OK F10A14.20. Arabidopsis thaliana (Mouse-ear Cress) Divermote: Viridial antes: Great Arabita (Embryonhyta, Tranheonhyta)	streptopnyta; Embryopnyta; yta; eudicotyledons; core eu	eurosids II; Brassicales; Brassicaceae; Arabidopsis. NCBI_TaxID=3702;	[1] SEQUENCE FROM N.A.	STRAIN=cv. Columbia; MEDLINE=21016719; PubMed=11130712;	Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O. Alonso J. Altafi H. Aranio R. Bowman C.J., Brooks S.Y.,	Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,	Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Dunn P., Etcu P., Feldblyum T.V., Feng JD., Fong B., Pujii C.Y.,	Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,	Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Miaykin B., Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,	Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li YP., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,	, Ogborne	Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,	llon L.J., Tambunga G., Toriumi M.J., Town C.D., Varabers M. Wassteleija V.S. Walker M.	<ol> <li>vall Akell S., vaysberg M., vysocskala v.s., mainer</li> <li>G., Fraser C.M., Venter J.C., Davis R.W.;</li> </ol>	and analysis of c	Lidalidae; Nature 408:816-820(2000).		MEDLINE=21608393; PubMed=11743104;		"Characterization of a tamily of Arabidopsis genes related to xyloqlucan fucosyltransferasel.";	Plant Physiol. 127:1595-1606(2001).	act as a fucosyltransferase.	-!- PATHWAY: Glycosylation. -!- SUBCELLULAR LOCATION: Type II membrane protein. Membrane-bound	form in trans cisternae of Golgi (By similarity).	seedlings.		erroneous gene model prediction.
RESU FUT7	422	Sad	888	888	88	RN	RX XX	RA PA	æ	ል	Z.	<b>2</b> 5	RA RA	Æ	A A	8 6 8	<b>S S</b>	RT	RE	R P	RX 6	88	R R	报	ខ្លួ	ខ្លួ	8 8	88	888	38

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C STRAIN-0157:H7 / RIMD 0509952;

X MEDLINE-21156231; PubMed=11258796;

MEDLINE-21156231; PubMed=11258796;

A Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.,

"Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

I DNA Res. 8:11-22(2001).

-!- FUNCTION: Endopeptidase that degrades small peptides of less than

7 Kab, such as glucagon and insulin (By similarity).

-!- CATALYTIC ACTIVITY: Preferential cleavage of 16-Tyr-| Leu-17 and

C -!- CATALYTIC ACTIVITY: Preferential cleavage of 16-Tyr-| Leu-17 and

C -!- CATALYTIC ACTIVITY: Preferential cleavage of 16-Tyr-| Leu-17 and

C -!- Tyr-26 bonds of oxidized insulin B chain. Also acts on
                                                                                                                                                                                                                                                                                  TIGHLEGGES, OLIVES, CALL WALL.

Signal-anchor; Golgi stack; Gell Wall.

DOMAIN 1 4 CYTOPLASMIC (POTENTIAL).

TRANSMEM 5 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P. S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
Protease III precursor (EC 3.4.24.55) (Pitrilysin) (Protease pi).
PTRA OR PTR OR 24138 OR ECS3678.
Bacteria coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
8F3B447551025FCD CRC64;
                                                                                                                                                                                                                              InterPro; IPR004938; XG_FTase.
Pfam, PF03254; XG_FTase; 1
Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
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Pred. No. 14;
0; Mismatches 1; Indels
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EMBL, AC068197; AAF79408.1; ALT_SEQ.
PIR, A86274; A86274.
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nes 7; Conservative
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CARBOHYD
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
-!- FUNCTION: Endopeptidase that degrades small peptides of less than -!- CATALYTIC ACTIVITY: Preferential cleavage of 16-Tyr-1 and 25-Phe-|-Tyr-26 bonds of oxidized insulin B chain. Also acts on other substrates of Mw less than 7 kDa such as insulin and
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STRAIN=06-HJ / CFTOT3 / AICC 700928;
MEDLINE=22388234; PubMed=12471157;
Melch R.A.; Butland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mabley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pfam, PF05193; Peptidase_M16_C; 2.
PROSTTE; PS00143; INSULINASE; Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
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Enterobacteriaceae; Escherichia.
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PTRA ECOLG STANDARD; PRT; 962 AA.

AC Q8CVS2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Protease III precursor (EC 3.4.24.55) (Pitrilysin) (Protease pi).
GN PTRA OR PTR OR C3415.

GN PTRA OR PTR OR C3415.

GN Escherichia coli 06.

SE Scherichia coli 06.
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substrates of Mw less than 7 kDa such as insulin and
                                    glucagon.
-- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-- SUBENIT: Monomer (By similarity).
-- SUBCELLULAR LOCATION: Periplasmic (By similarity).
-- SIMILARITY: Belongs to peptidase family M16.
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COFACTOR: Binds 1 zinc ion per subunit (By similarity).
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962 PROTEASE II.
918 ZINC (BY SIMILARITY).
91 ZINC (BY SIMILARITY).
92 ZINC (BY SIMILARITY).
169 ZINC (BY SIMILARITY).
107808 MW, 30785644CBF0E452 CRC64;
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InterPro, IPR001431, Peptidase_M16.
InterPro, IPR007863, Peptidase_M16_C.
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Matches 7; Conservative
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169 1
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Nucleic Acids Res. 14:8573-8582(1986).
        -!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
-!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
-!- SIMILARITY: Belongs to peptidase family M16.

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STRAIN=K12 / MG1655,
BELINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Caregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete nucleotide sequence of the Escherichia coli recB gene.";
                                                                                                                                                                                                                                                                          InterPro; IPR001431; Peptidase_M16.
InterPro; IPR007863; Peptidase_M16_C.
Edm; PF000675; Peptidase_M16; I.
Pfam; PF00193; Peptidase_M16_C;
Pfam; PF00193; Peptidase_M16_C;
PROSITE; PS00143; INSULINASE; I.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTRA_ECOLI STANDARD; PRT; 962 AA.
P05458; P78106;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protease III precursor (EC 3.4.24.55) (Pitrilysin) (Protease pi).
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=87040734; PubMed=3534791;
Finch P.W., Wilson R.E., Brown K., Hickson I.D., Emmerson P.T.;
"Complete nucleotide sequence of the Escherichia coli ptr gene encoding protease III.";
"Nucleic Acids Res. 14:7695-7703(1986).
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MEDLINE-87066729; PubMed=3537960;
Finch P.W., Storey A., Chapman K.E., Brown K., Hickson I.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 1; Length 962;
Pred. No. 26;
2; Mismatches 1; Indels
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Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                     23 BY SIMILARITY.
962 PROTEAGE III.
98 ZINC (BY SIMILARITY).
91 BY SIMILARITY.
92 ZINC (BY SIMILARITY).
169 ZINC (BY SIMILARITY).
1169 ZINC (BY SIMILARITY).
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H->R: LOSS OF ACTIVITY AND OF ZN-BINDING.
E->Q: LOSS OF ACTIVITY.
H->R: LOSS OF ACTIVITY AND OF ZN-BINDING.
E->Q: 20% LOSS OF ACTIVITY AND OF ZN-BINDING.
E->Q: LOSS OF ACTIVITY AND OF ZN-BINDING.
E->Q: NO LOSS OF ACTIVITY.
IIIHXVPA -> HYHSLRPW (IN REF. 4).

MW; 0558C68C2FIA0540 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzymes.";
Biochem. J. 292:137-142(1993).
Biochem. J. 292:137-142(1993).
--- FUNCTION: Endopeptidase that degrades small peptides of less than 7 kDa, such as glucagon and insulin.
--- CATALYTIC ACTIVITY: Preferential cleavage of 16-Tyr-|-Leu-17 and 25-Phe-|-Tyr-26 bonds of oxidized insulin B chain. Also acts on other substrates of Mw less than 7 kDa such as insulin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X04581; CAA28449.1; --

R EMBL; X04581; CAA28449.1; --

R EMBL; W10951; AAA294060.1; --

R EMBL; M17095; AAA29576.1; --

R ECOZDBASE; G095.0; 6TH EDITION.

R ECOZDBASE; G095.0; 6TH EDITION.

R ECOZDBASE; G095.0; 6TH EDITION.

R ECOZDBASE; PRO01483; Peptidase_M16.

R InterPro; IPR001431; Peptidase_M16.

R Pfam; PF00193; Peptidase_M16.

R Pfam; PF00193; Peptidase_M16.

R Pfam; PF00193; Peptidase_M16.

R Hydrolase; Machlloprotease; Magnesium; Periplasmic; Zinc; Signal;
                                                                       Kushner S.R.;
the protease III (ptr) gene of
                                                                                                                                                                                                                                                                                                                                                                   MUTAGENESIS, AND ACTIVE SITE.
MEDLINE-93277449; PubMed-8099278;
Becker A.B., Roth R.A.;
"Identification of glutamate-169 as the third zinc-binding proteinase III, a member of the family of insulin-degrading
                                                                                                                                                                     MUTGENESIS, AND ACTIVE SITE.
MUTGENESIS, AND ACTIVE SITE.

BECKET A.B., Roth R.A.;

"An unusual active site identified in a family of zinc metalloendopeptidases.";

Proc. Natl. Acad. Sci. U.S.A. 89:3835-3839(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucagon.
-!-COTTOR: Binds 1 zinc ion per subunit.
-!-SUBUNT: Monomer.
-!- SUBCELLULAR LOCATION: Periplasmic.
-!- SIMILARITY: Belongs to peptidase family M16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEASE III
                                          MEDILINE=888065781; PubMed=3308636;
Claverie-Martin F., Diaz-Torres M.R.,
"Analysis of the regulatory region of
Escherichia coli K-12.";
Gene 54:185-195(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107708 MW;
SEQUENCE OF 1-296 FROM N.A.
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1 693
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169
204
277
962 AA;
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SIGNAL
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METAL
METAL
METAL
MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIR=TY2 / Arcc 700931;
STRAIR=TY2 / Arcc 700931;
MEDLINE=25531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ". Bacteriol, 185:2330-2337(2003).
-!- FUNCTION: Endopeptidase that degrades small peptides of less than 7 kDa, such as glucagon and insulin (By similarity).
-!- CATALYITA ACTIVITY: Preferential cleavage of 16-Tyr-|-Leu-17 and 25-Phe-|-Tyr-26 bonds of oxidized insulin B chain. Also acts on other substrates of Mw less than 7 kDa such as insulin and
                                                                                                    Gaps
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Enterobacteriaceae; Salmonella,
NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Bel. 42, Last annotation update)
Procease III precursor (BC 3.4.24.255) (Pitrilysin) (Protease pi).
PTRA OR PTR OR STY3133 OR T2903.
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--- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
---- SUBUNIT: Monomer (By similarity).
---- SUBCELLULAR LOCATION: Periplasmic (By similarity).
---- SIMILARITY: Belongs to peptidase family M16.
                         Score 39; DB 1; Length 962;
Pred. No. 26;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        962 AA.
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InterPro; IPR001431; Peptidase_MI6.
InterPro; IPR001431; Peptidase_MI6_C.
Pfam; PF00675; Peptidase_MI6, I.
Pfam; PF05193; Peptidase_MI6, I.
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MEDLINE=21534947; PubMed=11677608;
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                                57.4%;
Query Match
Best Local Similarity 70.v.
Thes 7; Conservative
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                                                                                                                                                                                                                                   124 PYRTAFYLEV 133
                                                                                                                                                                     4 PYRTSRYLEL 13
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STRAIN=LT2 / SGSC1412 / ATCC 700720;

MIDDLINE=21534948; PubMed=11677609;

MEDLINE=21534948; PubMed=11677609;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 413:852-856(2001).

-!- FUNCTION: Endopeptidase that degrades small peptides of less than '-!- FUNCTION: Endopeptidase that degrades smallarity).

7 KDa, such as glucagon and insulin (By similarity).

-!- CATALYTIC ACTIVITY: Preferential cleavage of 16-Tyr-|-Leu-17 and 25-Phe-|-Tyr-26 bonds of oxidized insulin B chain. Also acts on other substrates of Mw less than 7 KDa such as insulin and
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protase III precursor (EC 3.4.24.55) (Pitrilysin) (Protease pi).
PTRA OR PTR OR STM2995.
Salmonellat typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AE008837; AAL21871.1; -.
Stydene; SG7277?; ptrA.
InterPro; IPR00143; peptidase_M16.
InterPro; IPR007863; Peptidase_M16_C.
Pfam; PF00675; Peptidase_M16; \overline{1}.
Pfam; PF005193; Peptidase_M16_C; 2.
PROSITE; PS00143; INSULTARSE; 1.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
PROSITE; PS00143; INSULINASE; FALSE NEG.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glucagon.
COFACTOR: Binds 1 zinc ion per subunit (By similarity).
                                                                                                                                                                                                             57.4%; Score 39; DB 1; Length 962; 70.0%; Pred. No. 26;
                                                        23 BY SIMILARITY.
962 PROTEASE III.
88 ZINC (BY SIMILARITY).
91 ZINC (BY SIMILARITY).
92 ZINC (BY SIMILARITY).
169 ZINC (BY SIMILARITY).
107524 MW; 5745C2C77F7F5832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
-!- SIMILARITY: Belongs to peptidase family M16.
                                                                                                                                                                                                                                                                                                                                                                                                                           962 AA
                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                             Local Similarity 70.0
                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                            124 PYRTAFYLEV 133
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                                                                            24 9
88 91
91 92
169 1
                                          Complete proteome.
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                                                                                                                ACT SITE
METAL
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                                                          SIGNAL
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PTRA SALTY
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      SPETER
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Complete proteome.

InterPro; IPR001431; Peptidase M16.
InterPro; IPR007863; Peptidase M16\_C.
Pfam; PF00675; Peptidase M16, 1.
Pfam; PF05193; Peptidase M16, 2.
PROSTIE; PS00143; INDIANSE; 1.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;

Complete proteome

SIGNAL

CHAIN

EMBL; AE016987; AAP18144.1;

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Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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STRAIN=2457T / ATC 700930 / Serctype 2a;
MEDLINE=22590274; PubMed=12704152;
MEDLINE=22590274; PubMed=12704152;
MEDLINE=22590274; PubMed=12704152;
A Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
A Wei J., Goldberg M.B., Purland V., Venkatesan M.M., Deng W.,
A Mau B., Perran N.T., Paynes S.M., Runyen-Janecky L.J., Zhou S.,
A Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of Shigella
I lexner; serctype 2a strain 2457T";
Infect. Immun. 71:2775-2786(2003):
Infect. Immun. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=301 / Serctype 2a, MEDLINE=22272406; PubMed=12384590; MEDLINE=22272406; PubMed=12384590; Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteòbacteria; Gammaproteòbacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Proctease III precursor (EC 3.4.24.55) (Pitrilysin) (Protease pi).
PTRA OR PTR OR SF2832 OR S3029.
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1 23 BY SIMILARITY.
24 962 PROTRAGE II.
88 2INC (BY SIMILARITY).
91 91 BY SIMILARITY.
92 92 ZINC (BY SIMILARITY).
169 169 ZINC (BY SIMILARITY).
169 2ZINC (BY SIMILARITY).
169 2ZINC (BY SIMILARITY).
962 AA, 107486 MW, 322ADGE87B873952 CRC64;
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||: |||:
124 PYRTAFYLEV 133
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   SIGNAL
CHAIN
METAL
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Gaps

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57.4%; Score 39; DB 1; Length 962; 70.0%; Pred. No. 26; tive 2; Mismatches 1; Indels

1 23 BY SIMILARITY.
24 962 PROTEASE III.
88 88 ZINC (BY SIMILARITY).
91 91 BY SIMILARITY.
92 92 ZINC (BY SIMILARITY).
169 169 ZINC (BY SIMILARITY).
962 AA, 107770 MM; 662041A5DCAOF254 CRC64;

METAL ACT SITE METAL METAL SEQUENCE

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STRAIN=Liverpool; TISSUE=Fat body;
STRAIN=Liverpool; TISSUE=Fat body;
MEDLINE=99124369; PubMed=9927179;
Lowenberger C.A., Smartt C.T., Bulet P., Ferdig M.T., Severson D.W.,
Tioffmann J.A., Christensen B.M.;
"Insect immunity: molecular cloning, expression, and characterization
of CONAs and genomic DNA encoding three isoforms of insect defensin in
Aedes aegypti.";
Linsect MOI. Biol. 8:107-118(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -: SUBCELLULAR LOCATION: Secreted.
-: TISSUB SPECIFICITY: Hemolymph.
-: DEVELOPMENTAL STAGE: Expressed 30 minutes after infection and remained present through to 21 days. Expressed in white or callow pupae during metamorphosis, but no expression was seen in larvae.
-: INDUCTION: By bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, INDUCTION, AND SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Liverpool; PubMed=7633471; Hetru C., Hodgeman B., Inverberger C., Bulet P., Charlet M., Hetru C., Hodgeman B., Christensen B.M., Hoffmann J.A.; Christensen B.M., Hoffmann J.A.; Insect immunity: isolation of three novel inducible antibacterial defensins from the vector mosquito, Aedes aegypti."; Insect Biochem. Mol. Biol. 25:867-873 (1995).
                                                                                    DEFC AEDAE STANDARD; PRT; 99 AA.
P81603; Q9Y0F0; Q9Y0F1;
P81603; Q9Y0F0; Q9Y0F1;
P81603; Q9Y0F0; Q9Y0F1;
13 - 0AT-2010 (Rel. 40, Last sequence update)
10 - 0CT-2003 (Rel. 42, Last annotation update)
Defensin C precursor.
Aedes aegypti (Yellowfever mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 60-99, AND INDUCTION.
                     ||||: |||:
124 PYRTAFYLEV 133
4 PYRTSRYLEL 13
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                                                                                    RESULT 8
DEFC_AEDAE
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EMBL; AE015297; AAN44319.1; -

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         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                    EMBL; Z48809; CAA88746.2; -. PIR; T24300; T24300.
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D87907; BAA22062.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrococcus kodakaraensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                           172 IKPYRLSRHL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   2 VRPYRTSRYL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || |||:||
501 YRLSRYIEL 509
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=69014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=KOD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYRKO
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MALQ_PYRKO
ID MALQ_P
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                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                          and C2.
-!- SIMILARITY: Belongs to the arthropod defensin family. Subfamily 1.
POLYMORPHISM: There are two defensin C isoforms, Cl (shown here)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Durbin R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-!- SIMILARITY: Belongs to the S14P family of ribosomal proteins.
                                                                                                                                                                                                                                                          EMBL; AF156092; AAD40116.2; -.

REMIL; AF156093; AAD40117.2; -.

RESP; 10891; 11CA.

RICEPTO; IPRO1642; Defensin_anpod.

IN therPro; IPRO1644; Knot1.

REMIL; SM01097; Arthro defensin; 1.

REMIL; SM01097; Arthro defensin; 1.

REMIL; SM01097; ARTHROPOD DEFENSINS; 1.

REMIL; PRO1719; ARTHROPOD DEFENSINS; 1.

REMIL; AND SM11; ARTHROPOD DEFENSINS; 1.

REMIL; SM01045; ARTHROPOD DEFENSINS; 1.
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Pred. No. 3.3;
1; Mismatches 4; Indels
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Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G -> E (IN ISOFORM C2).
P -> S (IN ISOFORM C2).
R -> G (IN REF. 2 AND 3).
A -> S (IN REF. 2 AND 3).
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Putative mitochondrial 40s ribosomal protein S14.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
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P49391;
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RT14_CAEEL
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                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                  Score 38, DB 1, Length 199;
Pred. No. 7.2;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.9%; Score 38; DB 1; Length 653; llarity 77.8%; Pred. No. 27; Conservative 1; Mismatches 1; Indels
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Pagn; PF03065; Glyco_hydro_57; 1.

Transferase; GlycosyLransFerase; Carbohydrate metabolism.

SEQUENCE 653 AA; 76664 WW; B0C4695613F29219 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
4-alpha-glucanotransferase (EC 2.4.1.25) (Amylomaltase)
(Disproportionating enzyme) (D-enzyme).
                                                                                                                                                      23414 MW; 2CC0021A618BCFF0 CRC64;
WormPep; T01E8.6; CE32923.
InterPro, IPR001209; Ribosomal S14.
Pfour; PF00253; Ribosomal S14; 1.
PROSITE; PS00527; RIBOSOMAL S14; FALSE_NEG.
Ribosomal protein; Mitochondrion.
SEQUENCE 199 AA; 23414 MW; 2CC0021A61BBC
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3503 AA.

Tue Oct 5 09:51:31 2004

C 24-25-2003 (Red. 14.) Created)
Dr. 13-FEB-2003 (Red. 14.) Least sequence update)
Dr. 13-FEB-20

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EMBL; 109811; AA479329.2;

DR RMBL; 109811; AA479329.2;

DR FUNDARS & AAF51468.3; ALT_INIT.

BR F104826; P15116; 1NCJ.

BR G0; GO:0005887; C:integral to plasma membrane, ISS.

BR G0; GO:0008283; P:calliun-dependent cell adhesion molecule ac. . .; ISS.

BR G0; GO:0008283; P:calliun-dependent cell adhesion, ISS.

BR G0; GO:0008283; P:calliun-morphogenesis during differentiation; IMP.

BR G0; GO:0045189; P:establishment of epithelial cell polarity; IMP.

BR G0; GO:0045189; P:establishment of cepithelial cell polarity; IMP.

BR G0; GO:0045189; P:establishment of cepithelial cell polarity; IMP.

BR G0; GO:0018149; P:eddherin.

BR G0; GO:0018149; Cadherin.

BR FRINTS: PRO0020; Cadherin.

BR FRANTS: PRO0020; CADHERIN 1. 20.

BR PROSITE; PSC0228; CADHERIN 1. 20.

BR ROSITE; PSC0289; CADHERIN 1. 20.

BR PROSITE; PSC0289; PSC02
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                                                                                                                                                                systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
-!- FUNCTION: Involved in morphogenesis. May also be involved in cell
                                                                                                                                                                                                                                                                                adhesion.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- TISSUE SPECIFICITY: Expressed in embryonic ectoderm. In larvae, expression is restricted to imaginal disks and brain.
-!- DEVELOPMENTAL STAGE: Expressed throughout embryogenesis where it is first detected during gastrulation. Also expressed in larvae
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.,
                                                                                                                       ๙
                                                                                          Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and adults.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 6.
CADHERIN 6.
CADHERIN 7.
CADHERIN 9.
CADHERIN 11.
CADHERIN 11.
CADHERIN 12.
CADHERIN 12.
CADHERIN 14.
CADHERIN 16.
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CADHERIN 16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-86013616; pubMed=3862932;

MEDLINE-860136168; pubMed=3862932;

Schnitz J., Faist G.;

"Comparative studies on the structural gene for the ribosomal protein S1 in ten bacterial species ";

MOI. Gen. Genet. 200:476-481(1985).

INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT SHINE-DAGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).

-!- SIMILARITY: Belongs to the S1P family of ribosomal proteins.
-!- SIMILARITY: Contains 5 S1 motif domains.
Pfam; PF05746; tRNA-synt_id_C; 1.
PRINTS; PR01038; TRNASYNTHARG.
TIGRPAMs; TIGR00456; argS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete proteome.
147 157 "HIGH" врагом
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Providencia.
                                                                                                                                                                                                                                                      54.4%; Score 37; DB 1; Length 620; 50.0%; Pred. No. 39; ive 4; Mismatches 2; Indels
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S1 NOTIF 2.
S1 NOTIF 3.
S1 NOTIF 4.
S1 NOTIF 5.
                                                                                                                                                                           157 "HIGH" REGION.
67206 MW; F51C3COC8CD9AB06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01.JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnoration update)
30S ribosomal protein S1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribosomal protein; Repeat; RNA-binding.
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HSSP; P05055; 1SRO.
InterPro; IPR008994; Nucleic acid OB.
InterPro; IPR00110; Ribosomal_S1.
InterPro; IPR003129; S1.
Pfam; PP00575; S1; 5.
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SMART; SM00316; S1, 4.
PROSITE; PS50126; S1; 5.
                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.v.
6; Conservative
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534 DRQPHKVARYLE 545
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                                                                                                                                                                                                    SEQUENCE 620 AA;
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259
346
378 AA;
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Best Local Similarity
Matches 7; Conserv
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P14128;
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SEQUENCE
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                        S T X X X X Y S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYR BIFLO STANDARD; PRT; 620 AA.
08G4V2.
10G4V2.
115-MAR-2004 (Rel. 43, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
Bifldobacterium longum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.9%; Score 38; DB 1; Length 3503; 60.0%; Pred. No. 1.7e+02; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     975B09F059F7EEF5 CRC64;
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7 -> 5 (IN REF.

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             CADHERIN 23.
CADHERIN 24.
CADHERIN 25.
CADHERIN 26.
CADHERIN 27.
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InterPro; IPR01278; Arg_tRNA-synt_lc.
InterPro; IPR005148; N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro; IPR008909; tRNA-synt_1d_C.
nterPro; IPR001412; tRNA-synt_I.
nterPro; IPR009080; tRNAsyn_1a_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                        379774 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF03485; N-Arg; 1.
PF00750; tRNA-synt_ld; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE014754; AAN25073.1; -.
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                                                                                                                       3028
1070
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11692 169
2029 2020
2210 221
2289 228
2836 283
2853 283
3038 3038
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HID DE REAL PROPERTIES OF THE PROPERTIES OF THE

Gaps .. 0 52.9%; Score 36; DB 1; Length 378; ilarity 58.3%; Pred. No. 34; Conservative 2; Mismatches 3; Indels

0

42709 MW; E0FD2A96E97E5D81 CRC64;

396 AA;

SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

A STRAIN=ATCC 15692 / PAO1;

A STRAIN=ATCC 15692 / PAO1

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

A Garber R.L., Golltry L., Tolentino E., Westbrock-Wadnan S., Yuan Y.,

B Prody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saler M.H., Hancock R.B.W., Lory S., Olson M.V.;

Reizer J., Saler M.H., Hancock R.B.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen."

I PODF STRAINS CATALYSE The overall synthetic reaction is composed of two sequential steps, AdoMet formation and the subsequent

two sequential steps, AdoMet formation and the subsequent

two sequential steps, AdoMet formation in to release of

AdoMet Erom the enzyme (By similarity).

C GATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +

AdoMet Erom the enzyme (By similarity).

C GATALYTIC ACTIVITY: ATP + L-methionine as amagnesium or cobalt, and

I potassium ion per subunit (By similarity).

LI PATHWAY: Activated methyl cycle.

LI STBELDIAR LOCATION: Cytoplasmic.

STBELLIAR LOCATION: Cytoplasmic.

SIMILARITY: Belongs to the AdoMet synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.
PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.
Transferase; One-carbon metabolism; ATP-binding; Magnesium; Potassium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
5-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine adenosylrransferase) (AdoMet synthetase) (MaT).
METK OR PA0546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAGNESIUM (BY SIMILARITY)
POTASSIUM (BY SIMILARITY)
POTASSIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
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HAMAP, MF 00086; -; InterPro; IRR002133; S-AdoMet_synt.
Pfam; PF00438; S-AdoMet_synt; 1.
Pfam; PF02772; S-AdoMet_syntD2; 1.
Pfam; PF02773; S-AdoMet_syntD2; 1.
TIGRFAM9; TIGR01034; meTK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteome.
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                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
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NP BIND 261 268
METAL 18 18
METAL 265 265
                                         ||||| | : :||
DVRPVRDTTHLE 43
                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=287;
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                                                                                                                                                                         RESULT 14
METK_PSEAE
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[2] SEGIBNCE FROM N.A. STRAIN-K12 / MG1655; SEGIBNS E. COll; STRAIN-K12 / MG1655; Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M., Chung E., Allen E., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Rederspiel N., Pyman R., Kalman S., Kohramm S., Davis R.W.; Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-E.coli, STRAIN-K12;
SPECIES-E.coli, STRAIN-K12;
MEDILNE-97061202; PubMed=8905232;
MEDILNE-97061202; PubMed=8905232;
Sinima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12-728.0 min region on the linkage map.";
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Griegor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-77 FROM N.A.

SEQUENCE SECOLI, STRAIN=B,

MEDINE=95113294; PubMed=7813889;

Michael N.P., Brehm J.K., Anlezark G.M., Minton N.P.;

Michael N.P., Brehm J.K., Anlezark G.M., Minton N.P.;

michael nord characterisation of the Escherichia coli B gene encoding nitroreductase and its over-expression in Escherichia coli K12.";

FEMS Microbiol. Lett. 124:195-202(1994).
                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jin Q., Yuan Z., Xu J., Wang Y., Shen X., Lu W., Wang J., Liu H.,
                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
 Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-12 FROM N.A.
SPECTES=E.coli; STRAIN=K12 / C600;
Zenno S., Koike H., Tanoka M., Saigo K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
DB 1;
36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES=S.flexneri, STRAIN=301 / Serotype 2a,
MEDLINE=22272406, PubMed=12384590;
                                                                                                                                                                                                                        939455; P77602;
01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 32, Last sequence update)
Hypothetical protein ybdG.
YBDG OR B0577 OR SF0483 OR S0492.
                                       Mismatches
   Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae; Escherichia
52.9%;
                                                                                                              336 DLRPYAITKMLDL 348
                                                                           1 DVRPYRTSRYLEL 13
                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                        Escherichia coli, and Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=562, 623;
   Query Match
Best Local Similarity
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                                         Matches
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us-09-805-290a-9.rsp

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                                                                                                                             "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."; Nucleic Acids Res. 30:4432-4441(2002).
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                 MEDIJIRE=22590274; PubMed=12704152; Mei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Darling A., Fournier G., Maylew G.F., Plunkett G. III, Rose D.J., Darling A., Schwartz D.C., Blattner F.R., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T."

Infect. Immun. 71:2775-2786(2003):
-! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.9%; Score 36; DB 1; Length 415; Best Local Similarity 50.0%; Pred. No. 38; Matches 6; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; Transmembrane; Complete proteome.
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C9A8A8A41CDC8F28 CRC64;
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; AE015080; AAAP12134.1; ALT_INIT.
; AE016979; AAP16008.1; -. G64790; G64790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; G64790; G64790.
EcoGene; EG12620; ybdG.
Interpro; IPR006685; MSion_channel.
Pfam; PF00241; MS_channel, 1.
Hypothetical protein; Transmembrane
TRANSMEM 25 45
POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AE000163; AAC73678.1; -. SEMBL, 108258; AAB40775.1; -. EMBL; D90700; BAS5217.1; -. EMBL; U07860; AAC43265.1; -.
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TRANSMEM
SEQUENCE
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SMBL;
SMBL;
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Search completed: October 5, 2004, 08:01:38 Job time: 2.16358 secs ::|| |||: |: 291 LKPYLTSRHQEI 302 Db

2 VRPYRTSRYLEL 13

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Gaps

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5, 2004, 07:34:11; Search time 6.88117 Seconds (without alignments) 596.081 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                            1017041 segs, 315518202 residues
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                                                       OM protein - protein search, using sw model
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sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_organelle:*
sp_phage:*
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sp bacteria:*
sp fungi:*
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Maximum DB seq length: 200000000
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68
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Q81aq8 arabidopsis Q8CON9 mus musculu Q7wqs bordetella Q7wqso bordetella Q7siy9 arabidopsis Q8x972 escherichia Q8x972 escherichia Q8x973 escherichia Q8x973 ercherichia Q8x974 artus norv Q91ul arabidopsis Q91ul arabidopsis Q9yhel brachydanio Q7wz84 nonomuraea Q2938 lolligo opal Q80652 arabidopsis Q9mlk7 arabidopsis Description SUMMARIES Q8C00 Q7WGG8 Q7W4Z0 Q9X1Y9 Q8X972 Q8U8Y6 Q35390 Q9LTU1 Q5Z001 Q25368 O80652 Q9M1K7 P91590 09YHE1 Q7WZ84 四 Length 217 258 303 Query Score Result No. 

| |:| |||:| DTHPHRMSRYIQL 109 1 DVRPYRTSRYLEL 13

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Q8tgz6 methanopyru	Q803r3 brachydanio	Q87bj7 xylella fas	Q8p8p5 xanthomonas	Q8pk77 xanthomonas	Q9paq7 xylella fas	Q84sf5 oryza sativ	Q7uw68 rhodopirell	Q89ab5 buchnera ap	Q9h9d2 homo sapien	Q9n575 caenorhabdi	Q92ru9 rhizobium m	Q7z3v7 homo sapien	Q971f2 clostridium	Q9jtu5 neisseria m	Q8pf48 xanthomonas	Q9t9h4 halocynthia	Q9vjy1 drosophila	Q8mz99 drosophila	Q82py4 streptomyce	054583 halobacteri	Q83fn0 tropheryma	Q974n2 sulfolobus	001792 caenorhabdi	Q8y294 ralstonia s	P93797 volvox cart	Q8imf0 drosophila	Q8g4v2 bifidobacte	Q9fn94 arabidopsis
Q8TGZ6	Q803R3	Q87BJ7	Q8P8P5	Q8PK77	Q9PAQ7	Q84SF5	Q7UW68	Q89AB5	Ф3Н9D2	Q9N575	Q92RU9	Q7Z3V7	Q97LF2	Q9JTUS	Q8PF48	Q9T9H4	Q9VJY1	Q8MZ99	Q82PY4	054583	Q83 FN0	Q974N2	001792	Q8Y294	P93797.	QBIMFO	Q8G4V2	Q9FN94
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57.4	57.4	57.4	57.4	57.4	57.4	57.4	55.9	55.9	55.9	55.9	55.9	55.9	55.9	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4
39	ن 9	39	39	39	39	39	38	38	38	38	38	38	38	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

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                                                Manages, 01-0CT-2002 (TrEMBLrel. 22, Created) 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 01-0CT-2002 (TrEMBLrel. 23, Last sequence update) 01-0CT-2003 (TrEMBLrel. 23, Last amoutation update) Hypothetical protein. Arabidopsis thaliana (Mouse-ear cress). Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.2%; Score 43; DB 10; Length 272; 53.8%; Pred. No. 8.2; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell
Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                          "Full-Length cDNA from Arabidopsis thaliana.";
submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY08971, AAM65208.1; -.
InterPro; IPR005162; Retrotrans_gag.
Pfam; PF03732; Retrotrans_gag; I.
Hypothetical protein.
SEQUENCE 272 AA; 30811 MW; 9C889BD760029D09 CRC64;
                                   PRT;
                                                                                                                                                                                                                                                                                                                       annotation.";
Genome Biol. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                   PRELIMINARY;
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Best Local Similarity
Matches 7; Conserv
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                                   Q8LAQ8
RESULT 1
Q8LAQ8
ID Q8LA
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Gaps

Q8C0N9

RESULT 2 Q8C0N9

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Bacteria; Profeobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 322;
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Indels
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Last sequence update)
Last annotation update)
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61.5%; Pred. No. 23;
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1, Mismatches
Mismatches
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EMBL; BX640433; CAE38800.1; -.
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                                                                  170 DVTPYRTDRLVAL 182
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Best Local Similarity 61...
8; Conservative
                                   1 DVRPYRTSRYLEL 13
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8; Conservative
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SEOUENCE 322 AA
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Matches
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In School S. Sanders M., Skelton J., Squares C., Bordetella pertussis, Mat. Genet. 35:30-40(2003).

REMBI, Bx640449; CAB34314.1; -.

W Complete proteome.

SEQUENCE 322 AA; 34669 MW; F6072C095666D3E6 CRC64;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIR=CS7BL/6J; TISSUE=Testis;
STRAIR=CS7BL/6J; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Nature 420:563-573 (2002).
Nature 420:563-573 (2002).
BMBL; ARG30414; BAC26805.1; -.
MGD; MGI:24444484; 4932703102Rik.
SEQUENCE 462 AA; 53199 MW; SEA81B9C5075E684 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2003 (TrEMBLrel. 25, Created)
1-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative transcriptional regulator.
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 AA
                                                                          462 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                          PRT;
                                                                                                                                                               Endo-alpha-D-mannosidase homolog.
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ilarity 61.5%;
Conservative
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                                                                          PRELIMINARY;
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Best Local Similarity
8; Conserve
                                                                                                                                                                                                    Mus musculus (Mouse)
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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01-MAR-2003
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Q7WGG8

RESULT 3

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Query Match

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 22827954; PubMed=12910271;

A Parkin! J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

A Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norbercak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,

A Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

A Unwin L., Whitehead S., Barrell B., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

"A Good of the standing of the genome sequences of Bordetella pertussis,

"A Maskell Baragertussis and Bordetella bronchiseptica.";
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STRAIN=CV. COlumbia;
STRAIN=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Fujii C.Y., Mason T.M., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Buell C.R., Kecchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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InterPro, IPR002104; Phage_integrase.
Pfam; PF00589; Phage_integrass; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 441 AA; 51923 MW; 788EE55CS8CD670D CRC64;
                                                                                Query Match
Best Local Similarity
Matches 8, Conserv
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STRAIN-C157.H7 / FINDD 0509952;

RATIN-C157.H7 / FINDD E., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

I ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

EMBL; AR005493; AAG57756.1;

EMBL; AR005493; AAG57756.1;

EMBL; AR005403; BAB36934.1; ALT_INIT.

PIR, H85911; H85911.

RO, GO:0005317; FINA binding; IEA.

GO; GO:0003377; FINA hinegration; IEA.

RO; GO:0005310; F:DNA integration; IEA.
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SEQUENCE FROM N.A.

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rosfai G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Melon R.A., Blattner F.R.;

"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";

Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
Copenhaver G.P., Freuss D., Nierman W.C., White O., Bisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana.";
                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                     Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC007020; AAD25679.1; -.
PIR; B84828; B64828; WAD25679.1; -.
PIR; B84828; B64828; WD40.
Pfam; PF0440; WD40; 4.
SWART; SM00320; WD40; 4.
PROSITE; PS0682; WD_REPEATS 1; 1.
PROSITE; PS0682; WD_REPEATS 2; 1.
PROSITE; PS0692; WD_REPEATS 2; 1.
PROSITE; PS0694; WD_REPEATS 3; 1.
                                                                                                                                                                                                                                                                                                              60.3%; Score 41; DB 10; Length 775; 66.7%; Pred. No. 59; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein 23943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 AA
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Best Local Similarity 66.,
Best Local Similarity 67.,
And 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       429 DLRPYPNSCYLE 440
                                                                      Nature 402:761-768(1999)
                                                                                                                                                                                                                                                                                                                                                                          1 DVRPYRTSRYLE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                              Lin X.;
Submitted (MAR-2000) to
                                                                                                 SEQUENCE FROM N.A. STRAIN=cv. Columbia;
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Q8X972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21608550; PubMed=11743193; Wonks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Woo L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clandenning J., Deatherage G., Gillet W., Grant C., Rutyavin T., Levy R., Li M. J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Kreepson W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                Gaps
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58.8%; Score 40; DB 16; Length 441; 61.5%; Pred. No. 50; ative 2; Mismatches 3; Indels
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58.3%; Pred. No. 50; 3; Indels
tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agrobacterium Tumefaciens (strain CSB / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium
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01-07N-2002 (TrEMBLrel. 21, Last sequence update)
01-07T-2003 (TrEMBLrel. 25, Last annotation update)
0xidoreductase.
ATU3952 OR AGR_L_1801.
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EMBL; AE008268; AAK89474.1; -.
PIR; AB3042; AD3042.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR006076; Fad oxred.
PICAFPO: IPR006205; NAD BS.
PF01266; DAO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                    Conservative
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418 KPFQTSRYLD 427
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1 DVRPYRTS 8
                      10 DVRPYKTS 17
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Best Local Similarity
6, Conserva
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Ciona intestinalis.
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SEQUENCE FROM N.A.
Cariello L.;
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Q52001
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P91590
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MEDLINE=98030622; PubMed=9361017;
Spiro M.J., Bhoyroo V.D., Spiro R.G.;
Spiro M.J., Bhoyroo V.D., Spiro R.G.;
"Molecular cloning and expression of rat liver endo-alpha-mannosidase, an N-linked oligosaccharide processing enzyme.";
J. Biol. Chem. 272:29336-29336.1997).
EMBI, AF020657; AABB6525.1;
SEQUENCE 451 AA, 51671 MW; SA997EFD07585066 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC
                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota, Metazca, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S., Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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EMBL; AB024034; BAB02796.1; -.

InterPro; IPR003871; DUP223.

InterPro; IPR005994; Nucleic_acid_OB.

Ffam; PF02721; DUP223; 1.

SEQUENCE 581 AA; 64867 MW; 5BCB4DB5B0E006DC CRC64;
                                                                                               035390;
01-JAN-1998 (TrEWBLrel. 05, Created)
01-JAN-1998 (TrEWBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Endo-alpha-D-mannosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
10-0CT-2003 (TrEMBLrel. 15, Last annotation update)
Replication protein Al-like.
Arabidopsis thaliana (Mouse-ear cress).
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                                                                                   451 AA
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MEDLINE-20277480; PubMed=10819329;
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415 DYRPHKPSLYLEI 427
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                                                                                  PRELIMINARY;
        421 DPRPYRYSRFFD
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Best Local Similarity
Matches 7; Conservat
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Q9LTU1
                                                    RESULT 8
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Schwarz F.V., Perreten V., Teuber M.;
"Sequence of the 50-kb conjugative multiresistance plasmid pRE25 from Enterococcus faecalis RE25.";
Enterococcus faecalis RE25.";
EMBL, 61:170-187(2001).
EMBL, L39769; AAA99466.1; -.
EMBL, X92945; CAC29179.1; -.
GO; GO:0006821; Caxrachromosomal DNA; IEA.
Interpro; IPR005053; MobA_MobL.
Pfam; PF03389; MobA_MobL.
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MEDLINE=97330926; PubMed=9187361;
Cariallo L., Ristoratore F., Zanetti L.;
A new transglutaminase-like from the ascidian Ciona intestinalis.";
FEBS Lett. 408:171-176(1997).
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Phlebobranchia, Cionidae, Ciona.
NCBI_TaxID=7719;
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SPECIES-Streptococcus sp.; STRAIN=PVA1702; PLASMID=pIP501;
MEDLINE=95362640; PubMed=7635806;
MEDLINE=95362640; PubMed=7635806;
MEDLINE=95362640; PubMed=7635806;
"Streptococcal plasmid plP501 has a functional oriT site.";
J. Bacteriol. 177:4199-4206(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 654;
                                                                                                                                                                               Streptococcus sp., and Streptococcus faecalis).
Entercoccus faecalis (Streptococcus faecalis).
Plaemid pIP501, and Plasmid pRE25.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                  01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES=E.faecalis; STRAIN=RE25; FLASMID=pRE25;
PubMed=11735367;
654 AA
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                                                         Created)
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PRT;
                                                      01-NOV-1996 (TrEMBLrel. 01,
PRELIMINARY;
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Local Similarity
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Kral L.G., Cornwell J.R. Jr., Barron C.S. III, Marty S.;
Intracellular protein tyrosine phosphatases expressed in zebrafish embryos: New members of PTP-1B and PTP-MEGI related protein tyrosine phosphatase sub-families.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR091483; AAC97944.1; -.
HSSP; P18031; 1PTV.
GO; GO:0004727; F:prorylated protein tyrosine phosphatase act. .; IEA.
GO; GO:0004727; F:prorylated protein tyrosine phosphatase act. .; IEA.
GO; GO:0006470; F:protein amino acid dephosphorylation; IEA.
InterPro; IRRO02242; Tyr_PP.
PRIMTS; PR00700; PRTYPHHASE.
PROSITE; PS50055; TYR_PHOSPHATASE_PPP; 1.
                                                                                                                                                                                                                                                                                                                                Gaps
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Protein tyrosine phosphatase 1B (EC 3.1.3.48) (Fragment).
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi; Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes, Cyprinidae; Danio.
NCBI_TAXID=7955;
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                                                                                                                                                                                                                                                                                 58.8%; Score 40; DB 5; Length 766; 77.8%; Pred. No. 89; 1.1ve 2; Mismatches 0; Indels
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(SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                         87194 MW; 7F90D921D87FDD1D CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative VanY-type carboxypeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 AA.
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                                                      InterPro; IPR001102; GlutransfG.
InterPro; IPR001102; Ig-like.
InterPro; IPR001101; Ig-like.
InterPro; IPR000918; Transglut.C.
InterPro; IPR000931; Transglutamin.C; I.
Pfam; PF00668; Transglutamin.N; 1.
Pfam; PF01841; Transglut.core; 1.
SMART; SM00460; TGC; 1.
SEQUENCE 766 AA; 87194 MW; 7F90D921D8
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                EMBL; Y10212; CAA71263.1; -. HSSP; P00488; 1GGU.
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                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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732 EVRPYRSSR 740
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Best Local Similarity
Local 8; Conserve
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NON TER
SEQUENCE
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Q9YHE1
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                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ATCC 3972;
STRAIN=ATCC 3972;
Sosio M., Stinchi S., Beltrametti F., Lazzarini A., Donadio S.;
The gene cluster for the biosynthesis of the glycopeptide antibiotic A40926 by Noncmuraea sp.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ561198; CAD91202.1;
ACyltransferase; Carboxypeptidase; Glycosyltransferase; Moncoxygenase.
SEQUENCE 196 AA; 22157 MW; 003AA44D19127982 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota, Metazoa, Mollusca; Cephalopoda, Coleoidea, Neocoleoidea,
Decapodiformes, Loliginidae, Loligo.
NCBI_TaxID=31211;
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Nonomuraea sp. ATCC 39727.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptosporangineae, Streptosporangiaceae, Nonomuraea.
NCBI_TaxID=93944;
                                                                                                                                                                                                                                                                                                                                                                            57.4%; Score 39; DB 2; Length 196; ilarity 58.3%; Pred. No. 33; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q25368;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomarev S.I., Chung S., Piatigorsky J.;
"Glutathione S-transferase and S-crystallins of ce from active enzyme to lens-refractive proteins.";
J. Mol. Bvol. 41:1048-1056(1995).
EMBL U19300; AAA97551.1;
HSSP; P46088; 2GSQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.4%; Score 39; DB 5; 50.0%; Pred. No. 36;
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InterPro; IPR004045; GST_Nterm.
InterPro; IPR003083; Scrystallin.
Pfam; PF00043; GST_C; I.
Pfam; PF02798; GST_C; I.
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MEDLINE=96139039; PubMed=8587103;
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SEQUENCE 217 AA; 26113 MW;
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Best Local Similarity
6; Conserv?
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us-09-805-290a-9.rspt

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STRAIN=cv. Columbia;
Federapiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,
Federapiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,
Au M., Araujo R., Buehler E., Dewar K., Feng J., Kim C., Li Y.,
Oji O., Osborne B.I., Shinn P., Sun H., Toriumi M., Vysotskaia V.S.,
Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (ESP-1998) to the EMBL/GenBank/DDBJ databases.
BMBL, AC004266; AAC34353.1;
InterPro; PRR006502; DUF plant_1615.
PIR; TO0447; T00447.
InterPro; PRR006502; DUF plant_1615.
Ffam; PF04720; DUF506, 1.
ITGRFAMS; TIGR01615; A thal 3542; I.
SEQUENCE 258 AA; 29578 WW; FBC341434DFA6380 CRC64;
Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702;
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Search completed: October 5, 2004, 08:13:13 Job time : 8.88117 secs

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Gaps

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57.4%; Score 39; DB 10; Length 258; 66.7%; Pred. No. 44; tive 3; Mismatches 0; Indels

Query Match
Best Local Similarity 66.77
Matches 6; Conservative

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5, 2004, 07:04:10 ; Search time 9.89043 Seconds (without alignments) 371.381 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                         - protein search, using sw model
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1 DVRPYRTSRYLEL 13 US-09-805-290A-9 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* A Geneseq 29Jan04:\* .: geneseqp1980s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp1990s:\* geneseqp2004s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Description	Aae10541	Aae10554	4	Ŋ	Aae1054(	Aae10552	Aae10543	Aag06656	10		Abp7565		-44	Ade54766	549	Aag31529	2	152	8	Abu33563	9	Abu45234	Abu32202	Aau57763	Abm54283
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ID GI	AAE10541	AAE10554	AAE10542	AAE10559	AAE10540	AAE10552	AAE10543	AAG06656	AAG06655	AAG06654	ABP75655	AAB45097	ADC01045	ADE54766	ABP35493	AAG31529	AAG31528	AAG31527	ABB90986	ABU33563	ABU27962	ABU45234	ABU32202	AAU57763	ARM542R2
DB	4	4	4	4	4	4	4	٣	m	٣	9	٣	۲-	۲	'n	٣	٣	~	M	v	9	9	9	4,	ų
% Query Match Length	13	130	13	130	13	130	13	252	272	281	90	142	437	451	57	208	238	258	509	558	727	944	196	22	C.R.
% Query Match	100.0	100.0	97.1	97.1	95.6	92.6	94.1	63.2	63.2	63.2	60.3	58.8	58.8	58.8	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	55.9	55.9
Score	68	68	99	99	65	65	64	43	43	43	41	40	40	40	99	39	9	ტ ტ	თ რ	ው የ	39	33	39	38	38
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Aae04256 Human gen	Adc89474 Ribosomal	Aab45098 Human sec	Aam47969 Human end	Aab95204 Human pro	Ade54768 Human Pro	Aag79783 Carbohydr	Adb08478 Alloiococ	Aaw54870 Super hea	Aae26420 Human tra	Abb66499 Drosophil	Aaw87540 Peptide d	Abg24628 Novel hum		Abm59451 Propionib	Aay73330 HTRM clon	Dro	Adc94988 E. faeciu	Aaw87531 An antitu	Abp66018 Bifidobac
AAE04256	ADC89474	AAB45098	AAM47969	AAB95204	ADE54768	AAG79783	ADB08478	: AAW54870	AAE26420	ABB66499	: AAW87540	ABG24628	AAU62932	. ABM59451	. AAY73330	ABB70887	ADC94988	: AAW87531	ABP66018
9	٣	43	29	06	290 7	78	80			3503 4					0	54	91	9	20
55.9	55.9	55.9	55.9	55.9	55.9	55.9	55.9	55.9	55.9	55.9	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4
38	38	38	38	38	38	38	38	38	38	38	37	37	37	37	37	37	37	37	37
			53		. 31			34	35	36	37	38	6	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 AAE10541

AAE10541 standard; peptide; 13 AA.

AAE10541;

(first entry) 10-DEC-2001

Llama species antibody VHH CDR3 #10.

Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3. 

Lama

EP1134231-A1.

19-SEP-2001,

20-FEB-2001; 2001EP-00200703.

14-MAR-2000; 2000EP-00200930.

(UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.

Tareilus De Haard JJW, Σ Van De Burg Bezemer S,

ы,

WPI; 2001-572718/65.

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Disclosure; Page 17; 37pp; English.

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region

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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHE) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region
                                                                                                                                                                                                                                                                                                                                                                                 Llama antibody; camelid, anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
  Length 130;
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                                        Indels
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100.0%; Score 68; DB 4; I
100.0%; Pred. No. 6.8e-05;
                                      0; Mismatches
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Best Local Similarity 92.3
Matches 12; Conservative
                                          13; Conservative
                                                                                                                   DVRPYRTSRYLEL
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PLC.
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  Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Tabel = CDR1 | Tabel = "Complementarity determining region 1"
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|Jabel= CDR3
|note= "Complementarity determining region 3"
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                                                                  Length 13;
                                                                                                       Indels
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                                                              Score 68; DB 4; L
Pred. No. 5.3e-06;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                       AAE10554 standard; peptide; 130 AA.
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                                                              100.0%;
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label= CDR2
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                                                                                                         Conservative
                                                                                                                                                                           1 DVRPYRTSRYLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NV.
PLC.
                                          WPI; 2001-572718/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIL ) UNILEVER (UNIL ) UNILEVER
                         Sequence 13 AA;
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EP1134231-A1

Region

Lama

Region

Region

10-DEC-2001 AAE10554;

RESULT 2 AAE10554

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AAE10559 standard; peptide; 130 AA.

Seguence 130 AA;

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Region

Region

Region

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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody; camelid; anorectic; heavy chain variable domain; VHH; dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; human gastric lipase; HGL; cosmetic control; body weight.
                                                     Llama artibody, camelid, anorectic, heavy chain variable domain, VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPL inhibiting VHH fragment, HPL #12 from llama species
                                                                                                                                                                                                                                                                                                                                                                                                                       Tareilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65; DB 4;
Pred. No. 2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cocation/Qualifiers
                Llama species antibody VHH CDR3 #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 17; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE10552 standard; peptide; 130 AA.
                                                                                                                                                                                                                                                                               20-FEB-2001; 2001EP-00200703.
                                                                                                                                                                                                                                                                                                                   14-MAR-2000; 2000EP-00200930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.6%;
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/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                     Bezemer S, Van De Burg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DVRPYRTSRYLEL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
                                                                                                                                                                                                                                                                                                                                                         (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-572718/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13 AA;
                                                                                                                                                                                                 EP1134231-A1
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                                                                                                                                                             Lama sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                food;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #30 from llama (camelid) species
                                                                                                              Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                //abel= CDR3
/note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                  "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                              'note= "Complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 130;
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Pred. No. 0.00016;
                                                                              HPL inhibiting VHH fragment, HPL #30 from llama species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De Haard JJW, Tareilus E;
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 10; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-2001; 2001EP-00200703
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                                                                                                                                                                                                                                                              11. .35
'label= CDR1
                                                                                                                                                                                                                                                                                                                                        'label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van De Burg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVRPYRTSRYLEI 110
                                      (first entry)
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                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 130 AA
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Best Local Simi
Matches 12;
                                      10-DEC-2001
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Bezemer S,

AAE10540;

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06-APR-1999;
08-APR-1999;
16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                         The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #12 from lama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human panoreatic lipase; HGL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.
                                                                                                                                                                                                                     New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                    2
                                                  /note= "Complementarity determining region 3"
50. .64
/label= CDR2
/note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                               95.6%; Score 65; DB 4; Length 130; 92.3%; Pred. No. 0.00025; ive 1; Mismatches 0; Indels
                                                                                                                                                                               Tareilus
                                                                                                                                                                               Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
13
/label= Val, Leu, Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Llama species antibody VHH CDR3 #12
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                                                                                                                                                                                                                                                                        Example 2; Page 9; 37pp; English.
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                                                                                                           20-FEB-2001; 2001EP-00200703.
                                                                                                                              14-MAR-2000; 2000EP-00200930.
                            98. .110
/label= CDR3
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                                                                                                                                                                              Van De Burg
                                                                                                                                                                                                   WPI; 2001-572718/65.
                                                                                                                                                 (UNIL ) UNILEVER
                                                                                                                                                                                                                                                   of light chains
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 130 AA;
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                                                                                        .9-SEP-2001
                                                                                                                                                                                 Bezemer S,
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                             Region
  Region
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Matches
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region
                                                                                                                                                                                                                                                                                                                                           New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.1%; Score 64; DB 4; Length 13; 100.0%; Pred. No. 3e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                        Tareilus E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 3507.
                                                                                                                                                                                                                                        De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG06656 standard; protein; 252 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 29; 37pp; English.
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99US-0123180P.
99US-0123548P.
99US-0125788P.
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990S-0126785P.
990S-0127462P.
990S-0128234P.
99US-0128714P.
                                                                                                     14-MAR-2000; 2000EP-00200930.
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                                                                                                                                                                                                                                           Bezemer S, Van De Burg
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PLC.
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Best Local Similarity
                                                                                                                                                        (UNIL ) UNILEVER (UNIL ) UNILEVER
                                                                                                                                                                                                                                                                                                                                                                                                   heavy chain vair
of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13 AA;
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09-MAR-1999;
23-MAR-1999;
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19-SEP-2001
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PR 19-APR-1999, 99US-01304049P, PR 21-APR-1999, 99US-0130449P, PR 23-APR-1999, 99US-0130449P, PR 23-APR-1999, 99US-0130449P, PR 23-APR-1999, 99US-0130449P, PR 23-APR-1999, 99US-013248P, PR 30-APR-1999, 99US-013248P, PR 30-APR-1999, 99US-013248P, PR 30-APR-1999, 99US-013248P, PR 40-MAY-1999, 99US-013248P, PR 15-MAY-1999, 99US-013248P, PR 15-MAY-1999, 99US-013421P, PR 15-MAY-1999, 99US-013421P, PR 24-MAY-1999, 99US-013421P, PR 24-MAY-1999, 99US-013421P, PR 24-MAY-1999, 99US-013421P, PR 24-MAY-1999, 99US-013424P, PR 19-JUN-1999, 99US-013445P, PR 24-JUN-1999, 99US-013443P, PR 24-JUN-1999, 99US-013443P, PR 24-JUN-1999, 99US-013443P, PR 24-JUN-1999, 99US-013443P, PR 24-JUN-1999, 99US-0140823P, PR 24-JU
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PR 20-UUL-1999; 99US-0144335P.
PR 20-UUL-1999; 99US-0144335P.
PR 20-UUL-1999; 99US-0144814P.
PR 21-UUL-1999; 99US-0144814P.
PR 21-UUL-1999; 99US-0144814P.
PR 21-UUL-1999; 99US-0145084P.
PR 22-UUL-1999; 99US-0145084P.
PR 23-UUL-1999; 99US-0147045P.
PR 23-UUL-1999; 99US-0147041P.
PR 23-UUL-1999; 99US-0147049P.
PR 23-UUL-1999; 99US-0147041P.

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9905-0132466F

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9905-0134218P

9905-01342118P

9905-0134211P

9905-0134211P

9905-0134211P

9905-0134211P

9905-0135229P

9905-0135229P

9905-0135228P

9905-0137502P

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01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
07-JUN-1999;
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10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
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23-JUN-1
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Pred. No. 8.4;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                      AAG06655 standard; protein; 272 AA
9905-0159330P.
9905-0159331P.
9905-0159638P.
9905-0160761P.
9905-0160768P.
9905-0160768P.
9905-0160768P.
9905-0160815P.
9905-0160815P.
9905-016088P.
9905-016088P.
9905-016088P.
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99US-0161992P.
99US-0161993P.
99US-0162142P.
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9903-0123180P.
9903-0125784P.
9903-0126264P.
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9903-012874P.
9903-012874P.
9903-0130891P.
9903-0130891P.
9903-0130891P.
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53.8%;
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DTHPHRMSRYIQL 89
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                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.8
Matches 7; Conservative
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 14-0CT-1999
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09-MAR-1999;
23-MAR-1999;
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01-APR-1999;
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16-APR-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Best Local Similarity 53.8%; Pred. No. 9.1;
Matches 7; Conservative 3; Mismatches
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99US-0123180P.
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99US-0126745P.
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99US-0126744P.
99US-0138444P.
99US-0131444P.
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99US-016070P
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99US-01608114P
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| DTHPHRMSRYIQL 109
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                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
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05-MAR-1999;
23-MAR-1999;
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21-OCT-1999;
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99US-015130P.
99US-015130P.
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99US-0150538P.

04-0CT-1999 06-0CT-1999 08-0CT-1999 12-0CT-1999 13-0CT-1999 13-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 12-0CT-1999 12-0CT-1999 13-0CT-1999 13-0CT us-09-805-290a-9.rag

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Gaps

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New human secretory proteins and polynucleotides, useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell proliferations or
                                                                                                                                                                                                                                                                                                                                                                                                                             Human; SPTW, autoimmune disorder; inflammatory disorder; AIDS; anaemia; asthma; Crohn's disease; neurological disorder; epilepsy; cancer; Huntington's disease; Alzheimer's disease; Crettzfeldt-Jakob disease; multiple sclerosis; Parkinson's disease; cell proliferative disorder; anti-inflammatory; immunosuppressive; neuroprotective; notropic; neuroleptic; antianaemic; cytostatic; antiparkinsonian; anxiolytic; antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J; Dufour GB, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR; Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin Fperalta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B; Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 839; 458pp + Sequence Listing; English
                                                                                                                                                          Length 281;
                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Human secretory polypeptide SPTM SEQ ID NO 839.
                                                                                                                                                       Score 43; DB 3;
Pred. No. 9.5;
3; Mismatches 3
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                                                                                                                                                                                                                                                                                                                   ABP75655 standard; protein; 90 AA.
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29-MAR-2001, 2001US-0280068P.
16-MAY-2001, 2001US-0291280P.
17-MAY-2001, 2001US-0291849P.
19-UNN-2001, 2001US-0299428P.
20-JUN-2001, 2001US-0299476P.
99US-0161404F.
99US-016140GP.
99US-0161369P.
99US-0161360P.
99US-0161360P.
99US-0161360P.
99US-0161920P.
99US-0161928P.
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                                                                                                                                                        Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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DTHPHRMSRYIQL 118
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N-PSDB; ABZ36098.
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 25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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28-0CT-1999;
28-0CT-1999;
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The invention relates to a secretory polynucleotide (designated sptm)

Comprising any of 567 polynucleotide sequences (AB25837-AB258463), a

naturally occurring polynucleotide sequence at least 90 % identical to

the polynucleotide sequence, a polynucleotide complementary to them or an

End of the polynucleotide sequence at least 90 % identical to

RNA equivalent of them. The polypeptide or polynucleotide are useful for

End of the sexpression of functional SPPM. These are particularly useful for

the expression of functional SPPM. These are particularly useful for

the expression of functional SPPM. These are particularly useful for

the expression of functional SPPM. These are particularly useful for

the expression of functional SPPM. These are particularly useful for

diagnosing, treating or preventing autoimmune/inflammatory disorders

(e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's

disease), neurological disorders (e.g. epilepsy, Huntington's disease,

multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,

children or annesia), or cell proliferative disorders (e.g.

schizophrenia or annesia), or cell proliferative disorders (e.g.

leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,

breast, cervix or prostate). The present sequence dison

for this patent did not form part of the printed specification, but was

cobtained in electronic format directly from WIPO at

cut the properties of the invention compart of the printed specification, but was

cobtained in alectronic gequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein; human; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nocropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; vulnerary; gene therapy; treatment; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; cerebrovascular disorder; wound healing; epithelial cell proliferation; transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 6.4;
1; Mismatches
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07-JAN-2000; 2000US-0174852P.
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Best Local Similarity 66.7
Matches 8; Conservative
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sequence represents an E. coli 0157:H7-specific polypeptide of the

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This invention describes novel isolated nucleic acid molecules (I)
encoding a human secreted proteins (II) which have immunosuppressive,
antiatthritic, antirhemuatic, antiproliferative, cycostatic, cardiant,
vasotropic, cerebroprotective, nootropic, neuroprotective, antibacterial,
virucide, fungicide, ophthalmological and vulnerary activity and can be
used for gene therapy. (I) and (II) are used to prevent, treat or
used for gene therapy. (I) and (II) are used to prevent, treat or
used for gene therapy. (I) and (II) are used in be
used to prevent, treat or
diagnosing a pathological condition or susceptibility to a pathological
condition. The antibodies to (II) can also be used in
condition. The antibodies to (II) can also be used in alleviating
symptoms associated with the disorders and in diagnostic immunoassays
of symptoms associated with the disorders and in diagnostic immunoassays
is condition. The artibodies to (II) can also be used in alleviating
system disorders which are diagnosed or treated include autoimmune diseases e.g.
rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest,
crebrovascular disorders e.g. carebral ischemia, angiogenesis,
crebrovascular disorders e.g. carebral ischemia, angiogenesis,
crebrovascular disorders e.g. corebral infections caused by bacteria,
polypeptides can also be used to aid wound healing and epithelial cell
proliferation, to prevent skin aging due to sunburn, to maintain organs
of the polypeptides can also be used to aid wound represent the content or and to the content of primary tissues,
content or an also be used to aid wound represent the content organs
of the content or and the content skin aging due to sunburn, to maintain organs
of the content or an also be used to subpring cell culture of primary tissues,
content or an also be used to subpring cell culture of primary tissues,
content or an also be used to subpring cell culture of primary tissues,
content or an also be used to aid wound healing and epithelial contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regenerate tissues and in chemotaxis. The polypeptides can also be
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Sequence 142 AA; 

Gaps ; Score 40; DB 3; Length 142; Pred. No. 17; 3; Indels 3; Mismatches 58.8%; Query Match
Best Local Similarity 53.00
Tr Conservative

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1 DVRPYRTSRYLEL 13

106 DYRPHKPSLYLEI 118

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ADC01045 standard; protein; 437 AA. ADC01045 ~GCCCCCXXXXBXXBXXBXXXXXXXXXXXXBXBXBXBXPX

(first entry) 04-DEC-2003 Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 1089.

enterohaemorragic; anti-bacterial

Escherichia coli; 0157:H7.

JP2002355074-A.

10-DEC-2002

24-JAN-2002; 2002JP-00015959.

2001JP-00112010. 24-JAN-2001;

(UYTS-) UNIV TSUKUBA.

WPI; 2003-451640/43

Claim 3; SEQ ID NO 1089; 2067pp; Japanese.

Enterohemorragic Escherichia coli 0157:H7-specific nucleic acid molecule and a polypeptide and its use, a polypeptide, a vector and a host cell.

The invention relates to a novel enterchaemorragic Escherichia coli 0157:H7-specific nucleic acid molecule. A polynucleotide of the invention has anti-bacterial activity. The polypeptide can be used in detection and/or treatment of 0157:H7 infection. The nucleotide sequence of the genome of Enterchaemorragic E coli 0157:H7 was determined. The present

The first of the composition comprising two or more isolated rate of this man polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit in craases or decreases the expression of the polymucleotide sequence that increases or decreases the expression of the polymucleotide sequence that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (chung), chronic constriction o O Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung. New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal. The invention discloses a composition comprising two or more isolated Gaps .. DB 7; Length 437; 58; 3; Indels 2; Mismatches Costigan M; Score 40; Pred. No. Rat Protein AAB86925, SEQ ID NO 571. ADE54766 standard; protein; 451 AA. Claim 1; Page; 1017pp; English. Befort K, 14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P. 14-AUG-2002; 2002WO-US025765. 58.8%; ilarity 61.5%; Conservative 317 DVRSERTNSYIEL 329 (first entry) (GEHO ) GEN HOSPITAL CORP. (FARE ) BAYER AG. 1 DVRPYRTSRYLEL 13 WPI; 2003-268312/26. GENBANK; AAB86925. D'urso D, Query Match Best Local Similarity Matches 8; Conserv Rattus norvegicus. Sequence 437 AA; WO2003016475-A2: 27-FEB-2003. 29-JAN-2004 invention. ADE54766; Woolf C, RESULT 14 ADE54766 88888 ð g 

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injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Sequence 451 AA;

DB 7; Length 451; 58.8%; Score 40; DB 53.8%; Pred. No. 60; tive 3; Mismatches 415 DYRPHKPSLYLEI 427 Query Match
Best Local Similarity 53.5Best Local 7; Conservative 1 DVRPYRTSRYLEL 13 à

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Gaps

.. 0

ABP35493 standard; protein; 57 AA. RESULT 15 ABP35493

ABP35493; 

Human ORF4466 protein, SEQ ID NO:8932. 08-JUL-2002 (first entry)

Human; ORF; open reading frame; ORFX; drug screening; diagnosis; implicases monitoring; cytokine; cell proliferation; cell differentiation; anglogenesis; activing; cytokine; regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombotytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; issue growth disorder; tissue regeneration disorder; disorder; all sorder; proliferative disorder; proliferation; vissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterolester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; cardiant; hypotensive; antidharosclerotic; anticoagulant; thrombolyfic; cardiant; hypotensive; antidharosclerotic; antidnamatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.

Homo sapiens,

WO200190366-A2.

29-NOV-2001

24-MAY-2001; 2001WO-US017076.

24-MAY-2000; 2000US-0206690P

(CURA-) CURAGEN CORP.

Leach MD, Shimkets RA;

MPI; 2002-106200/14. N-PSDB; ABN79519. Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation

Claim 10; Page 2475; 2508pp; English.

Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (Open reading frame) 1-4534, and sequences ABN7558-ABN75587 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORF1-ORF4534 S\$\$ identical to the ORF1-ORF4534 S\$\$ identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies

cc specific for OREX proteins, methods of detecting OREX polynucleotides and activity, and methods of screening individuals for a predisposition to an CCC activity, and methods of screening individuals for a predisposition to an CRPX-associated disorder. The OREX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haemacopoiesis regulation, tissue growth, angiogenesis, activity hamonicity, chemotactic/ chemokinetic activity, haemostatic activity, thrombolytic activity, chemotactic/ chemokinetic activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. OREX proteins, and antiinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. OREX proteins, contact acids and antibodies may be used in the treatment of cancers, cother proliferative disorders such as psoriasis and benign tumours, cother proliferative disorders such as epoilepsy and Alzheimer's disease, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester cardiovascular diseases, immune system disorders in the detection of ORFX genomic sequences cord primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous cordeness, in genetic diagnosis, and in forection and cloning of homologous curved may be useful for studying the function and cloning of ortivity of ORFX protein, and in drug screening. The ORFX proteins may be used as immunogens to generate specific antibodies, which are useful in the monitoring of ORFX-associated diseases immunogens to generate specific antibodies, which are useful in the configuration of ortives. 

Sequence 57 AA;

Gaps .. Length 57; 57.4%; Score 39; DB 5; 80.0%; Pred. No. 9.3; iive 0; Mismatches 8; Conservative Local Similarity Query Match Matches

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4 PYRTSRYLEL 13 7 2 PYRTSNNLEL ð g

5, 2004, 07:59:38 Search completed: October Job time : 11.8904 secs

(Oldan) Madig Edda Sign

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 5, 2004, 07:36:16; Search time 2.10648 Seconds (without alignments) 593.639 Million cell updates/sec Run on:

US-09-805-290A-10 68 1 DVRPYRTSRYLEI 13 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283366 seqs, 96191526 residues Searched: 283366

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78: \*
1: pir1: \*
2: pir2: \*
3: pir3: \*
4: pir4: \* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	cal prot	WD-40 1	lysin (EC	e III	einase	protease III precu	preductas	c	heti	O		cal r	l pro	ם	ransp	ybdG protein - Esc	ble me	al	_	tical	_		м.	hypothetical prote	Ψ	in-S	Γl Ωι	cal prot	hypothetical prote
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sult No.		7	m	4	S	φ	7	æ	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	60

60.3%; Score 41; DB 2; Length 775;

Query Match

conserved hypothet hypothetical prote	probable linB prot	plobable isociciac glutamate-tRNA lig	hypothetical prote	hypothetical prote	ribosomal protein	30S ribosomal prot		multiple transfera	probable dna-direc	cyclic beta 1-2 gl	hypothetical DNA-b	7	diol dehydrase (di
H70146 T00446	B70725	A/2658 F72200	T08541	E84465	B82141	C83250	G81825	E81051	T40607	H96974	A81857	E95298	AC1219
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52 52	22	52.7	52	22	52	52	52	52	52	52	51.5	51	51
36 36	36	9 P	36	36	36	36	36	36	36	36	35	ខា	3

## ALIGNMENTS

	RESULT 1 T47356 humotherical protein P18P9 140 - Arabidobais thaliana
	Typermetrical process that are mouse-ear cress C; Species: Arabidopsis that are mouse-ear cress C; Species: Arabidopsis that are mouse-ear cress C; Date: CDate: CD
	R.)Nyakatran, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; A. Masser, K. F. V.
	rays, n.r. to the Protein Sequence Database, April 2000 A,Reference number: 224458
	A.Accesion: 14/356 A.Status: preliminary A.Molecule type: DNA
	A,Residues: 1-303 «NYA» A,Cross-references: EMBL:AL138654 A,Experimental source: cultivar Columbia, BAC clone F18P9
	C;Genetics: A;Nap position: 3 A;Introns: 47/3; 103/3; 140/2; 182/1; 210/2; 241/3 A;Note: F18P9.140
	Query Match Best Local Similarity 46.2%; Pred. No. 7.9; Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
•	Oy 1 DVRPYRTSRYLEI 13
	Db 10 DIRPYKTSWRIQV 22
	RESULT 2
1	EG4828
	probable WD-40 repeat process (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Feb-2001 #secuence revision 02-Feb-2001 #text change 02-Feb-2001
	Claccesion: B84828
	Ribin, X.; Kaul, S.; Kounsley, S.D.; Shea, T.F.; Benico, M.I.; Lown, C.D.; Fulli, C.L.; M.; Koo, H.; Moffat, K.S.; Croini, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.d.
	Husb, D.; Nielman, W.C.; Mille, O.; Ersen, O.S.; Carrocis, C.E.; Creec, C.E.; Carrocis, C.E.;
	A, Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana. A, Reference number: A84420; MUID:20083487; PMID:10617197
	A, Accession: B84828 A. Status: preliminary
	^
	A; Cross-references: GB: AE002093; NID: 94586061; PIDN: AAD25679.1; GSPDB: GN00139
	Cyguelicis A,gan at2g40360 A,Wan nosition: 2

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Pred. No. 21; , Mismatches

66.78;

Best Local Similarity

Conservative 1 DVRPYRTSRYLE 12

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Matches

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DLRPYPNSCYLE 440

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proteinase III [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 0509952)
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Oct-2003
C;Accession: F9108
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G., DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genon A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F9108
A;Status: preliminary
A;Molecule type: DNA
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A;Molecule type: DNA
A;Rolecule type: CSTD>
A;Cross-references: GB:AB005174; NID:g12517303; PIDN:AAG57932.1; GSPDB:GN00145; UWGP:Z41:
A;Experimental source: strain O157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteinase III [imported] - Escherichia coli (strain 0157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: H85933
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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A)Residues: 1-962 - HAV>
A)Cross-references: GB:BA000007; PIDN:BAB37101.1; PID:g13363150; GSPDB:GN00154
A)Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC83678
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ilarity 70.0%;
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A, Cross-references: GB:M17095, NID:g147391, PIDN:AAA24436.1; PID:g147391
A, Experimental source: strain K12
A, Note: part of this sequence, including the amino end of the mature protein, was confir R, Finch, P.W.; Wilson, R.E.; Brown, K.; Hickson, I.D.; Emmerson, P.T.
R, Finch, P.W.; Wilson, R.E.; Brown, K.; Hickson, I.D.; Emmerson, P.T.
A, Mucleic Acids Res 14, 7695-7703, 1986
A, Title: Complete nucleotide sequence of the Escherichia coli ptr gene encoding protease A, Reference number: A25765, MUID:87040734; PMID:3534791
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S. Superfamily: insulin-degrading enzyme (IDE)

C. Superfamily: insulin-degrading enzyme (IDE)

C. Superfamily: insulin-degrading enzyme (IDE)

C. Superfamily: insulin-degrading enzyme (IDE)

F. 1-23 / Domain: signal sequence #status predicted <SIG>
F. 24 962/Product: pitrilysin #status experimental <MMT>

F. 88 92/Binding site: zinc (His) #status experimental

F. 91/Active site: Glu #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                     pitrilysin (EC 3.4.24.55) precursor [validated] - Escherichia coli (strain K-12) N'Alterante names: endopeptidase Pi; proteinase III (Species: Bscherichia coli (strain K-12) C;Species: Bscherichia coli (Species: Britis) (Species: Bscherichia coli (Species: Bscheri
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R;Becker, A.B.; Roth, R.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 3835-3839, 1992
A;Title: An unusual active site identified in a family of zinc metalloendopeptidases.
A;Reference number: A38854; MUID:92237263; PMID:1570301
A;Contents: annotation; active site
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                                                                      Gaps
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Pred. No. 26;
2; Mismatches 1; Indels
                                                             Indels
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A; Residues: 1-962 <FIN>

A,Gene: ptr A,Map position: 61 C,Function:

C;Genetics:

Molecule type: DNA

Accession: A25765

Molecule type: DNA

A; Accession: F65064

124 PÝRTAFÝLEV 133 RESULT 4 F91088 g

4 PYRTSRYLEI 13

60.3%;

Query Match Best Local Similarity Matches 7; Conserv

12

preliminary

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FAULDOSE: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis, thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C;Accession: A862701
C;Accession: A86270
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C;Date: 02-Mar-2001
C;Date: 02-Mar-2001
C;Date: 02-Mar-2001
C;Date: 03-Mar-2001
C;Date: 03-Ma
                                                                                                                                                                                                                Apporthetical protein T14N5.4 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 22-Oct-1999
C;Accession: 100447
R;Federspiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Araujo,; VyGotskala, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.
A;Reference number: Z14152
A;Accession: T00447
A;Status: translated from GB/EWBL/DDBJ
A;Ratus: translated from GB/EWBL/DDBJ
A;Rasidues: 1-28 FFED.
A;Accession: T0447
A;Kesidues: FFED.
A;Kesidues: EMBL:AC004260; NID:g3176694; PID:g3540203; GSPDB:GN00059; ATSP:T14N5.
A;Experimental source: cultivar Columbia
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87.5%; Pred. No. 33;
ive 0; Mismatches 1; Indels
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Pred. No. 16;
3; Mismatches
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Best Local Similarity 8/...
                                            421 DPRPYRYSRFFD 432
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Matches 6; Conservative
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A; Introns: 38/3; 106/1
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A,Molecule type: DNA
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: H98243
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 233-2328, 2001
A;Fitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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A;Nolecule type: DNA
A;Residues: 1-442 <KUR>
A;Cressreferences: GB:AE008689; PIDN:AAL44754.1; PID:G17742390; GSPDB:GN00187
A;Cressreference: strain C58 (Dupont)
C;Genetics:
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   A,Molecule type: DNA A,Residues: 1-962 <PRN>
A,Residues: 1-962 <PRN>
A,Crossidues: 1-962 <PRN>
A,Crossidues: GB:AL513382; PIDN:CAD02819.1; PID:g16504073; GSPDB:GN00176
C;Genetics: A,Gene: STY3133
C,Superfamily: insulin-degrading enzyme (IDE)
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Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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Pred. No. 18;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                 Length 962;
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Pred. No. 26;
2; Mismatches
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Best Local Similarity 70.0%;
Matches 7; Conservative
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Best Local Similarity be...
7; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-442 < KUR>
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A, Accession: B82559 A, Status: preliminary A, Molecule type: DNA

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S;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. B. 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: G90705

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-415 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34038.1; PID:g13360073; GSPDB:GN00154

A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Rocidues: 1-415 <STO>
A;Cross-references: GB:AE005174; NID:g12513462; PIDN:AAG54910.1; GSPDB:GN00145; UWGP:Z071
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      ribosomal protein S14 T01E8.6, mitochondrial [similarity] - Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-May-2002 R,Accossion: T24300 R,Accossion: T24
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A,Cross-references: EMBL:Z48809; PIDN:CAA88746.1; GSPDB:GN00020; CESP:T01E8.6
A,Experimental source: clone T01E8
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C,Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C,Accession: G90705
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Pred. No. 39;
3; Mismatches 2; Indels
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Pred. No. 9.5;
3; Mismatches
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C,Superfamily: Escherichia coli ribosomal protein
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Best Local Similarity 58.3%;
Matches 7; Conservative
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291 LKPYLTSRHQEI 302
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76 IKPYRLSRHL 85
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A;Gene: CESP:T01E8.6
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: B82559
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Aitle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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A;Residues: 1-569 <SIN>
A;Cross-references: GB.AE004052; GB:AE003849; NID:g9107617; PIDN:AAF85237.1; GSPDB:GN001
A;Cross-references: GB.AE004052; GB:AE003849; NID:g9107617; PIDN:AAF85237.1; GSPDB:GN001
A;Experimental source: strain 9a5c
B:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
B:Simpson, A.J.G.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramee, E.E.; Laigr
chado, M.A.; Madeixa, A.M.B.N.; Madeixa, H.W.F.; Marrino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Sulva, M.C.; Palmieri, D.A
A;Authors: da Silva, A.G. & Silva, F.R.; de Silva, S.R.; Salva Jr., W.A.; de Salva Jr., W.A.; verjovski-Almeida, S.; vettore, A.L.; Z., C., M.A., M.A.; de Salva Jr., Salva Jr., Salva Jr., W.A.; verjovski-Almeida, S.; vettore, A.L.; Z., Salva Jr., M.A.; de Salva Jr., V. V.B.; de Salva Jr., W.A.; verjovski-Almeida, S.; vettore, A.L.; Z., Salva Jr., M.A.; de Salva Jr., V. V.B.; 
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A;Molecule type: DNA
A;Molecule type: DNA
A;Rosiuse: 1-594 cPRU>
A;Cross-references: EMBL:AF003138; NID:g2088708; FID:g2088711; PIDN:AAB54155.1; GSPDB:GN
A;Experimental source: strain Bristol N2; clone F1286
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C,Species: Caenorhabditis elegans
C,Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
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A;Introns: 45/2; 146/3; 211/3; 316/1; 367/3; 407/3; 552/2
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C;Superfamily: Escherichia coli ribosomal protein Sl
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149 DVRPVRDPAYLE 160

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RESULT 12

Accession: T15202

8; Conservative 1 DVRPYRTSRYLE 12

Best Local Similarity

Matches

Query Match

289 DLSRÝŘÍSŘHTĚV 301

RESULT 13 T24300

1 DVRPYRTSRYLEI 13

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Conservative

Query Match Best Local Similarity 7; Conserve

A; Gene: CESP:F12B6.3

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A;Experimental source: strain 0157:H7, substrain EDL933 C;Genetics: A;Gene: ybdG
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0; Gaps Query Match

55.9%; Score 38; DB 2; Length 415;
Best Local Similarity 58.3%; Pred. No. 39;
Matches 7; Conservative 3; Mismatches 2; Indels

0;

Search completed: October 5, 2004, 08:16:50 Job time: 2.10648 secs

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GenCore version 5.1.6
Copyright (C) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 5, 2004, 07:29:35; Search time 1.16358 Seconds (without alignments) 581.749 Million cell updates/sec Run on:

US-09-805-290A-10 68 1 DVRPYRTSRYLEI 13 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ψ	٠À٠	P05458 escherichia	Q8z418 salmonella	Q8zmb5 salmonella	Q83qc3 shigella fl		P49391 caenorhabdi	escherich		pifid	aedes aeg	borre		mycobacter						P34306 caenorhabdi	_			_		arabidopsi	escherichi	3 buchnera a	36 influenza	luenz	74 intluenza	2 influenza
SUMMARIES		PTRA ECOS7	PTRA_ECOL6	PTRA_ECOLI	PTRA SALTI	PTRA SALTY	PTRA_SHIFL		RT14 CAEEL	YBDG ECOLI	DS_DROME	SYR BIFLO	DEFC AEDAE	LUXS BORBU	DHAA MYCBO	DHAA_MYCTU	RS1 PROSP	SYEZ THEMA	MALQ PYRKO	RPC1_SCHPO	Y14F BPT4	YKQA CAEEL	RHO HELPJ	RHO HELPY	CBPM HUMAN	V111_FOWPV	YLI1 MYCHO	œ		m	INBS	ı	P2_INB	RRP2_INBP9
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## ALIGNMENTS

1.1	ECOS7 STANDARD; PRT; 962 AA.	Concert 2003 (Rel. 42, Created) 10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Protease III precursor (EC 3.4.24.55) (Pitrilysin) (Protease pi). PRA OR PTR OR 24138 OR ECS3678.	hia cter	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-0.57:H7 / BDL933 / ATCC 700927; MEDLINE=21074935; PubMed=11206551; MEDLINE=21074935; PubMed=11206551; MEDLINE=21074935; PubMet G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";	SEQUENCE FROM N.A. STRAIN-0157:H7 / RIMD 0509952; STRAIN-0157:H7 / RIMD 0509952; MEDLINE-21156231; PubMed=11258796; MEDLINE-21156231; PubMed=11258796; MEDRINE-21156231; PubMed=11258796; Han CG., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";	ades in (B cleav insu 7 kDa ounit	-: SUBCELLULAR LOCATION: Periplasmic by similarity): SIMILARITY: Belongs to peptidase family Mis. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).  EMBL; AROSSSIO; AAGS7932.1;
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Pfam, PF05193; Peptidase_M16_C; 2.
PROSITE; PS00143; INSULINASE; 1.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
                                                                                                                                                                                                   Score 41; DB 1; Length 962;
Pred. No. 11;
2; Mismatches 1; Indels
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les 7; Conservative
                                                                                                                                                                                                                                                                                                  124 PYRTAFYLEV 133
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                                                                                                                                                                         962 AA;
                                                         Complete proteome SIGNAL 1
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ACT SITE
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                                                                                           CHAIN
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EMBL; AP002563; BAB37101.1; -.

FRIK; F91068; F91068.

InterPro; IPR001431; Peptidase_M16.

InterPro; IPR007663; Peptidase_M16.

Pfam; PF00675; Peptidase_M16; I.

Pfam; PF00193; Peptidase_M16; Z.

Pfam; PF00193; Peptidase_M16_C; Z.

PROSITE; PS00143; INSULINABE; I.

Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protease III precursor (BC 3.4.24.55) (Pitrilysin) (Protease pi).
PTRA OR PTR OR C3415.
Escherichia coli O6.
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-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
-!- SIMILARITY: Belongs to peptidase family MIG.
                                                                                                                                                                                                                                                                                 Score 41; DB 1; Length 962;
Pred. No. 11;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                    107808 MW; 30785644CBF0E452 CRC64;
                                                                                                                                                                  PROTEASE III.
ZINC (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                   ZINC (BY SIMILARITY). ZINC (BY SIMILARITY).
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InterPro; IPR001431, Peptidase M16.
InterPro; IPR007863; Peptidase M16_C.
Pfam; PP00675; Peptidase M16_T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CFT073 / ATCC 700928;
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                                                                                                                                                                                                                                                                                 60.3%;
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 70.vv,
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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SIGNAL 1
CHAIN 24
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Q8CVS2;
                                                                                                                                                                                                ACT SITE
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PTRA_ECOL6
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Gaps
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MEDINE=88065781; PubMed=3308636;
Claverie-Martin F., Diaz-Torres M.R., Kushner S.R.,
"Analysis of the regulatory region of the protease III (ptr) gene of Escherichia coli K.12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete nucleotide sequence of the Escherichia coli recB gene."; Nucleic Acids Res. 14:8573-8582(1986).
                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIANE=97426617, PubMed=9278503;
Blattner F.R., Flunkett G. III, Bloch C.A., Ferna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                PTRA ECOLI STANDARD; PRT; 962 AA.
P05458; P78106;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Procease III precursor (EC 3.4.24.55) (Pitrilysin) (Protease pi).
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A. MDMed=3534791; MDDLINE-87040734; PubMed=3534791; Finch P.W., Wilson R.E., Brown K., Hickson I.D., Emmerson P.T.; Finch P.W., Wilson R.E., Brown K., Hickson I.D., Emmerson P.T.; "Complete nucleotide sequence of the Escherichia coli ptr gene encoding protease III "; encoding protease III "; Nucleic Acids Res. 14:7695-7703(1986).
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Finch P.W., Storey A., Chapman K.E., Brown K., Hickson I.D.,
Emmerson P.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGENESIS, AND ACTIVE SITE.
MEDLINE-92237263; PubMed=1570301;
Becker A.B., Roth R.A.;
"An unusual active site identified in a family of zinc metalloendopeptidases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 89:3835-3839(1992)
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MEDLINE=1554947; PubMed=11677608; Thomson N.R., Pickard D., Wain J., Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebainia M., Baker S., Baaham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davis R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Lazren T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Minchead S., Minc
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ". Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: Endopeptidase that degrades small peptides of less than 7 kDa, such as glucagon and insulin (By similarity).
-!- CATALYTIC ACTIVITY: Preferential cleavage of 16-Tyr-1-Leu-17 and 25-The-1-Tyr-26 bonds of oxidized insulin B chain. Also acts on other substrates of Mw less than 7 kDa such as insulin and
                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; 
Enterobacteriaceae; Salmonella.
NCBI_TaxID=601;
10-OCT-2003 (Rel. 42, Last annotation update)
Protease III precursor (EC 3.4.24.55) (Pitrilysin) (Protease pl).
PTRA.OR PTR OR STY3133 OR T2903.
                                                                                                                                                                 SEQUENCE FROM N.A.
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ZINC.
H-SR. LOSS OF ACTIVITY AND OF ZN-BINDING.
E-90: LOSS OF ACTIVITY.
H-SR: LOSS OF ACTIVITY.
E-90: 20% LOSS OF ACTIVITY.
E-90: LOSS OF ACTIVITY.
E-90: NO LOSS OF ACTIVITY.
E-90: NO LOSS OF ACTIVITY.
ILIHYDA -> HYHGLERW (IN REF. 4).
                                                                                                                                                   Diochem. J. 292:137-142(1993).

-!- FUNCTION: Endopeptidase that degrades small peptides of less than 7 kDa, such as glucagon and insulin.

-!- CATALYTICA CTIVITY: Preferential cleavage of 16-Tyr-|-Leu-17 and 25-Phe-|-Tyr-26 bonds of exidized insulin B chain. Also acts on other substrates of Mw less than 7 kDa such as insulin and
                                                                                        residue in
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InterPro; IPR007863; Peptidase_M16_C.
Pfam; PF00675; Peptidase_M16, 1.
PR05193; Peptidase_M16, 1.
PR051TE; P800143; INSULINASE; 1.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
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              [6]
MUTAGENESIS, AND ACTIVE SITE.
MUEDLINE=93277449; PubMed=8099278;
BECKER A.B., Roth R.A.;
"Identification of glutamate-169 as the third zinc-binding proteinage III, a member of the family of insulin-degrading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.3%; Score 41; DB 1; Length 962; 70.0%; Pred. No. 11; 1; Indels .ive 2; Mismatches 1; Indels
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EMBL; U29581; AAB40468.1; ---
EMBL; X06207; CAA29560.1; ---
EMBL; X06207; CAA29576.1; ---
EMBL; MI7095; AAA24436.1; ---
MEROPS; MI6,001; ---
ECOLDBASE; G095.0; 6TH EDITION.
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Best Local Similarity 70.0
Matches 7; Conservative
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962 AA;
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CONFLICT
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InterPro; IPR001431; Peptidase_M16.
InterPro; IPR007863; Peptidase_M16_C.
Pfam; PF00675; Peptidase_M16; \(\bar{1}\).
Pfam; PF005193; Peptidase_M16; \(\bar{1}\).
PROSTIE: PS00143; INCUINASE; PLISE NEC.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
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glucagon.
--- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
--- SUBUNIT: Monomer (By similarity).
--- SUBCELLULAR LOCATION: Periplasmic (By similarity).
--- SIMILARITY: Belongs to peptidase family M16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 1; Length 962;
Pred. No. 11;
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962 , PROTRASE II.
91 ZINC (BY SIMILARITY).
91 BY SIMILARITY.
92 ZINC (BY SIMILARITY).
169 ZINC (BY SIMILARITY).
107524 MW, 5745C2C77F7F5832 CRC64;
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Best Local Similarity 70..
7, Conservative
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8

962 AA

STANDARD;

PTRA SALTI ID PTRA SALTI AC Q8Z4T8; DT 10-OCT-2003 ( DT 10-OCT-2003 (

RESULT 4

(Rel. 42, Created) (Rel. 42, Last sequence update)

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RESULT
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CATALYTIC ACTIVITY: Preferential Cleavage of 16-Tyr-|-Leu-17 and 25-Phe-|-Tyr-26 bonds of oxidized insulin B chaim. Also acts on other substrates of Mw less than 7 kDa such as insulin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534949; PubMed=11677609;
MEDLINE=21534949; PubMed=11677609;
MCClelland M. O. Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Alson R.K., "Lison R.K.," "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stygene, SG?????, ptrA.
InterPro, IPR001431; Peptidase_M16.
InterPro, iPR007663; Peptidase_M16.
Pfam, PF00675; Peptidase_M16.
Pfam, PF005193; Peptidase_M16.; 2.
PROSITE; PS00143; INSULINASE; 1.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protease III precursor (EC 3.4.24.55) (Pitrilysin) (Protease pi)
PTRA OR PTR OR SIM295.
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-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
-!- SIMILARITY: Belongs to peptidase family M16.
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ZINC (BY SIMILARITY).
1; 322AD6E87B873952 CRC64;
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PROTEASE III.
ZINC (BY SIMILARITY).
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                                                                                                                                                                                                     STANDARD;
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SEQUENCE FROM N.A.
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OBZMB5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Infect. Immun. 71:2775-2786 (2003).
-!- FUNCTION: Endopeptidase that degrades small peptides of less than -!- FUNCTION: Endopeptidase that degrades small peptides of less than 7 kDa, such as glucagon and insulin (By similarity).
-!- CAPLYTIC ACTIVITY: Preferential cleavage of 16-Tyr-|-Leu-17 and 25-Phe-|-Tyr-26 bonds of exidized insulin B chain. Also acts on other substrates of Mw less than 7 kDa such as insulin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=301 / Serotype 2a;
MEDLINE=22272406; Pubmed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Yang J., Xang Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=2457T / ATCC 700930 / Serotype 2a;
STRAIN=22590274; PubMed=12704152;
MEDLINE=22590274; PubMed=12704152;
Med J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T. Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T.";
Thfect. Immun. 71:2775-2786(2003).
                                                                                                                                                            Last annotation update)
r (EC 3.4.24.55) (Pitrilysin) (Protease pi).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE015297; AAN44319.1; -.
EMBL; AE015297; AAP18144.1; -.
EMBL; AE046987; AAP18144.1; -.
InterPro; IPRO01431; Peptidase_M16.
InterPro; IPRO07863; Peptidase_M16.C.
Pfam; PF00675; Peptidase_M16, I.
Pfam; PF00675; Peptidase_M16, I.
PROSTIE; PS00143; INGUINASE; I.
Hydrolase; Metalloprotease; Magnesium; Periplasmic; Zinc; Signal;
                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity)
-!- SUBUNIT: Monomer (By similarity)
-!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
-!- SIMILARITY: Belongs to peptidase family M16.
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PROTBAGE II.
ZINC (BY SIMILARITY).
BY SIMILARITY.
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
MW; 662041A5DCA0F254 CRC64;
                                    962 AA.
                                                                                                                                 update)
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962 PRO7
88 ZINC
91 BY 8
92 ZINC
169 ZINC
167770 MW; (
                                                                                                                                                                                       Protease III precursor (EC 3.4. PTRA OR PTR OR SF2832 OR S3029.
                                                                                             (Rel. 42, Created)
(Rel. 42, Last sequ
(Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                     Enterobacteriaceae; Shigella.
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962 AA;
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                                                                                                                                                                                                                                                         Shigella flexneri
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                                 SHIFL
PTRA_SHIFL
ID PTRA_SHII
AC Q83QC3;
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Gaps

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60.3%; Score 41; DB 1; Length 962; 70.0%; Pred. No. 11; indels iive 2; Mismatches 1; Indels

Conservative

Local Similarity les 7; Conserv

Best Loc Matches

Query Match

4 PYRTSRYLEI 13 PYRTAFYLEV

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LUMBRAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

8F3B447551025FCD CRC64;

60537 MW;

526 211 215 363

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363
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526 AA;
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P49391;
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SITAIN=CV. Columbia;

XI Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

XI Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

A Theologis A., Care J.R., Palm C.J., Federspiel N.A., Kaul S.,

A Theologis A., Chan D., Conway A.B., Chank R.F., Chin C.W.,

A Chung M.K., Conm D., Conway A.B., Conway A.B., Creasy T.H., Chan K.,

A Chung M.K., Conn D., Haas B., Hansen N.F., Hughes B., Fujii C.Y.,

A Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

A Lin X., Liu S.X., Liu Z.A., Lee J.M., Lenz C.A., Li J. H., I.Y.-P.,

A Lin X., Liu S.X., Liu Z.A., Lucos J.S., Maiti R., Marziali A.,

A Lin X., Liu S.X., Liu Z.A., Lucos J.S., Maiti R., Marziali J.,

A Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Whu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,

Whu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,

The Lin A. The Li
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MEDLINE-21608393; PubMed=11743104;
Sarria R., Wagner T.A., O'Neill M.A., Faik A., Wilkerson C.G.,
Segita K., Raikhel N.V.; Paiklel N.V.; Raikhel N.V.
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                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                             Score 41; DB 1; Length 962;
Pred. No. 11;
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O9XIB1, O9LMF2;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable fucosyltransferase 7 (EC 2.4.1.-) (AtFUT7).
FUT7 AT16114070 OR F7A19.15 OR F16A14.19 OR F16A14.28.
Arabidopsis thaliana (Mouse-ear cress).
                                                                               2; Mismatches
                             60.38;
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                                                                               7; Conservative
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                                                                                                                                 4 PYRTSRYLEI 13
                                                       Best Local Similarity
Matches 7; Conser
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                                  Query Match
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Score 39; DB 1; Length 526;
Pred. No. 13;
0; Mismatches 1; Indels
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Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last semnotation update)
Putative mitochondrial 40s ribosomal protein S14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WormPep, TOIE8.6, CE32923.
InterPro, IPR001209; Ribosomal S14.
Pfam, PR00233, Ribosomal S14, 1.
PR051TE, PS00527; RIBOSOMAL S14, 1.
Ribosomal protein; Mitochondrion.
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     Query Match 57.4%;
Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity
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imaginal disc morphogenesis in Drosophila.";
Genes Dev. 9:1530-1542(1995).
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291 LKPYLTSRHQEI 302
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Matches 7; Conserv
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SPECIES=E.coli; STRAIN=K12 / MG1655;
Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
Ederspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
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SPECIES=E.coli, STRAIN=K12;
MEDINE=97061202, PubMed=8905232;
MEDINE=97061202, PubMed=8905232;
MEDINE=97061202, PubMed=8905232;
KMINE S., Kibada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kinara S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Marina S., Miki T., Mizobuchi K., Sampei G., Seki Y., Tagami H., Takemoto H., Nishio Y., Saito N., Yano M., Horiuchi T.,
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=S.flexnerri, STRAIN=301 / Serotype 2a, MEDLINE=22272406; PubMed=12384590; Jin B.2272406; PubMed=12384590; Jin C., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang G., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=97426617; Pubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Oollado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene encoding
                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=E.coli; STRAIN=B; MEDLINE=95113294; PubMed=7813899; Michael N.P., Brehm J.K., Anlezark G.M., Minton N.P.; Prehm J.K., Anlezark Escherichia coli B gene encoding "Physical characterisation of the Escherichia coli B gene encoding nitroreductase and its over-expression in Escherichia coli K12."; FEMS Microbiol. Lett. 124:195-202(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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SPECUESE.coli; STRAIN=K12 / C600;
Zenno S., Koixe H., Tanckura M., Saigo K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 45, Last annotation update)
Hypotherical protein ybdG.
YBDG OR B0577 OR SF0483 OR S0492.
Escherichia coli, and
                                                                                                               415 AA
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                                                                                                               STANDARD;
172 IKPYRLSRHL 181
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                                                                 RESULT
YBDG_EC
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the PNBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDILNE=55324813; PubMed=7601355;
Clark H., Brentrup D., Schneitz K., Bieber A., Goodman C., Noll M.;
"Dachsous encodes a member of the cadherin superfamily that controls
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SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a; MEDLINE=22590274; PubMed=12704152; MEDLINE=22590274; PubMed=12704152; Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence and comparative genomics of Shigella flaxmer; serotype 2a strain 2457T.", Infect. Immun. 71:2775-2786(2003).
-!- SUBCELLUULAR LOCATION: Integral membrane protein (Potential).
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      Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 15;
3; Mismatches
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SOLITIFIER PRESENTATION OF THE PROPERTY OF THE
                                                                RED. SUDDITECT (WAY-1999) to the EWBL/GenBank/DDBJ databases.

RED. SUDDITECT RECOM N.N.

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RA Admas N.D. CallAfer S.E., Holf R.A., Forkins R.A., Galle R.F.,

RA Admas N.D. CallAfer S.E., Ratherds S. Amblucher N., Henderson S.N.,

S. Sutton G.G., Worthman J. R., Yandell N.D. Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pefeiffer B.D.

RA Abrill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballaw R.M., Basus A., Baxendale U., Brandari D., Bolishakov S.,

RA Ballaw R.C., Borger M., Barman B.P., Paraktarica R., Miklos G.L.G.,

RA Barlaw R., Bouse D.A., Berman B.P., Paraktarica S., Bolishakov S.,

Burtis K.C., Busam D.A., Bench B.P., Davamport L.B., Davise P.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chankr I.,

RA Burtis K.C., Busam D.A., Baller R., Down P., Brotcher A., Chankr I.,

RA Burtis K.C., Bragalista C.C., Berraz C., Perraz S.D., Dew I., Dietz S.M.,

RA Burtis K.C., Busam D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Burtis K.C., Busam D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Burtis K., Gong F., Gorrell J.H., Gu Z., Galbart W.M., Glasser K.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Morberson D.,

RA Hostin D., Houston K.A., Heiman T.J., Morberson D.,

RA Hostin D., Matrei B., Morloch T.C., Morberd N.P., Morberson D.,

RA Horin S.M. Moy M., Murthy B., Murphy L., Muzny D.M., Nalson D.L.,

RA Blazzollin A.E., Stem H.M., Saulber R., Wenter E., Shenh H.,

Raisko P., Lei Y., Lei Y., Rainer M., Stupski M.P., Saith T.,

Spier E., Spradling A.C., Stapleton M., Stupski M.P., Saith T.,

Spier E., Spradling A.C., Stapleton M., Stupski M.P., Saith T.,

RA Beng X.H., Zhong F.N., Zhong W., Zhong X., Zhu X., Zhu X., Smith H. G.,

RA Beng X.H., Zhong F.N., Stapleton M., Shong S., Zhu X., Smith H.,

Raisko M., When M., Raisko M., Ra
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Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
-!- FUNCTION: Involved in morphogenesis. May also be involved in cell
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TISSUE SPECIFICITY: Expressed in embryonic ectoderm. In larvae,
expression is restricted to imaginal disks and brain.
DEVELOPMENTAL STAGE: Expressed throughout embryogeneeis where it
is first detected during gastrulation. Also expressed in larvae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.I. Bettencourt B.R., Celniker S.E., de Grey A.D.M.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Annotation of the Drosophila melanogaster euchromatic genome: a
                                                          Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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(See http://www.isb-sib.ch/announce/
                                                                                              R F1928s; FBG0000497; ds.

R G0; G0:0005887; C:integral to plasma membrane; ISS.

R G0; G0:0005887; C:integral to plasma membrane; ISS.

G0; G0:000814; F:calcium-dependent cell adhesion molecule ac. . .; ISS.

R G0; G0:0008283; P:calcium-dependent cell-cell adhesion; ISS.

R G0; G0:0008283; P:calcium-dependent cell-cell adhesion; ISS.

R G0; G0:0008283; P:calcium-dependent cell-cell adhesion; IMP.

R G0; G0:0008284; P:calcium-morphogeneis during differentiation; IMP.

R G0; G0:0045198; P:catabiishment of epithelial cell polarity; IMP.

R G0; G0:0018149; P:protein-protein cross-linking; IPI.

R InterPro; IPR002126; Cadherin_C term.

R Ffam; PR0028; cadherin_C term.

R Pfam; PR0049; Cadherin_C term;

R Pfam; PR0049; Cadherin_C term;
                                                                                                                               molecule ac. . ,; ISS
                                                                                                                                                                                                                                                                                                                                SMART; SM00112; CA; 25.
PROSITE; PS00232; CADHERIN 1; 20.
PROSITE; PS50268; CADHERIN 2; 27.
Cell adhesion; Glycoprotein; Transmembrane; Calcium; Calcium-binding; Sepeat; Signal; Developmental protein.
SIGNAL 120
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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1.6e+02;
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1; Mismatches
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HSSP; P15116; 1NCJ.
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                                         EMBL; L08811; AAA79329.2;
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Best Local Similarity
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DOMAIN
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4

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Aedes aegypti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-REFM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=2224977; PubNed=12381787; Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Schell M.A., Karmirantzou M., Snel B., Dork P., Dolley M., Pridmore R.D., Arigoni F.; The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract."; The genome sequence of Bifidobacterium longum reflects its adaptation Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
-!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP + diphosphate + L-arginyl-tRNA(Arg).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Oftoplasmic.
-!- SUBCELLULAR Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                               15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                                                                                                                                                                 Bifidobacterium longum.
Bacteria, Actinobacteria, Actinobacteridae, Bifidobacteriales,
Bifidobacteriaceae, Bifidobacterium.
NCBI_TaxID=216816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.4%; Score 37; DB 1; Length 620; 50.0%; Pred. No. 37; ive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 157 "HIGH" REGION.
620 AA; 67206 MW; F51C3C0C8CD9AB06 CRC64;
                                                                                                                                                                        620 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_00123; -; 1.
InterPro; IPR001278; Arg_tRNA-synt_lc.
InterPro; IPR005148; N.
InterPro; IPR008909; tRNA-synt_ld_C.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR0016080; tRNA-synt_l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE014754; AAN25073.1; -.
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534 DRQPHKVARYLE 545
                                                                                                                                                                        STANDARD;
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                                            DLEPYNTORY 158
DVRPYRTSRY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  OR BL1272
                                                                                                                                                                        BIFLO
                                              149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                    RESULT 11
SY BIFLO
SY BIFLO
ONG GO GO BLAND
ON NAGS
ON SEQUE
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99 AA.

PRT;

STANDARD;

RESULT 12 DEFC\_AEDAE ID \_DEFC\_AEDAE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=56047965; PubMed=7568275;
A Chalk R., Albuquerque C.M., Ham P.J., Townson H.;
That R., Albuquerque C.M., Ham P.J., Townson H.;
The characterization of two insect defensins: immune and characterization of two insect defensins: immune peptides from the mosquito Addes aegypti.";

Proc. R. Soc. Lond., B. Biol. Sci. 261:217-221(1995).

- Proc. R. Soc. Lond., B. Biol. Sci. 261:217-221(1995).

- Proc. R. Soc. Lond., B. Biol. Sci. 261:217-221(1995).

- FUNCTION: Antibacterial peptide mostly active against Gram-postitive bacteria.

- SUBCELLULAR LOCATION: Secreted.

- ITISSUE SPECIFICITY: Hemolymph.

- IDSUED.PRINTAL STATES: Expressed 30 minutes after infection and remained present through to 21 days. Expressed in white or callow pupae during metamorphosis, but no expression was seen in larvae.

- INDUCTION: By bacterial infection.

- POLYMORPHISM: There are two defensin C isoforms, C1 (shown here)
                                                                                                                                                                                                                                                                    MEDITAL=99124369; PUNNEd=9927179; MEDITALE CT., Saverson D.W., Lowenberger C.A., Smartt C.T., Bulet P., Ferdig M.T., Severson D.W., Hoffmann J.A., Christensen B.M.; M. Section M.M., "Insect immunity: molecular cloning, expression, and characterization of contagning endomic DNA encoding three isoforms of insect defensin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the arthropod defensin family. Subfamily 1.
                                                                                                                                                                                                               SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, INDUCTION, AND SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Liverpool; Manda-7633471; Metru C., Hodgeman B., Lowenberger C., Bulet P., Charlet M., Hetru C., Hodgeman B., Christensen B.M., Hoffmann J.A.; Insset immunity: isolation of three novel inducible antibacterial defensins from the vector mosquito, Aedes aegypti."; Insect Blochem. Mol. Biol. 25:867-873(1995)
                                                                                                                        Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
NOSI_TaxID=7159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00425; ARTHROPOD DEFENSINS; 1.
nmunity; Antibiotic; Defensin; Signal; Polymorphism.
1 23 POTENTIAL.
P81603; O9YOFO; O9YOFI;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Defensin C precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFENSIN C.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF156092; AAD40116.2; --
EMBL, AF156093; AAD40117.2; --
HSSF, P10891; 11CA.
InterPro; 1PR001542; Defensin_anpod.
InterPro; 1PR001542; Defensin_anpod.
InterPro; 1PR003614; Knotl.
Pfam; PF01097; Arthro defensin; 1.
PRINTS; SM00505; Knotl; 1.
PROSITE; PS00425; ARTHROPOD_DEFENSINS;
                                                                                                           Aedes aegypti (Yellowfever mosquito)
                                                                                                                                                                                                                                                     STRAIN-Liverpool; TISSUE=Fat body;
                                                                                                                                                                                                                                                                                                                                                                                                   nsect Mol. Biol. 8:107-118(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 60-99, AND INDUCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insect immunity, Antibiotic; SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [3]
SEQUENCE OF 60-99.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAINCE FROM N.A.
STRAINCE FROM N.A.
STRAINCE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
8-ribosylhomocysteinase (EC 3.13.1.-) (Autoinducer-2 production protein luxs) (Al-2 synthesis protein).
                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_00091; -; 1.

InterPro.; TPR003815; LuxS.

Fram; PF02664; LuxS; 1.

PRINTS; PR01487; LUXSPROTEIN.

PRODom; PD013172; LuxS; 1.

Quorum sensing, Autoinducer synthesis; Iron; Metal-binding; Hydrolase; Complete proteome.
                                                                                                                                          Score 36; DB 1; Length 99;
Pred. No. 7.7;
2; Mismatches 4; Indels
                                                                                                                                                                                         4; Indels
  G -> E (IN ISOFORM C2).
P -> S (IN ISOFORM C2).
R -> G (IN REF. 2 AND 3).
A -> S (IN REF. 2 AND 3).
                                                                                               CRC64;
                                                                                            7C3566A68F4548ED
                                                                                                                                                                                                                                                                                                                                                                                                          157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFACTOR: Iron (By similarity).
SUBUNIT: Homodimer (By similarity).
SIMILARITY: Belongs to the luxS family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001143; AAC66762.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4,5-dihydroxy-2,3-pentanedione.
26
34
83
83
PR
91
A 10696 MW;
                                                                                                                                            52.9%;
                                                                                                                                                                                                                                                                     31 DVRPYANSLFDEL 43
                                                                                                                                                                                                                                         1 DVRPYRTSRYLEI 13
                                                                                                                                                                   Local Similarity 53.8
es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
  26
34
83
91
99 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          LUXS BORBU
050164;
                           VARIANT
CONFLICT
                                                                                            SEQUENCE
                                                                                                                                               Query Match
                                                                        CONFLICT
     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                     LUXS BORBU
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a
     FTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEPURE 22709107; PubMed=12788972; Medina N., Mansoor H., MEDINE=22709107; PubMed=12788972; MEDINE=22709107; PubMed=12788972; Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

-: FUNCTION: Catalyzes hydrolytic cleavage of carbon-halogen bonds in halogenated aliphatic compounds, leading to the formation of the corresponding primary alcohols, halide ions and protons (By
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
CATALYTIC ACTIVITY: 1-haloalkane + H(2)0 = a primary alcohol
                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       halide.
SUBUNIT: Monomer (By similarity).
SIMILARITY: Belongs to the haloalkane dehalogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MU11;
besenska A., Rychlik I., Pavlik I., Damborsky J.,
"Distribution of haloalkane dehalogenase genes among bovine
mycobacteria.";
                                                                               Score 36; DB 1; Length 157;
Pred. No. 13;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOPHILE (BY SIMILARITY). ACID (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
RON (BY SIMILARITY).

RON (BY SIMILARITY).

RON (BY SIMILARITY).

89C3844C37BB7504 CRC64;
                                                                                                                                                                                                                                                                DHAA MYCBO STANDARD; PRT; 300 AA. 09xB14; 28-FBB-2003 (Rel. 41, Created) 15-WAR-2004 (Rel. 42, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update) Haloalkane dehalogenase (BC 3.8.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF_01231; -; 1.
InterPro; IPR000073; A/b_hydrolase.
InterPro; IPR00639; Bpox_hydrolase.
InterPro; IPR006379; Ser_Setrs.
Pfam; PF00561; abhydrolase; 1.
PRINTS; PR00412; EPOXHYDRLASE.
 IRON
                                   IRON
                                                                                                                  4;
53 IR
57 IR
124 IR
18098 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ243259; CAB45532.1; -. EMBL; BX248343; CAD94795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase, Complete proteome.
ACT_SITE 109 109
ACT_SITE 133 133
                                                                                 52.9%;
46.2%;
                                                                                                                                                                              133 DMAKYESSKYLQI 145
                                                                                                                                                1 DVRPYRTSRYLEI 13
                                                                                                                    Conservative
53
57
124
157 AA;
                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium bovis.
                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Subfamily 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1765;
                                                                                                                                                                                                                                                                                                                                                                    DHAA OR MB2610
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                                 METAL
SEQUENCE
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DHAA MYCBO
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X MEDINE=89295997; PubMed=9634230;

X MEDINE=89295997; PubMed=9634230;

A Gordon S.V., Erglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Gordon S.V., Erglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Gordon S.V., Banham D., Brown D., Chillingworth T., Connor R.,

A Badcock K., Banham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

RA Oliver S., Seeger K., Skelton S., Squares R.,

RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the

RT complete genome sequence.";

RT Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CDC 1551 / Oshkosh,
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Feterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 184:5479-5490(2002).
-!- FUNCTION: Catalyzes hydrolytic cleavage of carbon-halogen bonds is halogenated aliphatic compounds, leading to the formation of the corresponding primary alcohols, halide ions and protons (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
CATALYTIC ACTIVITY: 1-haloalkane + H(2)0 = a primary alcohol +
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                       Length 300;
BASE (BY SIMILARITY).

T -> A (IN REF. 1).

N -> K (IN REF. 1).

BCFA71EC43529F7B CRC64;
                                                                                    Score 36; DB 1;
Pred. No. 26;
1; Mismatches 4
                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DHAA OR RV2579 OR MT2656 OR MTCY227.22C.
                                                                                                                                                                                                                                                                                     300 AA
 273 273 BA
96 96 T
120 120 N
300 AA; 33730 MW;
                                                                                       52.9%;
                                                                                                                         7; Conservative
                                                                                                                                                             2 VRPYRTSRYLEI 13
                                                                                                                                                                                 | || :| :| | VEPYGQPKYLEI 17
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laboratory strains."
                                                                                                      Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                 DHAA MYCTU
Q50642;
 ACT SITE
CONFLICT
CONFLICT
SEQUENCE
                                                                                       Query Match
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EMBL; Z77724; CAB01264.1; -

-!- SUBUNIT: Monomer (By similarity). -!- SIMILARITY: Belongs to the haloalkane dehalogenase family. Subfamily 2.

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                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                       ;
                                                                                                                                                                               DB 1; Length 300;
26;
                                                                                                                        NUCLEOPHILE (BY SIMILARITY).
ACID (BY SIMILARITY).
BASE (BY SIMILARITY).
                                                                                                                                                                                                       4; Indels
                                                                                                                                                          E8F4854749F22562 CRC64;
                                                                                                                                                                                 Score 36; DB 1
Pred. No. 26;
1; Mismatches
                                                                                                                                                                                                                                                                                      5, 2004, 08:01:39
                              Tuberculist; Rv2579; -.
HAMAP; MF 01231; -; 1.
HAMAP; MF 01231; -; 1.
InterPro; JPR000073; A/b hydrolase.
InterPro; JPR0000379; Ser_estrs.
Ffam; PR00561; abhydrolase; 1.
Ffam; PR00412; BPOXHVDRLASE.
HYdrolase; Complete proteome.
ACT_SITE
EMBL; AE007099; AAK46969.1; -. PIR; B70725; B70725.
TIGR; MT2656; -.
                                                                                                                                               273 273 E
300 AA; 33728 MW;
                                                                                                                                                                                 52.9%;
                                                                                                                                                                         2 VRPYRTSRYLEI 13
                                                                                                                                                                                                                                                     6 VEPYGQPKYLEI 17
                                                                                                                                                                                                                                                                                      Search completed: October
Job time: 2.16358 secs
                                                                                                                                                ACT SITE
SEQUENCE
 STTTT SO STATE SO
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methanopyru

Q974n2 sulfolobus 001792 caenorhabdi

Q87bj7 xylella fas
Q87bj7 xylella fas
Q8pk7 xanthomonas
Q8pk7 xanthomonas
Q8pk8 crathomonas
Q84sf5 cryza sativ
Q84sf5 cryza sativ
Q84sf5 cryza sativ
Q84x1 pseudomonas
Q8x24 escherichia
Q8x24 escherichia
Q8x34 escherichia
Q8x37 escherichia
Q8x972 escherichia
Q8x973 drosophila
Q8w8f2 drosophila

Q8lre0 oryza sativ

1

OM protein

Run on:

Sequence:

Minimum DB R Maximum DB R

Searched:

Database :

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SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
STRAIN=Sprague-Dawley;
MEDLINE=98030622; PubMed=9361017;
Spiro M.J. Bhoyrov V.D., Spiro R.G.;
"Molecular cloning and expression of rat liver endo-alpha-mannosidase, an N.linked oligosaccharide processing enzyme.";
J. Biol. Chem. 272:29356-29363(1997).
EMBI: AF023657; AABB6925.1;
SEQUENCE 451 AA; 51671 MW; 5A987EFD07585066 CRC64;
                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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Pred. No. 22;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                           451
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091N47
09YHE1
08PF48
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Q22600
Q8LRE0
                                     Q8PK77
Q9PAQ7
Q84SF5
Q7UW68
Q884I1
Q884I1
                                                                                                            Q92RU9
Q8X972
                                                                                                                             Q9QLJ3
Q8IRJ0
Q86LF2
Q9WOR3
Q8WSF2
                      Q87BJ7
Q8P8P5
                                                                                     Q8XBX4
Q8FK34
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                                                                                                                                                                                                    Q84AM7
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01-JAN-1998 (TrEMBLrel. 05, La
01-NOV-1998 (TrEMBLrel. 08, La
Endo-alpha-D-mannosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative 2
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DYRPHKPSLYLEI 427
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                                                                                                              Rattus norvegicus (Rat)
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035390
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081ag8 arabidopsis

09m1x7 arabidopsis

09m1y7 arabidopsis

09siy9 arabidopsis

08u8y6 agrobacteri

08c0n9 mus musculu

08c0n9 mus musculu

08c0n9 musculu

08c0n1 streptococc

07x284 nonomuraea

02v3s8 loligo opal

02v3y1 drosophila

03v3y1 drosophila

08m299 drosophila

08m299 bordetella

07w320 bordetella
                                                     October 5, 2004, 07:34:11; Search time 6.88117 Seconds (without alignments) 596.081 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                              1017041
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                              1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                       protein search, using sw model
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Q8LAQ8
Q9MLK7
Q9LTU1
Q9SLY0
Q8U8Y6
Q8U8Y6
Q8CON9
Q52001
P91590
Q52001
Q0XX84
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sp_human:*
sp_inveriebrate:*
sp_mammal:*
sp_mno:*
sp_organelle:*
sp_phage:*
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sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext
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sp_bacteriap:*
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1: sp_archea:*
2: sp_bacteria:*
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                                                                                    US-09-805-290A-10
68
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seq length: 2000000000
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sp rodent:*
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Perfect score:
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Gaps

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Created) Last sequence update) 272 AA

(TrEMBLrel. 22, (TrEMBLrel. 22,

OSLAQ8 QSLAQ8; 01-OCT-2002 ( 01-OCT-2002 (

Q8MZ99 O80652 Q7WGG8 Q7W4Z0

Result No.

PRT;

PRELIMINARY;

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"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Eujii C.Y., Mason T.M., Bowman C.L., Barnstead M.B., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.B., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Salzberg S.L., Fraser C.M., Venter J.C.,
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                          Entaryoca, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Makaryota, Viridiplantae, Streptophyra, Embryophyta; Tracheophyta; Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                       Sato S., Nakamura Y., Kaneko T., Kato E., Asamizu E., Tabata S.; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                      01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Replication protein Al-like.
Arabidopsis thaliana (Mouse-ear cress).
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Pred. No. 44;
4; Mismatches
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DNA Res. 7:131-135(2000).

EMBL; AB024034; BAB02796.1; -.

InterPro; IPR003871; DUF223.

InterPro; IPR008954; Nucleic_acid_OB.

Pfam; PF02721; DUF223; 1.
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MEDLINE=20277480; PubMed=10819329;
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01-JUN-2003 (TrEMBLrel. 24, La:
Putative WD-40 repeat protein.
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53.8%;
  10 DIRPYKTSWRIQV 22
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Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                      NCBI TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Columbia;
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                     Hypothetical protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Etreptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                            SEQUENCE FROM N.A.
Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome annotation.";
Genome Biol. 0:0-0(2002).
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Pred. No. 22;
5; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                 Troukhan M., Alexandrov N., Lu Y.-P., Flavell
                                                                                                                                                                                                                                                                                                                            Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Feldmann K.;
Feldmann K.;
Full-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR.2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY087671; AAM65208.1;
InterPro; IPR005162; Retrotrans_gag.
Ffam, PF0372; Retrotrans_gag. I.
Hypothetical protein.
SEQUENCE 272 AA; 30811 MW; 9C889BD760029D09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVALUATION AND ACTION OF THE EMBL/GenBank/DDBJ databases. Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; All38654; CAB86685.1; -147356; T47356; T47356. T17556. InterPro; IPR003871; DUF223. InterPro; IPR008994; Nucleic_acid_OB. Pfam; PF02721; DUF223; 1. Hypothetical protein. SEQUENCE 303 AA; 34913 MW; SFFESC14628BA2E7 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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DTHPHRMSRYIQL 109
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Best Local Similarity 46.2
Matches 6; Conservative
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Hypothetical protein.
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01-OCT-2000
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DD BREAR READERS OF THE READERS OF T

RESULT 3

Best Loc Matches

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Nature 402:761-768(1999),

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Gaps

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SEQUENCE
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MEDLINE=2160855; PubMed=11743194;
MEDLINE=2160855; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
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MEDLINE=21608550; PubMed=11743193;

Mod D.E., Kitajima J.P.,

Mod D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Mod D.W., Setubal J.C., Kaul R., Mod G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Rutyavin T., Levy R., Lim M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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ATU3952 OR AGR L 1801.
ATU3952 OR ACR S AFF ATU3952 OR ACR S ATU3051 AND ATU3051 AND ATU3051 AND ATU3051 AND ATU3051 ATU3051 AND ATU3051 ATU305
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1; Mismatches 3; Indels
                                                                                                                                                                                       Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC007020; AAD25679.1; -.
PIR; B84828; B84828.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 4.
PROSITE; SM00120; WD40; 4.
PROSITE; PS50082; WD REPEATS 1; 1.
PROSITE; PS50082; WD REPEATS 2: 1.
PROSITE; PS50082; WD REPEATS 2: 1.
REPEAT: JS 980094; WD REPEATS REGION; 2.
REPEAT: MD REPEATS SEQUENCE 775 AA; 88051 MW; CBFC6F54B528F4EA CRC64;
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EMBL, AE008288; AAK89474.1; --
PIR, AD3042; AD3042.
PIR, H98243;
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 66...
Best Local 8; Conservative
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[2]
SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
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STRAILS-CAPEL/G17 IISSUE=Testis;
STRAILS-CAPEL/G17 IISSUE=Testis;
The FANTOM Consortium,
The FANTOM Consortium,
The RANTOM Consortium,
The RANTOM Consortium,
The ALEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:653-573 (2002).
MGD, MGI:2444484; 4932701.02Rik.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                            58.8%; Score 40; DB 16; Length 442; 58.3%; Pred. No. 51; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus sp., and
Entercoccus faecalis (Streptococcus faecalis).
Plasmid piPSOJ, and Plasmid pRE25.
Bacteria, Pirmicutes, Lactobacillales, Streptococcaceae;
                                                                             442 AA; 48309 MW; B074DB4BCFFBB62D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462 AA; 53199 MW; 5EA81B9C5075E684 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2003 (TrEMBLrel. 23, Last sequence update) 01-UTN-2003 (TrEMBLrel. 24, Last annotation update) Endo-alpha-D-mannosidase homolog. 4932703LK.

Mus musculus (Mouse)
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Last annotation update)
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SPECIES=E.faecalis; STRAIN=RE25; PLASMID=PRE25.
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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InterPro; IPR000205; NAD_BS.
Pfam; PF01266; DAO; 1.
Complete proteome.
SEQUENCE 442 AA; 48309 MW
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Best Local Similarity 53.0-
7; Conservative
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                        421 DPRPYRYSRFFD 432
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NCBI_TaxID=1306, 1351;
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MEDINE-96139039; PubMed-8587103;
MEDINE-96139039; PubMed-8587103;
MEDINE-96139039; PubMed-8587103;
Glutathione S-transferase and S-crystallins of cephalopods: evolution from active enzyme to lens-refractive proteins.";
J. Mol. Evol. 41:1049-1056(1995).
BMBL; U19300; AAA97551.1;
HSSP; P46088; 2680.
                                                                                                                                                                              STRAIN=ATCC 39727;
Sosion M., Straichi S., Beltrametti F., Lazzarini A., Donadio S.;
Sosion M., Straichi S., Beltrametti F., Lazzarini A., Donadio S.;
Sosion M., Straichi S., Beltrametti P., Lazzarini A., Donadio S.;
A40926 by Nonomuraea sp.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ561198; CAD91202.1;
EMBL, AJ561198; CAD91202.1;
ACYltransferase, Carboxypeptidase, Glycosyltransferase, Monooxygenase.
SEQUENCE 196 AA; 22157 MW; 003AA44D19127982 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loligo opalescens (California market squid).
Eukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea,
Decapodiformes, Loliginidae, Loligo.
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                                           Nonomuraea sp. ATCC 39727.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.
NCBI_TaxID=93944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.4%; Score 39; DB 2; Length 196; 58.3%; Pred. No. 34; 7ative 3; Mismatches 2; Indels
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Last sequence update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
S-crystallin.
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InterPro; IPR004045; GST_Nterm.
InterPro; IPR003033; S_CTystallin.
Pfam; PP00043; GST_C; I.
Pfam; PP00798; GST_N; I.
PRINTS; PR01269; SGRXSTALLIN.
SEQUENCE 217, AA; 26113 MW; 66D4D
Putative VanY-type carboxypeptidase
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
CG16848 protein.
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Best Local Similarity 58.5.
The 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=31211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Q25368
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0
           Schwarz F.V., 'Perreten V., Teuber M.;
"Sequence of the 50-kb conjugative multiresistance plasmid pRE25 from "Sequence of the 50-kb conjugative multiresistance plasmid pRE25 from Entercooccus facealis RES5.";
Plasmid 46:170-187(2001)
EMBL; L39769; AAA99466.1; --
EMBL; X2945; CAC20179.1; --
EMBL; X2945; CAC20179.1; --
EMBL; X2945; CAC20179.1; --
EMBL; PS09591; P:unidirectionsomal DNA; IEA.
GO; GO:0009291; P:unidirectional conjugation; IEA.
InterPro; IPR005053; MobA_MobL.
Pfam; PF03389; MobA_MobL; 1.
Plasmid.
SEQUENCE 654 AA; 76493 MW; C3EE5B8B84468600 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=97330926; PubMed=9187361;
Cariallo L., Ristoratore F., Zanetti L.;
An new transglutaminase-1186 from the ascidian Ciona intestinalis.";
FEBS Lett. 408.171-176(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ciona intestinalis.
Bukaryota: Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
NCBI_TaxID=7719;
                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; Y10212; CAA71263.1; -.
HSSP; P00488; IGGU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB Pred. No. 77; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR00858; Transglut C.
InterPro; IPR002931; Transglumase like.
Pfam; PF00827; Transglutamin C; I.
Pfam; PF00868; Transglutamin C; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01841; Transglut_core; 1.
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                                                                                                                                                                                                                                                                                                                                                                                  58.8%;
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Best Local Similarity 60...
Best 5; Conservative
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nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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KPFQTSRYLD 427
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EVRPYRSSR 740
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  PubMed=11735367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transglutiminase
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01-0CT-2003
01-0CT-2003
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RESULT 10

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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-EV. Columbia, Federspiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R., Au M., Araujo R., Buehler E., Dewar K., Feng J., Kim C., Li Y., Oji O., Osborne B.I., Shinn P., Sun H., Toriumi M., Vysotskaia V.S. Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AC004266, AAG34353.1; BIR; T00447; T00447.
                                                                                                                                                      SEQUENCE FROM N.A.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Konmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                   Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Nooptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBL TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Length 254;
                                                                                                                                                                                                                                                                                         Celniker S.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AY113289; AAM29294.1;
FlyBase; FBRD032522; CG16848.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
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TIGRPAMS; TIGRO1615; A_thal 3542; 1.
SEQUENCE 258 AA; 29578 MW; FBC341434DFA6380 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002500; PAPS reduct.
Pfam; PF01507; PAPS reduct; 1.
SEQUENCE 254 AA; 29730 MW; 37F06F7895A282C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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ilarity 66.7%; Pred. No. 45;
Conservative 3; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.4%; Score 39; DB 72.7%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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PWRTSRYMQ 207
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nes 8; Conserv
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es 6; Conser
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., Gutton G.R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Button G.R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Button G.R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Bandon R.C., Rogers Y.-H.C., Blazej R.G., Champpe M., Pefelffer B.D., Randon R.C., Bearen A., Barendale M.D., Ballew R.M., Basu A., Barendale J., Glazej R.G., Champe M., Pefelffer B., Ballew R.M. Basu A., Barendale J., Barman B.P. Bhandari D., Belbhakvi D., Ballew R.M. Basu A., Barendale J., Barman B.P. Bhandari D., Belbhakvi B. Buttis R.C., Budam D.A., Buller H., Cadeu E., Center A., Chandra I., R. Berson K.Y., Bernos P.V., Berman B.P., Bhandari D., Bolbhakvi S., Dahlke S., Dulkovy B., Durbin R.J. Cawley S., Dahlke C. Davengort Lib., Davis E., Downes M. Dugan-Rocha S., Dunkov B.C., Dunn P. R. Durbin K.J. Camley S., Dahlke S., Gelbart M.M., Glaser K., Alleris M.L., Harvey D., Hermande J., Berrison D.L., Roop F., Gorrell J.H., Guz Z., Guan P., Harris M.L., Harvey D., Hermande J.R., Med M.-H., Ibegam C., Allali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z., Liang Y., Mattel B., McInchen G.H., Ke Z., Kulp D., Lai Z., Liang Y., Mattel B., McInchen G.H., Kravitz S., Kulp D., Lai Z., Liang Y., Mattel B., McInchen G.H., Weller B., McInchen G.H., Weller B., McInchen G.H., Weller B., McInchen G.H., Weller B., McInchen G.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Mattel B., McInchen G., Mulkhin N., Mulkhin N., Mulkhin N., Mulkhin N., Mulkhin N., Mulkhin H., Mulkhin H., Mattel B., McInchen G., Milshin N., Mulkhin H., Mattel B., McInchen G., Milshin N., Mulkhin H., Mattel B., Spradling A.C., Stapleton M., Stupe R., Sun B., Spitekas R., Moodage T., Worley K., Wun Suppak, M., Wang Z.-Y., Wasarman D.A., Wang Z.-Y., Wasarman D.A., Walliams S.M., Woodage T., Wooday S., Shulkhin Wang Z.-Y
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0
                Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 5; Length 254;
Pred. No. 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002500; PAPS reduct.
Pfam; PF01507; PAPS reduct; 1.
SEQUENCE 254 AA; 29723 MW; 3D5164772719F06F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003640; AAF53304.1; -
FlyBase; FBGn003252; CG16648
GO; OG:0016740; F:transferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
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Best Local Similarity 72...
8; Conservative
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RHYRTSRWLHI
                                                                                                                                                        SEQUENCE FROM N.A.
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AT21573p.
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01-OCT-2002
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CG16848
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Gaps

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Indels

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RESULT 13

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08M299 1D 08 AC 08 DT 01 DT 01 DE AT

Length 258;

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Gaps

· 0

2; Indels

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AC O7WGG8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE clain the transcriptional regulator.

BD orderella bronchiseptica (Alcaigenes bronchisepticus).

CA Alcaigenaceae; Bordetella.

CA SEQUENCE FROM N.A.

RA BELINE-22827954; PubMed=12910271;

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., RA Achtman M., Atkin R., Hamlin N., Hauser H., Holroyd S., Jagner Hell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagner C., Rabinowitsch E., Rothers S., Sanders B., Squares S., Stevens K., RA Leather S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Numbin L., Whiteheed S., Barrell B.G., Maskell D.J.;

CA Comparative analysis of the genome sequences of Bordetella pertussis, R. Bentles Bricklats; Bricker S., Rabinowitsch C., Standers S., Sanders S., Stevens K., Complete proteoner 322 AA; 34669 MW, F6072C095666D3E6 CRC64;

SQUENCE 322 AA; 34669 MW, F6072C095666D3E6 CRC64;
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Db 170 DVTPYRTDRLVAL 182

1 DVRPYRTSRYLEI 13

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0; Gaps

Query Match 57.4%; Score 39; DB 16; Length 322; Best Local Similarity 53.8%; Pred. No. 57; Matches 7; Conservative 2; Mismatches 4; Indels

Search completed: October 5, 2004, 08:13:14 Job time: 7.88117 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model - protein search, OM protein

October 5, 2004, 07:04:10 ; Search time 9.89043 Seconds (without alignments) 371.381 Million cell updates/sec Run on:

US-09-805-290A-10 68

1 DVRPYRTSRYLEI 13 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:\* Database :

geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2002s:\*
geneseqp2003as:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STEAMMER

SUMMARIES	D Description	E10542 Aae10542	AAE10559 AAE10559 HPL inhib	AAE10540 Aae10540 Llama spe	AAE10552 HPL inhib	41 Aae10541	AAE10554 APL inhib	AAE10543 Aae10543 Llama spe	AAB45097 Aab45097 Human sec	Ade54766	'n	Aag06655	554	962	ABU45234 Protein	$\Delta$	555	529	Aag31528 Arabi	330	987	AAG31527 Arabidops	Abb90986	63 Abu33563	щ	
	H	4 A			4 A	4 Y	4 Z		3	·	·					6 A							•	•	4	
	Length DB	13	130	13	130	13	130	13	142	451	252	272	281	727	944	961	90	208	238	250	254	258	509	558	52	
de	ery	100.0	100.0		œ.	97.1	۲.	94.1	ä	ä	60.3	ö		60.3	60.3	60.3	57.4	57.4	57.4	,57.4	57.4	57.4	57.4	٠.	55.9	
	Score	9	68	67	67	99	99	64	42	42	41	41	41	41	41	41	39	39	99	39	9	39	39	39	38	
	Result No.	1	7	m	4	2	9	7	60	on	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	

Adc89474 Ribosomal Adc01045 Enterohae			Abg13829 Novel hum	Abb57915 Drosophil		Aau75885 Human adh	Aae26420 Human tra	Abb66499 Drosophil	Abp35493 Human ORF	Aaw87540 Peptide d	Abg24628 Novel hum	Aau62932 Propionib	Abm59451 Propionib	Abul8705 Protein e	Abul7607 Protein e	Adc94988 E. faeciu	Abu22918 Protein e	Aaw87531 An antitu
ADC89474	ABM67347	ABG24803	ABG13829	ABB57915	ABG99907	AAU75885	AAE26420	ABB66499	ABP35493	AAW87540	ABG24628	AAU62932	ABM59451	ABU18705	ABU17607	ADC94988	ABU22918	AAW87531
7	· vo	4	4	4	9		w	4	Ŋ	N	4	4	ø	_	9	•	9	01
103	009	614	841	916	967	1441	1718	3503	57	58	79	91	91	262	270	391	465	266
55.0	55.9	55.9	55.9	55.9	55.9	55.9	55.9	55.9	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4
3 8 8 8	8 8	38	38	38	38	38	38	38	37	37	37	37	37	37	37	37	37	37
26	. 2	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

AAE10542 standard; peptide; 13 AA. AAE10542

RESULT 1

AAE10542;

(first entry) 10-DEC-2001 Llama species antibody VHH CDR3 #11.

Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; muman dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cometic control; body weight; complementarity determining region 3; CDR3.

Lama sp.

EP1134231-A1.

19-SEP-2001.

20-FEB-2001; 2001EP-00200703.

14-MAR-2000; 2000EP-00200930.

(UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.

Œ, Tareilus De Haard JJW, Bezemer S, Van De Burg M,

WPI; 2001-572718/65.

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Disclosure; Page 17; 37pp; English.

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human discary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipse (HPL) or human gastric lipse (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region 

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Gaps

.; 0

Score 68; DB 4; Ler Pred. No. 7.5e-05;

100.0%; Fr. 100.0%;

AAE10540 standard; peptide; 13 AA.

AAE10540;

98 DVRPYRTSRYLEI 110

1 DVRPYRTSRYLEI 13

13; Conservative

Query Match Best Local Similarity Matches 13; Conserv

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Llama antibody, camelid, anorectic, heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11. .35
/label= CDR1
/note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region
                                             100.0%; Score 68; DB 4; Length 13; 100.0%; Pred. No. 5.8e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPL inhibiting VHH fragment, HPL #30 from llama species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49. .64
/label= CDR2
/note= "Complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tareilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                              AAE10559 standard; peptide; 130 AA
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/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2001; 2001EP-00200703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                           1 DVRPYRTSRYLEI 13
                                                                                                                                                                                              DVRPYRTSRYLEI 13
                                                                                                      13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
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                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            light chains
Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1134231-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bezemer S,
                                                                                                                                                                                                                                                                                                                                                                                                 AAE10559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lama sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Llama
                                                                                                      Matches
                                                                                                                                                                                                                                                                                        RESULT 2
AAE10559
IN AAE10559
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AAC1
AAE1
DT 10-D
DE HPL
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                                                                                                          Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; miman dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 67; DB 4; Length 13;
Pred. No. 8.9e-06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                              Tareilus
                                                                                                                                                                                                                                                                                                                                                                                                              De Haard JJW,
                                                                              Llama species antibody VHH CDR3 #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 17; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE10552 standard; peptide; 130 AA.
                                                                                                                                                                                                                                                                                              20-FEB-2001; 2001EP-00200703.
                                                                                                                                                                                                                                                                                                                             14-MAR-2000; 2000EP-00200930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.5%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                               ΣÌ
                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVRPYRTSRYLEI 13
                                                                                                                                                                                                                                                                                                                                                                                                              Van De Burg
                                                                                                                                                                                                                                                                                                                                                             (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-572718/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13 AA;
                                               10-DEC-2001
                                                                                                                                                                                                                               EP1134231-A1.
                                                                                                                                                                                                                                                              .9-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                               Bezemer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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AAE10552
ID AAE1
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #30 from lama (camelid) species

Sequence 130 AA;

Example 2; Page 10; 37pp; English.

Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.

Llama species antibody VHH CDR3 #10.

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                                                                                 Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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/label= CDR3
/note= "Complementarity determining region 3"
                                                                                                                                                                                                                          'note= "Complementarity determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 130;
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Pred. No. 0.00012;
1; Mismatches 0; Indels
                                                       HPL inhibiting VHH fragment, HPL #12 from llama species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      De Haard JJW, Tareilus E;
                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 9; 37pp; English.
                                                                                                                                                                                                                                        50. .64
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2001; 2001EP-00200703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.5%;
                                                                                                                                                                                                 31. .35
/label= CDR1
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nes 12; Conservative
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                          10-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNILEVER NV.
UNILEVER PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-572718/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heavy chain var:
of light chains
                                                                                                                                                                                                                                                                                                                                                    EP1134231-A1.
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AAE10552
                                                                                                                                                  Lama sp
                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                               Key
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New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid

Disclosure; Page 17; 37pp; English.

of light chains.

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Tareilus

De Haard JJW,

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Bezemer S, Van De Burg (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.

WPI; 2001-572718/65.

20-FEB-2001; 2001EP-00200703. 14-MAR-2000; 2000EP-00200930.

EP1134231-A1.

Lama sp.

19-SEP-2001.

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                                                                                                                                                                                                                                                                                                                                                                        The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody; camelid; anorectic; heavy chain variable domain; VHH; dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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//label= CDR1
//nabel= CORplementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 66; DB 4; Length 13;
Pred. No. 1.4e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPL inhibiting VHH fragment, HPL #14 from llama species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE10554 standard; peptide; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.1%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVRPYRTSRYLEI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Llama antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE10554;
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Region
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Matches
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AAE10541 standard; peptide; 13

RESULT 5

AAE1054

(first entry)

10-DEC-2001

AAE10541;

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DVRPYRTSRYLEV 110

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1 DVRPYRTSRYLEI 13

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19-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #14 from lama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Llama antibody, camelid, anorectic, heavy chain variable domain, VHH, uhuman dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL, food; human gastric lipase; HGL, cosmetic control; body weight; complementarity determining region 3; CDR3.
                                                                                                                                                                                                                                                                                                                                                                       ntibody or its fragments for inhibiting human dietary enzymes, I for cosmetic control of body weight of human beings, comprises chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
50. 64
/label= CDR2
/note= "Complementarity determining region 2"
                                               98. 110
/label= CDR3
/note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 66; DB 4; Length 130
Pred. No. 0.00018;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                          Tareilus
                                                                                                                                                                                                                                                                                                          De Haard JJW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Llama species antibody VHH CDR3 #12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE10543 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 9; 37pp; English.
                                                                                                                                                                                      20-FEB-2001; 2001EP-00200703.
                                                                                                                                                                                                                     14-MAR-2000; 2000EP-00200930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 92.3%,
Conservative
                                                                                                                                                                                                                                                                                                        Van De Burg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DVRPYRTSRYLEI 13
                                                                                                                                                                                                                                                    (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
                                                                                                                                                                                                                                                                                                                                         WPI; 2001-572718/65.
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Misc-difference 13
                                                                                                                                                                                                                                                                                                                                                                                                                             of light chains,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 130 AA;
                                                                                                                   EP1134231-A1
                                                                                                                                                                                                                                                                                                                                                                             antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1134231-A1
                                                                                                                                                    19-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                           useful
 Region
                                                    Region
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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted protein, human; immunosuppressive, antiarthritic; antirheumatic; antiprollerative, eytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; vulnerary; gene therapy; treatment; autoimmune disease; hyperprollerative disorder; cardiovascular disorder; cardiovascular disorder; cerebrovascular disorder; nervous system disorder; infection; skin aging; wound healing; epithelial cell proliferation; transplantation; skin aging;
                                                                                                                                                                                                                                 New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic, control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                   Tareilus E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein encoded by gene 31 homologue.
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Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                 De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB45097 standard; protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.1%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 29; 37pp; English
20-FEB-2001; 2001EP-00200703.
                                         14-MAR-2000; 2000EP-00200930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-1999; 99US-0126506P.
07-JAN-2000; 2000US-0174852P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000WO-US007723
                                                                                                                                                   Van De Burg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
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                                                                                  NV.
PLC.
                                                                                                                                                                                          WPI; 2001-572718/65.
                                                                                (UNIL ) UNILEVER (UNIL ) UNILEVER
                                                                                                                                                                                                                                                                               heavy chain vari
of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13 AA;
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                                                                                                                                                   Bezemer S,
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Best Local S
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Matches
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Komatsoulis G;

Rosen CA, Ruben SM,

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This invention describes novel isolated nucleic acid molecules (1)
encoding a human secreted proteins (II) which have immunosuppressive,
antistribritic, antirhenuatic, antiprofilerative, cytostatic, cardiant,
vasotropic, cerebroprotective, nootropic, neuroprotective, antibacterial,
virucide, fungicide, ophthalmological and vulnerary activity and can be
used for gene therapy. (I) and (II) are used to prevent, treat or
used for gene therapy. (I) and (II) are salso used in
diagnosing a pathological condition in e.g. humans, mice, rabbits, goats,
horses, cats, dogs, chickens or sheep. (I) and (II) are also used in
diagnosing a pathological condition or susceptibility to a pathological
condition. The antibodies to (II) can also be used in alleviating
symptoms associated with the disorders and in diagnostic immunoassays
e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA).
Disorders which are diagnosed or treated include autoimmune diseases e.g.
rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest,
cerebrovascular disorders e.g. cerebral ischemia, anglogenesis, nervous
system disorders e.g. Alzheimer's disease, infections caused by bacteria,
viruses and fungi and ocular disorders e.g. cardiac arrest
colliferation, to prevent skin aging due to sumburn, to maintain organs
before transplantation, for supporting cell culture of primary tissues,
to regenerate tissues and in chemotaxis. The polypeptides can also be
to regenerate tissues and in chemotaxis. The polypeptides
to regenerate tissues and in chemotaxie to increase or decrease storage Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers. Disclosure; Page 404-405; 418pp; English capabilities

61.8%; Score 42; DB 3; Length 142; 61.5%; Pred. No. 7.2; 1.1ve 2; Mismatches 3; Indels 1 DVRPYRTSRYLEI 13 Best Local Similarity 61.5 Matches 8; Conservative Sequence 142 AA; Query Match

| ||:: | |||| DYRPHKPSLYLEI 118

(first entry) 29-JAN-2004 Rat Protein AAB86925, SEQ ID NO 571.

Rattus norvegicus

WO2003016475-A2.

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ADE54766 standard; protein; 451 AA ADE54766; 

Rat, pain, neuronal tissue, gene therapy, spinal segmental nerve injury, chronic constriction injury, CCI, spared nerve injury, SNI; Chung.

27-FEB-2003.

14-AUG-2002; 2002WO-US025765

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P.

(GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.

Costigan M; Befort K, Woolf C, D'urso D, 

WPI; 2003-268312/26. GENBANK; AAB86925.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, or human polynucleotides or a polynucleotide acid sequence. Also claimed are a vector comprising the movel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method; an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the regulates the activity of one or more of the cativity in an animal of one or mean of the polypeptides given in the specification, a method for identifying a compound useful in treating contribution, and a pharmaceutical composition comprising the or or more of the cativity is useful for preparing a medicament for treating collypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating collypeptides or their antibodies. The polymucleotide or the compound that the regulates the activity is useful for preparing a medicament for treating collypeptides or their antibodies. The polymucleotide or the compound that the regulates the sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at compound the part of the propersed development of the propersed development of the propersed

Sequence 451 AA;

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Gaps ô

Gaps 0; 61.8%; Score 42; DB 7; Length 451; 61.5%; Pred. No. 26; ive 2; Mismatches 3; Indels Query Match Best Local Similarity 61.5 Matches 8; Conservative

1 DVRPYRTSRYLEI 13

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AAG06656 standard; protein; 252 AA. AAG06656;

Arabidopsis thaliana protein fragment SEQ ID NO: 3507.

(first entry)

17-OCT-2000

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence. 

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000

25-FEB-2000; 2000EP-00301439

99US-0121825P. 25-FEB-1999; 05-MAR-1999;

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- APP - APP	11 - MAY- 14 - MAY- 14 - MAY- 14 - MAY- 14 - MAY- 15 - MAY- 20 - MAY- 21 - MAY- 22 - MAY- 25 - MAY- 27 - MAY-		
\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	. <b>ጜ ፟፠ ጜ ፟፠ ፟፠ ፟፠ ፟፠ ፟፠ ፟፠ ፟፠ ፟፠ ፟፠ ፟፠ ፟፠ ፟፠ ፟፠ </b>	# # # # # # # # # # # # # # # # # # #	

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5-70L-199 6-70L-199 6-70L-199 9-70L-199 9-70L-199 9-70L-199 9-70L-199 1-70L-199	11-001-195 11-001-195 11-001-195 11-001-195 12-001-195 13-001-195	ANGO ANGO ANGO ANGO ANGO ANGO ANGO ANGO
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                                                      990S-0130449P.
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990S-0131449P.
990S-0132484P.
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990S-0132488FP.
990S-0132488FP.
990S-013248PP.
990S-0134218P.
990S-0134218P.
990S-0134218P.
990S-0134218P.
990S-0134221P.
990S-0134370P.
990S-0134370P.
990S-013532P.
990S-013532P.
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
16-APR 11999;
19-APR-11999;
23-APR-11999;
23-APR-11999;
30-APR-11999;
31-APR-11999;
31
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10-JUN-1999;
10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 3506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG06655 standard; protein; 272 AA.
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99US-0123180P.
99US-0125784BP.
99US-0126264P.
99US-0126785P.
99US-0126785P.
99US-0126785P.
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990S-0161359P.
990S-0161359P.
990S-0161360P.
990S-0161920P.
990S-0161922P.
990S-0161932P.
      9908-0157865P

9908-0158023P

9908-0158232P

9908-0159239P

9908-0159239P

9908-0159239P

9908-0159330P

9908-0159331P

9908-0159637P

9908-0159637P

9908-0160741P

9908-0160741P

9908-0160741P

9908-0160741P

9908-0160741P

9908-0160741P

9908-0160741P

9908-0160741P

9908-0160741P

9908-0160770P

9908-0160981P

9908-0160981P

9908-0160981P
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illarity 46.2%;
Conservative 4
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DTHPHRMSRYIQL 89
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Best Local Similarity
Matches 6; Conserv
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05-MAR-1999;
09-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
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         06-0CT-1999;
07-0CT-1999;
13-0CT-1999;
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13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
12-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
23-0CT-1999;
26-0CT-1999;
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RR 19-7UV-1999 9905-0144133.P.

RR 20-7UV-1999 9905-014413.P.

RR 21-7UV-1999 9905-014448.P.

RR 21-7UV-1999 9905-014448.P.

RR 21-7UV-1999 9905-014448.P.

RR 22-7UV-1999 9905-014508.P.

RR 22-7UV-1999 9905-014508.P.

RR 22-7UV-1999 9905-014508.P.

RR 22-7UV-1999 9905-01453.P.

RR 23-7UV-1999 9905-01453.P
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 3505.
                                                                                                                                                                                                                                       core 41; DB 3; 1
red. No. 23;
Mismatches 3.
                                                                                                                                                                                                                                        Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                        AAG06654 standard; protein; 281 AA
99US-0159329P.
99US-0159331P.
99US-0159633P.
99US-0159638P.
99US-0160741P.
99US-016076P.
99US-016076P.
99US-016078P.
99US-016081P.
99US-016081P.
99US-016098P.
99US-016098P.
99US-0161905P.
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99US-0161905P.
99US-0161905P.
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990S-0123180P.
990S-0125748P.
990S-0126264P.
990S-0126264P.
990S-0128234P.
990S-0128234P.
990S-0128234P.
990S-0130810P.
990S-0130810P.
990S-0130810P.
                                                                                                                                                                                                                                        60.3%;
46.2%;
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97 DTHPHRMSRYIQL 109
                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                          1 DVRPYRTSRYLEI 13
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Best Local Similarity 46.2
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
12-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
26-0CT-1999;
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05-MAR-1999;
06-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
116-APR-1999;
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23-APR-1999;
28-APR-1999;
30-APR-1999;
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AAG06654
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US-0132407P US-01324867P US-01324867P US-01324867P US-01324867P US-0134218P US-0134218P US-0134219P US-0134219P US-0134219P US-0134219P US-0134219P US-0134219P	9905-0136629F 9905-0136629F 9905-0137222F 9905-0137222F 9905-0137228F 9905-0137244F 9905-0137744F 9905-0137744F 9905-0139452F 9905-0139452F 9905-0139452F 9905-0139452F 9905-0139452F 9905-0139452F 9905-0139456F 9905-0139456F 9905-0139456F 9905-0139456F 9905-0139462F 9905-0139462F 9905-0139462F 9905-0139462F 9905-0139462F	103-0140354 103-01406354 103-0140821 103-0141287 103-0141287 103-0141287 103-01420554 103-01420554 103-01420554 103-01420554 103-01420554 103-01420554 103-01420554 103-014205 103-0143624 103-0144325 103-0144333
- APR-1999 - MAY-1999	25 - MAY - 1999; 25 - MAY - 1999; 26 - MAY - 1999; 27 - MAY - 1999; 28 - MAY - 1999; 29 - MAY - 1999; 21 - MAY -	
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PR 21-JUL-1999; 99US-014508P.
PR 22-JUL-1999; 99US-014508P.
PR 22-JUL-1999; 99US-014508P.
PR 22-JUL-1999; 99US-014508P.
PR 23-JUL-1999; 99US-014513P.
PR 23-JUL-1999; 99US-014730P.
PR 03-AUG-1999; 99US-014730P.
PR 03-AUG-1999; 99US-014730P.
PR 13-AUG-1999; 99US-014730P.
PR 13-AUG-1999; 99US-014730P.
PR 13-AUG-1999; 99US-014730P.
PR 13-AUG-1999; 99US-014730P.
PR 23-AUG-1999; 99US-014932P.
PR 23-AUG-1999; 99US-015130P.
PR 23-AUG-1999; 99US-015130P.
PR 23-AUG-1999; 99US-015130P.
PR 23-AUG-1999; 99US-01550SP.
PR 23-

(3) an isolated

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continued actual (1) an antibody capable of specifically binding antisense nucleic actd; (4) an antibody capable of specifically binding cantisense nucleic actd; (4) an antibody capable of specifically binding cantisense nucleic (5) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the agene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene product for cellular proliferation or the biological services or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a companion acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits states the product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation in cells other than S. typhimurium, control discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, the target prokaryotic essential genes. Note: The sequence data for this proliferation fermat directly from Wilpo at the printed specification, but was obtained for the wind int/wh/hublished not sequence as a for the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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  acid; (2) a host cell containing the vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #30761.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU45234 standard; protein; 944 AA.
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Carr GJ,
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2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 70.0
Lea 7, Conservative
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Trawick JD,
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N-PSDB; ACA49104.
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08-FEB-2002;
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Wall D,
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18 ABU45234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #13489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
24;
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 3
Pred. No. 24;
4; Mismatches
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Carr GJ,
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2001US-00948993.
2001US-0342923P.
2002US-00072851.
                                             990S-0160770P.
990S-0160814P.
990S-0160815P.
990S-0160980P.
990S-0160989P.
990S-016194P.
990S-0161404P.
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99US-0161360P.
99US-0161361P.
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99US-0160767P
99US-0160768P
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46.2%;
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DTHPHRMSRYIQL 118
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Trawick JD,
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N-PSDB; ACA31832.
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Best Local Similarity
Matches 6; Conserv
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25-OCT-2001;
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28-OCT-1999;
29-OCT-1999;
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25-OCT-1

21-OCT-22-OCT- ABU27962,

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Gaps .. 0 Zyskind JW; Xu HH;

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Claim 25;

(ELIT-) 'n,

Wang | Wall |

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

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for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                        Protein encoded by Prokaryotic essential gene #17729.
                   Claim 25; SEQ ID NO 73158; 1766pp; English
                                                                                                                                                                                                                                                                                                                                 ABU32202 standard; protein; 961 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-00815242.
2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
                                                                                                                                                                                                                                                          60.3%;
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 70...
7, Conservative
                                                                                                                                                                                                                                                                                                 PYRTAFYLEV 124
                                                                                                                                                                                                                                                                                   4 PYRTSRYLEI 13
                                                                                                                                                                                                                                                                                                                                                                                                  Klebsiella pneumoniae
                                                                                                                                                                                                                                              Sequence 944 AA,
                                                                                                                                                                                                                                                                                                                                                                                                               WO200277183-A2.
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08-FEB-2002;
06-MAR-2002;
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                                                                                                                                                                                                                                                                                                  115
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the 6213 antisense sequences given in the specification where expression of the muchec acid inhibits proliferation of a cell. Also included are:

of the muchec acid inhibits proliferation of a cell. Also included are:

closed a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) inhibiting cellular proliferation or the activity of a gene in an operon required for luciplication or that has an activity against a biological pathway required for that has an activity against a biological pathway required for that has an activity against a biological pathway in which a proliferation or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of the pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits prolification of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound, a activity; (11) a culture comprising strains in which the gene or medication of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound, a clivity; (11) a culture comprising strains in which the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the contrains; or (13) identifying the target of a compound acids required for collection of an organism. The antisense nucleic acids are useful for for cellular proliferation of an organism are candidate molecules got are useful for for cellular proliferation of an organism or candidate molecules for a candidate molecules for a citiental acids required for cellular candidate molecules for a candidate molecules for a candidate molecules for a candidate molecules for a candidate molecules activity and a candidate and candidate molecules for a candidate activity 
                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.3%; Score 41; DB 6; Length 961; 70.0%; Pred. No. 94;
                                                                                             Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 60126; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                     Malone C,
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Best Local Similarity 70.0.
                                 (ELIT-) ELITRA PHARM INC.
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Trawick JD,
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                                                                                  Wang L,
Wall D,
à
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                                                                                                                                                                                   The first needs to an isolated muciacis acid comparising any one of the 6213 antisease sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisease nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisease nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway concludent for proliferation or that has an activity against a biological pathway in which a proliferation or the the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) prolifing the extent to organism acts; (9) manufacturing an antibiotic; (10) prolification of an organism acts; (9) manufacturing an antibiotic; (10) prolification of an organism acts; (9) manufacturing an antibiotic; (10) prolification of an organism; or (13) identifying the target of a compound that inhibits the towhich each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the confident is overappressed or underexpressed; (12) determining for solidate molecules for rational dangines or proliferation in cells other than S. aureus, S. typhimurium, C. prequired for proliferation in cells other than S. aureus, S. typhimurium, C. the present dayed prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the sequences.
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                                                                                                                                                                        The invention relates to an isolated nucleic acid comprising
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Pred. No. 92;
2; Mismatches 1; Indels
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Gaps

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1; Indels

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AP2416
hypochetical protein all4886 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Date: 14-Dec-2001 #sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <RCHR>A;Residues: 1-152 <RCHR>A;Experimental source: strain PCC 7120
C;Genetics:
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aldehyde dehydroge
L-2,4-diaminobutyr
phospholipase C -
endoglucanase I (E
cellulase (EC 3.2.
cellulase (EC 3.2.
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                                                                      October 5, 2004, 07:36:16; Search time 2.10648 Seconds (without alignments) 593.639 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                283366 segs, 96191526 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                - protein search, using sw model
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AB1205
D61794
G690678
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G71095
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A38165
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Gapop 10.0 , Gapext 0.5
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68
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Maximum DB seq length: 2000000000
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Match Length DB
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317
317
334
452
2237
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          Copyright
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1: pir1:*
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Perfect score:
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Gaps ő

58.8%; Score 40; DB 2; Length 152; llarity 54.5%; Pred. No. 6.1; Conservative 3; Mismatches 2; Indels

Local Similarity

beta-lactoglobulin outer membrane pro	membrane	netical pr			lactaldehyde dehyd	aldehyde dehydroge	periplasmic glucan	protein W09G3.4 [i	vrlC protein - Dic	hypothetical prote		vitellogenin - yel	9	glucagon-36 - spot		(Schizosaccharomyces pombe)		#text_change 03-Dec-1999	2	מיטיי ממודפודי מ				COCCUR. GGGCC	carbs: anocoas;			Length 1225;	4; Indels 0; Gaps 0;		
A05144 B81932		A97396												GCFI	ALIGNMENTS	- fission yeast		evision 03-Dec-1999	F	e.; mcbougail, A.; Kajamuream, a Library, August 1999		ed from GB/EMBL/DDBJ		A LONGRO MATE	972h-; cosmid pYUK71			Score	; Fred. No. 24; 2; Mismatches		
131 2		293 2								526		139				family protein	Schizosaccharomyces pombe	#sequence_revision		or, c., mo Data Libr		translated		(E)	strain 9		. 030	61	53. rative	SDYTNY 13	  DYTRY 208
36 52.9	52.	52	6 52.	6 52.	6 52.	6 52.	6 52.	6 52.	6 52.	6 52.	6 52.	6 52.	5 51.	5 51.		domain fan			1: T39255	the EMBL	number: Z	layzaa eliminary	Tpe: DNA	1-1225 <ste></ste>	al source:		SPAPYUK71 on: 1	E	Simi 7;	1 OVRVRESSDYTNY	: :
90 110 110		9.6														RESULT 1 T39255 probable C2 o	C;Species: Sc	C; Date: 03-Dec-1999	C; Accession:	submitted to	A; Reference number: Z21838	A;Accession: 139233 A:Status: preliminary:	A, Molecule type: DNA	A;Residues: 1-1225 <ste></ste>	A/Closs-Ielelences: Embu:Aulos A/Experimental source: strain	C;Genetics:	A;Gene: SPDB:SPAPYUK71 A;Map position: 1	Query Match	Best Local Matches	Qy	Db 196

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13 92

RVRFSSDYTNY RIRFIGDYRSY

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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Baccissi Escherichia coli
E;Bacsion: G90678
A;Retescher Complete genome sequence of enterohemczrhagic Escherichia coli O157:H7 and genom
A;Rite: Complete genome sequence of enterohemczrhagic Escherichia coli O157:H7 and genom
A;Retescher number: A99629; MUD:21156231; PMID:11258796
A;Recession: G90678
A;Recidues: 1-317 cHAY>
A;Residues: 1-317 cHAY>
A;Residues: 1-317 cHAY>
A;Residues: 1-317 cHAY>
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Genetics:
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 161714
B;Ayer, D.E.; Lawrence, Q.A.; Eisenman, R.N.
Cell 80, 767-776, 1995
A;Title: Mad-Max transcriptional repression is mediated by ternary complex formation with A;Reference number: A56068; MUID:95196269; PMID:7889570
A;Accession: 161714
A;Accession: 161714
A;Accession: Lelminary; translated from GB/EMBL/DDBJ
A;Residues: 1-954 cRES>
A;Residues: 1-954 cRES>
C;Genetics: A;Gene: mSIAB
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Cispecies: Escherichia coli

Cispecies: Escherichia coli

Cispecies: I6-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

Cispecia, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca,

Mature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
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A;Molecule type: DNA
A;Residues: 1-317 <STD>
A;Cross-references: GB:AE005174; NID:g12513180; PIDN:AAG54695.1; GSPDB:GN00145; UWGP:Z044
A;Experimental source: strain 0157:H7, substrain EDL933
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Pred. No. 31;
1; Mismatches
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64;
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Pred. No.
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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A, Gene: Z0442
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson F;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson J; Pieischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Reterence number: A69250; MUID:98049343; PMID:9389475
A;Reterence number: A69250; MUID:98049343; PMID:9389475
A;Reterence number: A69250; MUID:98049347; PMID:9389475
A;Reterence number: A69250; MUID:98049347; PMID:9389475
A;Cross-treferences: GB:AE001024; GB:AE000782; NID:92689347; PIDN:AAB90089-1; PID:9264943
C;Superfamily: phosphoribosylamine-glycine ligase; phosphoribosylamine-glycine ligase homology <PGL>
                                                                                                                                                                                                   RESULT 3
AB1205
mologoperin biosynthesis protein moeA homolog lmo1042 [imported] - Listeria monocytoge (;Species: Listeria monocytogenes C;Species: Listeria monocytogenes C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Accession: AB1205
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AB1205
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker ; Dominguez-Bernal, G.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karser, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MuID:21837279; PMID:11679669
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-407 GGLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: GB:NC_003210, PIDN:CAC99120.1; PID:g16410444; GSPDB:GN00177 A,Experimental source: strain EGD-e C;Genetics:
C;Genetics:
A;Gene: lmo1042
C;Superfamily: molybdenum cofactor biosynthesis protein moeA-2
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Pred. No. 26;
2; Mismatches 2; Indels
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57.4%; Local Similarity 63.6%; les 7; Conservative 2

Query Match

330 QVRAKMASDYT 340

1 OVRVRESSDYT 11

8 qq Query Match
Best Local Similarity 70.0
Matches 7; Conservative

EVEMRESSDY 368 1 QVRVRFSSDY 10

359

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co-repressor protein - mouse

RESULT 5

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8 g

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Sry-related sequence - Tarentola mauritanica (fragment)
C;Species: Tarentola mauritanica
C;Species: Tarentola mauritanica
C;Species: Tarentola mauritanica
C;Sate: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 24-Sep-1999
C;Sacession: 151369
R;Picardo, A.M.; Mueller, U.; Harry, J.L.; Uwanogho, D.; Sharpe, P.T.
PCR Methods Appl. 2, 218-222, 1992
A;Fitle: PCR amplification of SRY-related gene sequences reveals evolutionary conservatic
A;Reference number: 150019; MUID:93184703; PMID:8443573
A;Accession: 151369
A;Estutus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-72 PIC;
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21087
B;Harris; B
B;Ha
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A;Introns: 48/3; 115/3; 181/3; 282/3; 369/1; 524/3; 661/3; 760/3; 839/2; 1065/2; 1278/3;
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C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C,Accession: T21086
B,Harris, B.
R,Harris, B.
R,Harris, B.
R,Accession: T21086
A,Reference number: Z19371
A,Accession: T21086
A,Reference prealiminary; translated from GB/EMBL/DDBJ
A,Rolecule: type: DNA
A,Rolecule: T245 < WIL>
A,Rolecule: T245 < WIL>
A,Rolecule: CESP.F18C12.2a
A,Gene: CESP.F18C12.2a
A,Gene: CESP.F18C12.2a
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C;Genetics:
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Best Local Similarity 87.5
Matches 7; Conservative
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T21086
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Al2071
hypothetical protein all2127 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Accession: Al2071
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A)Status: preliminary
A;Molecule type: DNA
A;Residues: 1-452 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB73826.1; PID:g17131218; GSPDB:GN00179
A;Genetics: A;Geneti
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A;Cross-references: EMBL:U64848; PIDN:AAB04881.1; GSPDB:GN00023; CESP:C50E3.4
A;Experimental source: strain Bristol N2; clone C50E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pypothetical protein C5083.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T29672
B;Geisel, C; Bradshaw, H.
Submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid C50E3.
A;Reference number: Z20662
A;Accession: T29672
A;Accession: T29672
A;Accession: T29672
A;Accession: T29672
A;Accession: Data
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A,Gene. (25SP:C50E3.4
A,Map position: 5.71: 110/3; 140/2; 276/2
A,Introns: 15/3; 53/1; 110/3; elegans hypothetical protein C50E3.4
C,Superfamily: Caenorhabditis elegans hypothetical protein C50E3.4
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Pred. No. 32;
5; Mismatches 0; Indels
           Query Match 55.9%; Score 38; DB 2; Length 317; Best Local Similarity 58.3%; Pred. No. 31; Matches 7; Conservative 1; Mismatches 4; Indels
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T21087
hypothetical protein F18C12.2b - Caenorhabditis elegans
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Best Local Similarity 54.5%;
Matches 6; Conservative
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13 VRVKFASEFSN 23
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Best Local Similarity
Matches 6; Conserva
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1 QVRVRFSSDYTNY 13
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                               RESULT 13

D96947

Dypothetical protein CAC0387 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: D96947

R;Nolly, J.; Brenctt, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S70355
R;Bignell, G.R.; Bruce, I.J.; Evans, I.H.
Curr. Genet. 30, 83-88, 1996
A;Title: Blectrophoretic karyotype of the amylolytic yeast Lipomyces starkeyi and clonin A;Reference number: S70355; MUID:96269334; PMID:8662214
A;Accession: S70355
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A;Residues: 1-92 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK78367.1; PID:g15023237; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: TRP1
C,Superfamily: phosphoribosylanthranilate isomerase; trpF homology
C,Keywords: intramolecular oxidoreductase; isomerase; tryptophan biosynthesis
F;14-228/Domain: trpF homology <TRF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-232 & BLG>
A;Cross-references: EMBL:268292; NID:gl134847; PIDN:CAA92584.1; PID:gl161576
A;Note: the authors translated the codon GCC for residue 211 as Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Lipomyces starkeyi
C;Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
                                                                                     Gaps
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                                         Length 72;
                                                                                  3; Indels
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Pred. No. 13;
3; Mismatches
                                       Score 37; DB 2;
Pred. No. 9.9;
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Pred. No. 34;
3; Mismatches
F;1-72/Domain: HMG box homology (fragment) <HMG>
                                                                                  4; Mismatches
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46.2%;
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                                                                                  6; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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                                       Query Match
Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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RESULT 15 G71095 hypothetical protein PH1028 - Pyrococcus horikoshii

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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C;Accession: G71099
C;Accession: G71095
M; Diduku, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
M; Obfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic an
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-281 <KAW>
A;Residues: 1-281 <KW
A;Residues: 1-
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Pred. No. 41;
3; Mismatches
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 5, 2004, 07:29:35; Search time 1.16358 Seconds (without alignments) 581.749 Million cell updates/sec Run on:

US-09-805-290A-11 68 1 QVRVRFSSDYTNY 13 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	0 8	18 arch	1	075182 homo sapien	12	8	63	92 cavia po	2	34 C	74	33 C	54	65	Q92665 homo sapien	Q8xff6 salmonella		shallot					human	human					dict		Q96pz7 homo sapien	tarentola	Q57785 methanococc
SUMMARIES	ID	YKH3 SCHPO	PUR2 ARCFU	SN3B_MOUSE	SN3B_HUMAN	MG42 TARMA	TRPF_LIPST	ALDA_ECOLI	ATHL_CAVPO	C8BA_BACUK	GUNI_CLOTM	GUNB_CALSA	MANB_CALSA	LG27_EUBMA	RS8 ARCFU	RT31 HUMAN	OPGG_SALTY	SYGB_BUCAP	RRPO_SHVX	VIT1_AEDAE	GLUC CALMI	GLUC_HYDCO	YES7_HAEIN	E320_ADE1A	E320_ADE1P	E320_ADE35	LYCM_STRGL	ARGC_STAAM	GP63_LEIMA	CLH DICDI	CSM1 MOUSE	1	44	Y339_METUA
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d	% Query Match	61.8	57.4	57.4	57.4	54,4					53.7	~:	53.7	ς.	~;	٥.	52.9	∾.	ď	ď	ä	ä	i,	ä	ij	ä	ä	Ξ.	ä	i.	ä	51.5	•	50.0
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	Result No.	7	7	٣	4	ហ	v	7	œ	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P14985 chloris str 008237 vibrio angu P06111 vibrio chol 031112 methanococc P54129 caenorhabdi Q7vas4 prochloroco Q82009 chlamqophi P5658 bos taurus Q9pano xylella fas Q87bg9 xylella fas P46249 cyanidium c Q9rwg7 deinococcus
COAT CSMV OMPV_VIBAN OMPV_VIBAN OMPV_VIBAN PWDC, METMP SRG7_CAEEL DDL, FRONA DDL, FRONA ADA_EOVIN METX_XYLFA METX_XYLFA SECY_CYACA VATB_DETRA
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# ALIGNMENTS

0;

Gaps

.; 0

DOMAIN DOMAIN

Matches

8 g

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SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).

TISSUE=ammmary gland, and Salivary gland;

MEDLINE=22388257; Pubbmed=12477932.

Krausberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Diatchenko L., Marusina K., Peares G.J., Abramson R.D., Mullahy S.J.,

R. Brownstein M.J., Usdin T.B., Deltywik S., Carninci P., Prange C.,

R. Raha S.S., Loqquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A. (ISOFORM 2), FUNCTION, AND INTERACTION WITH FOXK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Inte winged-helix/forkhead protein myocyte nuclear factor beta (MNF-beta) forms a co-repressor complex with mammalian Sin3B.";
Biochem. J. 345:335-343(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, SUBUNIIT, AND SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ayer D.E., Lawrence Q.A., Bisenman R.N., "Mad-max transcriptional repression is mediated by ternary or formation with mammalian homologs of yeast repressor Sin3."; (ell 80:767-776(1955).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Heart;
MEDLINE-20088666; PubMed=10620510;
Yang Q., Kong Y., Rothermel B., Garry D.J., Bassel-Duby R., Williams R.S.,
                                                                                                                                                                                                                                                                                                                                                                                      Length 470;
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            HAMP, MF 00138; atypical; 1.
InterPro_ IPR000115; Gars.
Pfam; PF001071; GARS; 1.
Pfam; PF02842; GARS; 1.
Pfam; PF02844; GARS_N; 1.
Pfam; PF02844; GARS_N; 1.
TIGREMA; TIGR00877; purD; 1.
PROSITE; PS00184; GARS; FALSE NEG.
Pwine blosynthesis; Ligase; Complete proteome.
DOWALN
SEQUENCE 470 AA; 51750 MW; C3B90CED22DCD353 GR
                                                                                                                                                                                                                                                                                                                                                                                   57.4%; Score 39; DB 1; 70.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             062141; 054976; 039VCB8; 039VD25; 10-0CT-2003 (Rel. 42, Created)
11-0CT-2003 (Rel. 42, Last sequence update)
11-VAR-2004 (Rel. 43, Last annotation update)
Paired amphipathic helix protein Sin3b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION.
TISSUB=Kidney;
MEDLINE=95196269; PubMed=7889570;
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 70...
Rest Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-RAY-2000 (Rel. 41, Last amotation update)
Phosphoribosylamine-glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase).
PURD OR AF1157.
Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-VC-16 / DSM 4104 / ATCC 49558;
MEDLINE-96049343; PubMed=9389475;
MEDLINE-96049343; PubMed=9389475;
MEDLINE-96049343; PubMed=9389475;
Klenk H.-P., Clayton R.J., Tomb J.-F., White O., Nelson K.E.,
Klenk H.-P., Clayton R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocapne J.D., Weidman J.F., McDonald L., Utterback T.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.W., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 1; Length 1225; 
Pred. No. 11; 
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      7041FCAA5A6D7B96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                         Pfam; PF00168; C2; 4.

PRINTS; PR00360; C22DOMAIN.

SMART; SM00239; C2; 4.

PROSITE; PS00499; C2_DOMAIN_1; 1.

PROSITE; PS50004; C2_DOMAIN_2; 3.

Hypothetical protein; Transmembrane; Repeat.

Hypothetical protein; Transmembrane; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 AA
                                                                                                                                                                                                                                                                                      167 187 POTENTIAL.
414 518 C2 DOMAIN 1.
691 72 DOMAIN 2.
1024 1121 C2 DOMAIN 3.
1225 AA; 135781 MW; 7041FCAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                   GenebB_SPombe, SPAPYUK71.03c, -.
InterPro, IPR000008, C2.
InterPro, IPR008973, C2_Calb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001024; AAB90089.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 RVKVNFKDDYTRY 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVRVRFSSDYTNY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 53.8
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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HSSP; P15640; 1GSO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUR2 ARCFU
029108;
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                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
SEQUENCE
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Gaps

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4,

Mismatches

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7; Conservative

Matches

REMEL; 138622; AA659774.1; -.
REMEL; AF038848; AAC04821.1; -.
REMEL; BC020169; AAH2106.1; -.
REMEL; BC0714; IG1714
REMEL; BC07005138; -.
REMEL; BC07005138; -.
REMEL; BC07005138; -.
REMEL; BC07000514; Firanscription co-repressor activity; IDA.
GO; GO:000514; Firanscription co-repressor activity; IDA.
GO; GO:000514; Firanscription of transcription, DNA-d. ..; IDA.
REPERO; IRRO3822; PAH;
REPERO; REMEL; REPERSSOR; Repeat; Nuclear protein;
Alternative splicing; 3D-structure.
REPERT PAH 1. PAH 2. RAKKIRGTKOLSIAAVGKY -> VGLQLKCAVVWFGYCTAE KKMKLRGTKDLSIAAVGKYGTLQEFSFF -> VLVHVWVLP AHGRSGVEAQAAGEPEARA (in isoform 3). /FTId=VSP\_008227.
Missing (in isoform 3).
/FTId=VSP\_008228.
A - G (IN REF. 2).
S - P (IN REF. 2).
W, 31F4BE14523EA213 CRC64; E (in isoform 2).
/FTId=VSP 008225.
Missing (In isoform 2).
/FTId=VSP 008226. 230 A -> 233 S -> 109393 MW; 3 954 302 954 230 233 954 AA; 294 303 CONFLICT CONFLICT SEQUENCE REPEAT VARSPLIC VARSPLIC **JARSPLIC** VARSPLIC REPEAT NAME OF THE PROPERTY OF THE PR

Score 39; DB 1; Length 954; Pred. No. 29;

57.4%;

Query Match Best Local Similarity

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STATESTEE OF 2-353 AND 711-1130 FROM N.A.

SECURISCE OF 2-353 AND 711-1130 FROM N.A.

TISSUE=Lung, and Skin,

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,

Altasner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Logelland N.A., Ferens G.G., Abrameon R.D., Mullahy S.D.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Logellano N.A., Perers G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Alting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahaseley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rahaseley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rahaseley A.C., Grimwood J., Schmutz J., Myers R.M.,

Radinger A.C., Schmut J.E., Jones S.J.M., Marra M.A.;

Reneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse CDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16803(2002).
-!- FUNCTION: Acts as a transcriptional repressor. Interacts with MXII
- to repress MYC responsive genes and antagonize MYC oncogenic
activities. Interacts with MAD-MXX heterodimers by binding to MAD.
The heterodimer then represses transcription by tethering SIN3B to
DNA. Also forms a complex with FOXKI which represses transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I. SUBUNIT: Interacts with FOXKI/MNF, MXII and MAD (By similarity).
-I. SUBCELLUIAR LOCATION: Nuclear (By similarity).
-I. SIMILARITY: Contains 3 PAH (paired amphipathic helix) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
MEDLINE=98403880; PubMed=9734811;
Isbikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
Isbikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. X.
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                SN3E HUMAN STANDARD, PRT, 1130 AA.

ID SN3B HUMAN STANDARD, PRT, 1130 AA.

O 05182, QRHB34, Q9BSC8,
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Paired amphipathic helix protein Sin3b.
GN SIN3B OR KIAA0700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB014600; BAA31675.1; ALT_INIT.
STATES OVENESSDYTHY 13
                                                43 QVKIRFGSDPATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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Query Match
Best Local Similarity
Matches 7, Conserv
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=29829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
                                                                                TRPF LIPST
Q01128;
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                                           RESULT 6
TRPF_LIPST
ID _TRPF_L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALDA ECOLI
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                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=53184703; bubmed=8443573;

CODIAL A.M., Mueller U., Harry J.L., Uwanogho D., Sharpe P.T.;

"PCR amplification of SRY-related gene sequences reveals evolutionary conservation of the SRY-box motif.";

PCR Methods Appl. 2.218-222(1993).

-! SUBCELLULAR LOCATION: Nuclear (Potential).

-! SIMILARITY: Contains 1 HMG box domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Gekkota, Gekkonidae, Tarentola.
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                MIM, 607777; -
InterPro, 187003822; PAH.
Pfam, PRO3671; PAH, 3
Transcription regulation; Repressor; Repeat; Nuclear protein.
                                                                                                                                                                                                                                                           57.4%; Score 39; DB 1; Length 1130;
53.8%; Pred. No. 35;
tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                               321 367 PAH 3.
1130 AA; 129359 MW; B767339317ECC96D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9E2364AA414751F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1;
Pred. No. 4.4;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 31, Last sequence update) (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M86337; AAA49621.1; -.
PIR; 151369; 151369.
HSSP; P48436; 1SX9.
InterPro; IPR000135; Highmoblty 12.
InterPro; IPR000135; Highmoblty 12.
PFan; PR0055; HMG box; 1.
PRINTS; PR00886; HIGHMOBLTY12.
SMART; SM00398; HMG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HMG BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRY-related protein MG42 (Fragment).
                                                                                                                                                        PAH 1.
PAH 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50118; HMG_BOX_2; 1.
DNA-binding; Nuclear protein.
NON_TER 1 1
DNA_BIND 1 69 HM
NON_TER 72 72
EMBL; BC005113; AAH05113.1; -. EMBL; BC025026; AAH25026.1; -. Genew; HGNC:19354; SIN3B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Gecko)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 AA; 8814 MW;
                                                                                                                                                                                                                                                                                                                                                   1 OVRVRESSDYTNY 13
                                                                                                                                                                                                                                                                                                                                                                                          50 OVKIRFGSDPATY 62
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                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                        105
236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tarentola mauritanica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
'... 6; Conserve
                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8569;
                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
SEQUENCE
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                             Query Match
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P40651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
MG42_TARMA
MG42_TARMA
MG42_TARMA
MG42_TARMA
MG62_TARMA
MG
                                                                                                                                                                            REPEAT
                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                       Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene.";
Cur. (Genet. 30:83-88(1996).
-!- CATALYTIC ACTIVITY: N-(5-phospho-beta-D-ribosyl)-anthranilate = 1-
(2-carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate.
-!- PATHWAY: Tryptophan biosynthesis; third step.
-!- SIMILARITY: Belongs to the tryP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase A (EC 1.2.1.22) (Lactaldehyde dehydrogenase).
ALDA OR ALD OR B1415.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=KL2;

MDDLINE=92011371; PubMed=1917845;
Hidalgo E., Chen Y.-M., Lin E.C.C., Aguilar J.;
"Molecular cloning and DNA sequencing of the Escherichia coli K-12
                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
N-(5'-phosphoribosyl)anthranilate isomerase (EC 5.3.1.24) (PRAI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
SEQUENCE TO 1436;
MEDIAIN=9626934; Pubmed=8662214;
Bignell G.R., Bruce I.J., Evans I.H.;
Bignell G.R., Bruce ic karyotype of the amylolytic yeast Lipomyces stanand cloning, sequencing and chromosomal localization of its TRP1
                                                                                                                                                                           Lipomyces starkeyi.
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Lipomycetaceae, Lipomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·
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Pfam, PF00697, PRAI, 1.
Isomerase, Tryptophan biosynthesis.
SEQUENCE 232 AA, 24625 MW, EGFFIB4EA7D7A9E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 1;
Pred. No. 15;
3; Mismatches
232 AA
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HSSP; Q56320; 1DL3.
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STANDARD;
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1 QVRVRFSSDYTNY 13
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064392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEXEMINE STAILS. | ENG2:

MEDLINE=97443975; PubMed=9298646;
Link A.J., Robison K., Church G.M.;
Link A.J., Robison K., Church G.M.;
Link A.J., Robison K., Church G.M.;
In the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
-:- FUNCTION: ACTS ON LACTALDEHYDE AS WELL AS OTHER ALDEHYDES.
-:- CATALYTIC ACTIVITY: (S)-lactaldehyde + NAD(+) + H(2)O = (S)-
-:- SUBNUHT: Homoretramer.
-:- SUBNUHT: HOMORETRANE.
-:- INDUCTION: BY GROWTH ON FUCOSE, RHAMNOSE, ARABINOSE AND AMINO
ACIDS SUCH AS GLUTAMATE.
-:- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
                                                  SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=9745617; PubMed=9278503;
MEDLINE=9745617; PubMed = 9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                      MEDINE=97251357; PubMed=9097039; MEDINE=97251357; PubMed=9097039; MEDINE=97251357; PubMed=9097039; MEDINE=97251357; PubMed=9097039; Kitagawa H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori H., Mori H., Mori H., Moria K., Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda U., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; Yamamoto Y., Horiuchi T.; Senome Corresponding to the 28.0-40.1 min region on the linkage map."; DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAD (ADP PART) (BY SIMILARITY)
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BY SIMILARITY.

OBSDF44B29E87F4A CRC64;
   l gene encoding aldehyde dehydrogenase.";
Bacteriol. 173:6118-6123(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro, IPR002086; Aldehyde_dehydr.
Pfam; PF00111; Aldedh; 1.
PROSITE; PS00070; ALDEHYDE DEHYDR CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
Oxidoreductase; NAD; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M64541; AAA23427.1;
EMBL; AE000239; AAC74497.1;
EMBL; D90780; BAA15032.1;
EMBL; D90781; BAA15037.1;
PIR; A28165; A38165.
HSSP; P56533; LA4S.
SWISS-27PAGE; P2553; COLI.
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250
284
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250 2
284 2
478 AA;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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NP BIND
ACT SITE
ACT SITE
SEQUENCE
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WEDLINE-90084400.1 PubMed=9872395;

RA MEDLINE-90084400.1 PubMed=9872395;

RA Pestov N.B., Romanova L.G., Korneenko T.V., Egorov M.V., Kostina M.B.,

RA Sverdlov V.E., Askari A., Shakhparonov M.I., Modyanov N.N.;

The combaint sensitive H.K.-Arpase: tissue-specific expression of the mammalian genes encoding the catalytic alpha subunit.";

The companies encoding the catalytic alpha subunit.";

TEBS Lett. 440:320-324(1998).

The FEBS Lett. 440:320-324(1998).

The FONTION: Catalyzes the hydrolysis of ATP coupled with the exchange of H(+) and K(+) ions across the plasma membrane.

The CATALYTIC ACTIVITY: ATP + H(2)0 + H(+)(In) + K(+)(out) = ADP + Dibosphate + H(+)(out) + K(+)(In).

The SUBCRITIC Composed of two subunits: alpha (catalytic) and beta.

The SUBCRITICITY: Found in skin, kidney and distal colon.

The SUBCRITICITY: Found in skin, kidney and distal colon.

The SUBCRITICITY: Found in skin, kidney and distal colon.

The SUBCRITICITY: Belongs to the cation transport ATPases family (P-type ATPASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                                                                                                     i Y.;
guinea
                                      15-UTL-1999 (Rel. 38, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
10-CTL-2003 (Rel. 42, Last annotation update)
10-CTL-2003 (Rel. 42, Last annotation update)
pump) (Non-gastric H-/K+ ATPase alpha chain 2 (EC 3.6.3.10) (Proton ATP12A OR ATP1AL1.
                                                                                                                                                                      Cavia porcellus (Guinea pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Cavildae, Cavia.
NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                  STRAIN=Hartley;
Watenabe T., Saco M., Kaneko K., Suzuki T., Yoshida T., Suzuki "Isolation and characterization of cDNA encoding the putative gpig distal colon H+, K+ -ATPase alpha subunit.";
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R InterPro; IPR00157; ATPase E1-E2.

R InterPro; IPR006069; Cation_ATPase.

InterPro; IPR006069; Cation_ATPase.

InterPro; IPR0060414; Cation_ATPase.

InterPro; IPR008250; E1-E2_ATPase_N.

InterPro; IPR008250; E1-E2_ATPase_N.

R InterPro; IPR005834; HydroJase.

R InterPro; IPR005834; HydroJase.

R Pfam; PF00689; Cation_ATPase_alph.

R Pfam; PF00689; Cation_ATPase_N; 1.

Pfam; PF00122; B1-E2_ATPase, 1.

R Pfam; PF00122; B1-E2_ATPase, 1.

R Pfam; PR00121; ATPASE E1.

R Pfam; PR00119; CATATPASE.

R TIGRRAMS; TIGR01494; ATPASE E1. E2; 1.

R PROSTIE; PS00154; ATPASE E1. E2; 1.

R Hydrolase; Potassium transport; Hydrogen ion transport; Tran Hydrolase; Potassium transport; Tran Hydrolase; Potassium transport; Hydrolase; DOMAIN I DOMAIN I DOMAIN.
1033 AA.
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STANDARD;
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CAVPO
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Gaps

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6; Conservative

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U04365; AAA21118.1; -.

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Score 37; DB 1;
Pred. No. 84;
7; Mismatches
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INTERPRO; IPPRON9965; CelTul bind.
INTERPRO; IPPRON1701; G1yCo_hydro. 9.
INTERPRO; IPPRON9701; G1yCo_trans_6hp.
Pfam; PP00759; G1yCo_trans_6hp.
Pfam; PP00759; G1yCo_hydro_9; 1.
PRODOM; PR001947; CBD_3; 1.
PROSITE; PS00592; GLYČOSYL HYDROL_F9_1; 1.
PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                879 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 56-69
                                                                                                                                                                                                       54.4%;
                                                                                                                                                                                   Query Match
Best Local Similarity 38.50,
Best Local Similarity 38.50,
Conservative
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                                                                                                                                                                                                                                                                                                 573 RIRIRYASNETSY 585
                                                                                                                                                                                                                                                                         1 QVRVRFSSDYTNY 13
                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium thermocellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A47704; A47704.
HSSP; P26221; 1TF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1515;
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                                                                                                                                                                                                                                                                                                                                                                                                CLOIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolates.";
Patent number MO9315206, 05-AUG-1993.
-- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
-- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
-- BETTHELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABABED BEFILES.
-- DEVELOPMENTAL STAGE: The crystal protein is produced during sportlation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
With CAEEP72D83C1F40C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the spore coat. MISCELLANBOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Michaels T.E., Foncerrada L., Narva K.E.; "Process for controlling scarab pests with Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry8Ba (Insecticidal delta-endotoxin CryVIIIB(a)) (Crystaline entomocidal protoxin) (134 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 1; Length 1033; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringiensis (subsp. kumamotoensis).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
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                                               CYTOPLASMIC (POTENTIAL)
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                                                                                                                 CYTOPLASMIC (POTENTIAL)
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                                                                                  (POTENTIAL).
                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                      LUMENAL (POTENTIAL).
              CUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                54.4%;
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01-FBB-1995 (Rel. 31, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Endoglucanase I precursor (EC 3.2.1.4) (EGI) (Endo-1,4-beta-glucanase)
(Cellulase I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Gene sequence and properties of Cell, a family E endoglucanase from Clostridium thermocellum.";
J. Gen. Microbiol. 139:307-316(1993).
-!- FUNCTION: THIS ENZYME CAPALYZES THE ENDOHYDROLYSIS OF 1,4-BETA-GLUCANS. PRINCIPALLY ACTIVE AGANTST BARLEY BETA-GLUCAN.
-!- CATALYTIC ACTIVITY: Bndohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucosidic linkages in cellulose degradation.
-!- PATHWAT: Cellulose degradation.
-!- SATHWATY: Belongs to cellulase family E (family 9 of glycosylhydrolases).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                              Length 1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=NCIB 10682;
MEDLINE=93171873; PubMed=8436949;
Hallewood G.P., Davidson K., Laurie J.I., Huskisson N.S.,
InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PF00555; endotoxin, 1.
Pfam; PF03944; endotoxin, 2.
Pfam; Sporulation.
Sporulation.
SEQUENCE 1169 AA; 133543 MW; 22EEFCF5BD699909 CRC64;
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ACT_SITE
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SEQUENCE
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Best Local
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DOMAIN
DOMAIN
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MANB_CALSA
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AMEDLINE=80909838; PubMed=2789517;

Saul D.J., Williams L.C., Love D.R., Chamley I.W., Bergquist P.I.;

Saul D.J., Williams L.C., Love D.R., Chamley I.W., Bergquist P.I.;

Saul D.J., Williams L.C., Love D.R., Clamley I.W., Bergquist P.I.;

"Nucleotide Sequence of a gene from Caldocellum saccharolyticum

"Nucleotide Sequence of 17439-439 (1989).

"Incleic Acids Res. 17,439-439 (1989).

"Incleic Acids Res. 17,439-439 (1989).

"Incleic Acids Res. 17,439-439 (1989).

"Incleic Action Research Company Company Company Is and Endocuble Action Proceeding Company Incleases in Cellulose and Cellulose, Lichenia and Cereal beta-D-glucosidic linkages in Calulose and Cellulose, Lichenia section; belongs to cellulase family contenting ends of the Chains Section; belongs to Cellulase family Company Sould State Company In the Noteminal Section; belongs to Cellulase Family Company Sould State Company State Company State Company State Company State Company State State Company State Sta
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                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endoglucanase (Acoglucanase Brecursor (Includes: Endoglucanase (EC 3.2.1.4) (Endo-1.4-beta-glucanase) (Cellulase)
(Cellobiohydrolase); Exoglucanase (EC 3.2.1.91) (Exocellobiohydrolase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caldocellum saccharolyticum (Caldicellulosiruptor saccharolyticus).
Bacteria, Firmicutes, Clostridia, Clostridiales, Syntrophomonadaceae,
Caldicellulosiruptor.
                                                                                                                                                                                              Gaps
                                                              (BY SIMILARITY).
                                                                                                                                                                                              ..
                                                                                                                                                               DB 1; Length 879;
                                                                                                                                                                                              Indels
                                                                                                                             35A60069A514A927 CRC64;
Hydrolase; Glycosidase; Signal
                                                CATALYTIC.
CELLULOSE-BINDING (
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                               Score 36.5; DE
Pred. No. 76;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                 PRT; 1039 AA
                                                                                                 SIMILARITY. SIMILARITY.
                                 ENDOGLUCANASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, Q06851; INBC.
InterPro; PR001956; CBD 3.
InterPro; IPR001956; Cellul bind.
InterPro; IPR001000; Glyco_hydro_10.
InterPro; IPR001847; Glyco_hydro_5.
Pfam; PF00942; CBM 3; 1.
Pfam; PF00150; cellulase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00331; Glyco_hydro_10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X13602; CAA31936.1; -.
                                                                                                                 BY
                                                                                                                                 97796 MW;
                                                                                                                                                                53.7%;
                                                                                                                                                                                                                                                      :|::||| |::||
839 EVQIRFSKEDWSNY 852
                                                                                                                                                                                                                                 1 QVRVRFS-SDYTNY 13
                                                                                                                                                                                  Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                               879
879
448
486
   degradation;
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                                                                                                                                   A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=44001;
                               879
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   Cellulose
               SIGNAL
CHAIN
DOMAIN
ACT SITE
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CALSA
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-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caldocellum saccharolyticum (Caldicellulosiruptor saccharolyticus). Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae; Caldicellulosiruptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93119139; PubMed-1476429;
Gibbs M.D., Saul D.J., Luthi E., Bergquist P.L.;
"The beta-mannanase from 'Caldocellum saccharolyticum' is part of
                                                                                                                                                               ENDOGLUCANASE/EXOGLUCANASE B.
THR/PRO-RICH, TANDEM REPEATS OF T-P.
CELLUIGSE-BINDING (BY SIMILARITY).
THR/PRO-RICH, TANDEM REPEATS OF T-P.
PROTON DONOR (POTENTIAL).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-40G'.1991 (Rel. 19, Created)
01-40G-1993 (Rel. 26, Last sequence update)
01-40L-1993 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Beta-mannanase/endoglucanase A precursor [Includes: Mannan endibeta-mannosidase A (EC 3.2.1.78) (Beta-mannanase) (Endo-1,4-mannanase); Endo-1,4-beta-glucanase (EC 3.2.1.4) (Cellulase)].
                                                                                                                                                                                                                                                                                                                                                     Score 36.5; DB 1; Length 1039;
Pred. No. 91;
7; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linkages in mannans, galactomannans, glucomannans, and
                                                                                                                                                                                                                                                                                                                    117641 MW; 0E0378171594DDAE CRC64;
PRINTS; PR00134; GLHYDRLASE10.
ProDom; PD01947; CBD 3; 1.
SMART;:SM00633; Glycollo; 1.
PROSITE; PS00659; GLYCOSYL HYDROL F10; 1.
PROSITE; PS00659; GLYCOSYL HYDROL F5; 1.
Cellulose degradation; Hydrolase; Glycosidase; Repeat; Multifunctional enzyme; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1331 AA.
                                                                                                                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FAMILY 44 OF GLYCOSYL HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                              53.7%;
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                                                                                                                                                                                                                                                                                                                                                                                  42.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVRVRFS-SDYTNY 13
                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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376 41
417 57
571 61
177 177 2285
792 AA;
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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P22533;
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us-09-805-290a-11.rsp

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HSSP; P56209; 1SEI.
TIGR; AF1910; -.
HAMAP; MF 01302; -; 1.
                                                                                                                                                                                                                                                RS8_ARCFU
028369;
                                                                                                            NON TER
SEQUENCE
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Best Local
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RS8_ARCFU
                                                                                                                                                             Matches
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                     CATALYTIC (MANNAMASE ACTIVITY).
PRO/SER/THR-RICH (PT BOX).
SUBSTRATE-BINDING (POTENTIAL).
PRO/SER/THR-RICH (PT BOX).
SUBSTRATE-BINDING (POTENTIAL).
PRO/SER/THR-RICH (PT BOX).
CATALYTIC (ENDOGLUCANASE ACTIVITY).
PRO/DON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
T - P (IN REF. 2).
T - P (IN REF. 2).
T - P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRY-related procein LCZZ7 (Fragment).
Eublepharis macularius (Leopard gecko).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Gekkota; Eublepharidae;
Eublepharus.
                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                  Score 36.5; DB 1; Length 1331;
Pred. No. 1.2e+02;
7; Mismatches 0; Indels 1;
                                                                                                                                                                                               BETA-MANNANASE/ENDOGLUCANASE
                                                                                InterPro; IPR001956; CBD 3.

InterPro; IPR001956; CBD 3.

IN InterPro; IPR001956; CBIJul bind.

InterPro; IPR001547; Glyco_hydro_5.

R Pfam; PF00150; cellulase; 1.

R Prodom; PD001947; CBD 3; 2.

R PROSITE; P800659; GLYCOSYL HYDROL F5; 1.

R Hydrolase; Glycosidase; Cellulose degradation; Signal; Multifunctional enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L01257; AAA71887.1; -.
EMBL; M36063; AAA72861.1; -.
                                                                                                                                                                                                                                                                                                                                    53.78;
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                                                                                                                                                                                                                                                                                                                                                                                    670 EIQIRFNKSDWSNY 683
                                                                                                                                                                                                                                                                                                                                                                          1 QVRVRFS-SDYTNY 13
                                                                                                                                                                                                                                                                                                                                            Local Similarity 42.9
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                                                                            PIR; A48954; A48954.
HSSP; Q06851; INBC.
                                                                                                                                                                                                                                                                                                       340 34
1331 AA;
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ACT_SITE
CONFLICT
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STRAIN=VC2.16 / DSW 4104 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
MEDLINE=98049343; PubMed=9389475;
MA Klenk H.-P., Clayton R.J., Gwinn M., Hickey E.K., Peterson J.D.,
A Richardson D.L., Kerlavage A.R., Graham D.E., Kyrphdes N.C.,
A Richardson D.L., McKenbush J., Lee N.H., Sutton G.G., Gill S.,
A Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
A Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
A Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
A Peterson S., Reich C. I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-!- FUNCTION: One of the primary rRNA binding proteins, it binds directly to 165 rRNA central domain where it helps coordinate assembly of the platform of the 308 subunit (By similarity).
-!- SUBUNIT: Part of the 308 ribosomal subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBINIT: Part of the 30S ribosomal subunit.
-!- SIMILARITY: Belongs to the S8P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 1; Length 71; Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                            23D2076B6C29F71A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last seguence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                               HMG BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
EMBL, M86335, AAA92978.1; -. PIR; ISO541. ISO541. ISO541. ISO541. InterPro; IRX9. InterPro; IPR000910; HMG 12 box. Pfam; PF00505; HMG box; I. SMART; SM00398; HMG; 1. DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seqn
28-FEB-2003 (Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                               52.9%;
                                                                                                                                                                                                                                                                                                                                                      71 71
71 AA; 8919 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30S ribosomal protein S8P. RPS8P OR AF1910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VRVRFSSDYTNY 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausmer R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Butcow K.H., Schefer C.F., Bhat N.K.,
A Diatchento L., Marueina R., Farmer A.A., Rubin G.M., Haieh F.,
A Diatchento L., Marueina K., Farmer A.A., Rubin G.M., Hang L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McDwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
Human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koc E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.;
"The small subunit of the mammalian mitochondrial ribosome:
"Independent of the full complement of ribosomal proteins present.";
J. Biol. Chem. 276:19363-19374 (2001).
-!- SUBUNIT: Component of the mitochondrial ribosome small subunit
(285) which comprises a 128 rRNA and about 30 distinct proteins.
-!- SUBCELLUMAR LOCATION: Mitochondrial.
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                  RT31_HUMAN STANDARD, PRT; 395 AA.
092665; QBWTV8;
28-FEB-2003 (Rel. 41, Created)
10-0CT-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
28 ribosomal protein S31, mitochondrial precursor (S31mt) (MRP-S31)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB=Skin;
Hutcon J.C., Roep B.O.;
"Human Imogen 38. T-cell and antibody responses in newly diagnosed
diabetic subjects.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
InterPro; IPR000630; Ribosomal S8.
Pfam; PF00410; Ribosomal S8; 1.
ProDom; PD001099; Ribosomal S8; 1.
PROSITE; PS00053; RIBOSOMAL S8; 1.
Ribosomal protein; RNA-binding; rRNA-binding; Complete proteome. SEQUENCE 131 AA; 14684 MW; E1B413B376449B3E CRC64;
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                                                                                                                                 Score 36; DB 1; Length 131;
Pred. No. 13;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION.
MEDLINE=21276436; Pubmed=11279123;
                                                                                                                                       52.9%;
                                                                                                                                                         Local Similarity 58.3 tes 7; Conservative
                                                                                                                                                                                                                 2 VRVRFSSDYTNY 13
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Best Local
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RT31_HUMAN
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Search completed: October 5, 2004, 08:01:41 Job time: 3.16358 secs

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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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Pred. No. 41;
4; Mismatches 4; Indels
                                                                                                    EMBL; Z68747; CAA92951.1; -.
EMBL; Z68747; CAA92951.1; -.
EMBL; BC022045; AAH20245.1; -.
Genew; HGNC:16632; MRPS31.
GO; GO:0005739; C:mitochondrion; TAS.
Ribosomal protein; Mitochondrion; TAS.
Ribosomal protein; Mitochondrion; TAS.

Ribosomal protein; Mitochondrion; TAS.

Ribosomal protein; Mitochondrion; TAS.

Ribosomal protein; Mitochondrion; TAS.

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Ribosomal protein; Mitochondrion; TAS.

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Ribosomal protein; Mitochondrion; TAS.
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Description	Q86568 streptococc Q8dzq0 streptococc Q8dzq0 streptococc Q8dy2 yobrio para Q8dy3 yobrio para Q8dy5 pseudomonas Q8mp7 anabaena sp Q8fmt6 corynabacte Q81985 hellanthus Q8439 bacteroides Q9yzn8 japanese ya Q9dy108 japanese ya Q9dy108 japanese ya Q9dy10 japanese y
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	PRT;	Creat	Last	Last		erotype I	bacillale					1,1	354221;	rieser C.	E., Lalioui L.,		coccus ag	• •	3 (2002).	;		IEA.	F:ATP binding; IEA.	F:ATP-binding cassette (ABC)	Finucleotide binding;	, IEA.	Pase.	ansporter		porter; 1		PORTER 1;	PORTER_2;		
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LT 1	Q8E5E8 O8E5E8	01-MAR-2003	01-MAR-2003	01-001-2003	Hypothetical GBS1084.	Streptococcus agalactiae (serotype III).	Bacteria; Fi	Streptococcus	NCBI_TaxID=216495;	[1]	SECUENCE FROM N.A.	STRAIN=NEM316	MEDLINE=22242508; PUDMed=12354221;		Msadek T., 2	Kunst F.;	"Genome sequence of Streptococcus	invasive neonatal	Mol. Microbiol. 45:1499-1513(2002)	EMBL; AL766848; CAD46743.1;	Sagalist; gbs1084;			GO; GO:0004009;	GO; GO:00001			InterPro; IE	Pfam; PF00005; ABC	ProDom; PD00006; ABC transporter;	SMART; SM00382; AAA;	PROSITE; PS00211; ABC_TRANSPORTER_1;	PROSITE; PS	Hypothetical protein; Complete	
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Matches 7; Conservative
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MEDLINE=2222988; PubMed=1220647;
Tetrelin H., Masignani V. Cicelewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkec D.M., Daucherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Lacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                               Gaps
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EMBL; AE014240; AAM9931.1;
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GO, GO:0005524; F:ATP binding; IEA.

GO, GO:0004009; F:ATP-binding cassette (ABC) transporter acti.

GO, GO:0000466; F:Nucleotide binding; IEA.

GO, GO:00006810; P:transport; IEA.

InterPro; IPR003593; AAA ATPase.

InterPro; IPR003593; AAA ATPase.

Probom; PR00005; ABC_transporter.

Probom; PR00006; ABC_transporter.

Probom; PR00006; ABC_transporter.

PROBOM; SM00382; AAA; Z.
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                   63.2%; Score 43; DB 16; Length 513; 70.0%; Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-JUN-2003 (TIEMBLrel. 24, Last sequence update)
01-OCT-2003 (TIEMBLrel. 25, Last annotation update)
Putative IcmF-related protein.
                                                                                                                                                                                                                                                 513 AA
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                                                           2; Mismatches
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2; Mismatches
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Query Match
Best Local Similarity 70.v-
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ATP-binding; Compenions 513 AA;
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Q87PU3;
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087PU3
ID 087PI
AC 087PI
DT 01-JI
DT 01-JI
DT 01-JI
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Gaps
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STRAIN=RIMD 2210633 / Serctype O3:K6;
MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Ilijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.; "Genome sequence of Yibrio parahaemolyticus: a pathogenic mechanism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-224306; PubMed=12534463;
MEDINE-224306; PubMed=12534463;
Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback P., Rizzon M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hohelsel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 16; Length 1129;
Pred. No. 55;
3; Mismatches 3; Indels (
Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1129 AA; 128541 MW; 7D12799A09BA89D9 CRC64;
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Environ. Microbiol. 4:799-808(2002).
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01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Penicillin-binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                       distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
EMBL, AP005078, BAC59671.1; -
GO, GO:0006364; P:RNA processing; IEA.
InterPro; IPR006238; Rib bind factA.
PROSITE; PS01319; REFA, I.
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Pfam; PF00905; Transpeptidase; 1
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NCBI_TaxID=160488;
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DB 16; Length 773;

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POTENTIAL.
1,2-BETA-FRUCTAN 1F-FRUCTOSYLTRANSFERASE; F4D7465955406DB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, aster campanulids, Asterales, Asteraceae, Asteroideae, Heliantheae,
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
NCBI_TaxID=818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 10; Length 615; Pred. No. 1e+02;
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STRAIN-VPI-5482 / ATCC 29148;
STRAIN-PI-5482 bubMed=12653928;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K., Chiang H.C., Hooper L.V., Gordon J.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Putative outer membrane protein, probably involved in
                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update
1,2-beta-fructan IF-fructosyltransferase precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1067 AA.
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Helianthus tuberosus (Jerusalem artichoke)
                                                                                                                                                                                                                615
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Best Local Similarity 58.3
7; Conservative
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                          3 RVRFSSDYTNY 13
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                                                 132 RERFEGDYANY
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081985
ID 081985
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Q8A3P9
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STRAIN-YS-314 / AJ 12310 / DSW 44549 / JCM 11189;
STRAIN-YS-314 / AJ 12310 / DSW 44549 / Xikuchi H., Nakamura Y.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
Usuda Y., Sudjamoto S.;
Usuda Y., Sudjamoto S.;
Usuhe artire genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, APOG522, BAG1923.1;
BMBL, APOG522, BAG1923.1;
BMBL, APOG522, BAG1923.1;
BMBL, APOG522, BAG1923.1;
SEQUENCE 346 AA, 36872 MW; 9243CB84E9EF6049 CRC64;
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MEDLINE=21959285; PubMed=11759840;

MEDLINE=21959285; PubMed=11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.;

"Complete genomic sequence of the filamentous nitrogen-fixing

cyanobacterium Anabaena sp. strain PCC 7120.";

DNA Res. 8:205-213(2001).
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.8%; Score 40; DB 16; Length 152; 54.5%; Pred. No. 23; 2; Indels 2; Indels
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NCBI_TaxID=103690;
                          Indels
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152 AA; 17008 MW; B376E02EFCFDB4E5 CRC64;
                                                                                                                                                                                                                                                                 Q8YMP7, PRELIMINARY, PRT, 152 AA.
Q8YMP7,
Q1-MAR-2002 (TEBWBLrel. 20, Created)
O1-MAR-2002 (TEBMBLrel. 20, Last sequence update)
O1-UJV-2003 (TEBWBLrel. 24, Last annotation update)
Hypothetical protein All4886.
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Last annotation update)
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Pred. No. 85;
0; Mismatches
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88.9%;
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Similarity 88.5
8; Conservative
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Best Local Similarity
Matches 7; Conserval
                                                                              VRVRFSSDY
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Best Local
Matches
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Pfam; PF00851; Peptidase_C
Pfam; PF00767; Poty_coat;
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SEQUENCE FROM N.A.
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Q9QN08
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"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."; Science 299:2074-2076(2003).
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Arch. Virol. 144-231-240(199).
-!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
EMBL; AB016500; BAA36278.1;
-- MERCPS; C06.001;
MERCPS; C06.001;
MERCPS; S10.001;
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Japanese yam mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
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RGO; GO: 0005524; F:ATP binding; IEA.

RO; GO: 0008028; F:ATP binding; IEA.

RO; GO: 0008026; F:ATP binding; IEA.

RO; GO: 0008026; F:ATP binding; IEA.

RO; GO: 0008026; F:ATP binding; IEA.

RO; GO: 00016787; F:CYSteine-type endopeptidase activity; IEA.

RO; GO: 000579; F:CYSteine-type endopeptidase activity; IEA.

RO; GO: 0005198; F:RNA-directed RNA polymerase activity; IEA.

RO; GO: 0005198; F:RNA-directed RNA polymerase activity; IEA.

RO; GO: 0005198; F:RNA-directed RNA polymerase activity; IEA.

RO; GO: 0005199; F:RNA-directed RNA polymerase activity; IEA.

RO; GO: 0005199; F:RNA-directed RNA polymerase activity; IEA.

RO; GO: 0005199; F:RNA-directed RNA polymerase.

RILECTPO: IPRO0140; Peptidase_C4.

RILECTPO: IPRO0159; Peptidase_C5.

RILECTPO: IPRO0159; RNA-pol DS PS.

RILECTPO: IPRO01205; RNA-pol DS PS.

RILECTPO: IPRO01605 RNA-pol DS PS.

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                                                   EMEL: AE0162919 AC078011.1; -.

EMEL: AE0162919 AA078011.1; -.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0004784; F:superoxide dismutase activity; IEA.

GO; GO:000601; F:superoxide metabolism; IEA.

InterPro; IPR001869; CarboxypepD_reg.

InterPro; IPR001869; Golsmutase.

ProDom; PD000475; SODismutase.

PROSITE; PS00018; BF_HAND; 1.

Complete proteome.

SEQUENCE 1067 AA; 119530 MW; 9B3DEAPC654C968A CRC64;
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Last sequence update)
Last annotation update)
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MEDLINE=99399236; Pubmed=10470250;
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01-MAY-1999 (TrEMBLrel. 10,
01-OCT-2003 (TrEMBLrel. 25,
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400 EVKVRFQADFDDY 412
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Matches 6; Conservative
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SEQUENÇE FROM N.A.
STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
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LMO1042.
                                                                                                          57.4%;
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                                                                                               1 OVRVRESSDYTNY 13
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nes 7; Conserv
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TISSUE=Skin;
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  NCBI_TaxID=173;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Q8Y875;
                                                                                                                                                                                                                                 Q8TB34
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Matches
                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                      Q8TB34
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Proglucagon (Fragment).
Ambloplites rupestris (Rock bass).
Evkaryota, Metazoa, Chordata, Cramiata, Vertebrata; Euteleostomi, Acanthomorpha; Acanthoperrygii, Teleostei; Buteleostei; Acanthomorpha; Acanthopererygii, Teleostei; Buteleostei; Recomorpha; Acanthopererygii, Percomorpha; Perciformes; Percoidei, Noble TaxID=109273;
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LA6234.
Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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0
                                                                                              Query Match
58.8%; Score 40; DB 12; Length 3132;
Best Local Similarity 70.0%; Pred. No. 5.7e+02;
Matches 7; Conservative 2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 13; Length 96; Pred. No. 22;
Pfam; PF01577; Poty P1; 1.
Pfam; PF00680; RNA dep RNA pol; 1.
PRINTS; PR00966; NTAPOTYPTĀSE.
SWART; SM00487; DEXDC; 1.
SWART; SM00490; HELICC; 1.
PROSITE; PS00125; SER THR PHOSPHATASE; 1.
ATP-binding; Coat protein; Helicase; Hydrolase.
SEQUENCE 3132 Aa; 356199 MW; 2597B7197CF047C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Al-Mahrouki A.A., Irwin D.M., Youson J.H.;
Al-Mahrouki Bass Proglucagon.";
Submitred (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF1994999; AAG16778.1;
HSSP; PO1274; IGCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 AA; 11225 MW; 6435033EBDDC00CE CRC64;
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GLUCAGON-LIKE PEPTIDE 1.
GLUCAGON-LIKE PEPTIDE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005179; F:hormone activity; IEA.
IncerPro; IPRO00523; Glucagon.
Ffan; PF00121; hormone2; 2.
PRINTS; PR00275; GLUCAGON.
SWART; SM00070; GLUCA; 1.
PROSITE; PS00260; GLUCAGON; 1.
CHAĪN TER 1 >29 GLUCAGON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                        Local Similarity 75.0
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×70
×96
                                                                                                                                           2 VRVRFSSDYT 11
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FINDYINY 13
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
Q8F9G1
1D Q8F9G
AC Q8F9G
DT 01-MA
DT 01-MA
DT 01-MA
DT HYDOL
GN LA023
OS BECTE
OS BACTE
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Q9DG43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=21537279; PubMed=11679669;
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Blocker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
                                                                                                                                                                                   Score 39; DB 16; Length 336;
Pred. No. 81;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.4%; Score 39; DB 4; Length 352; 53.8%; Pred. No. 85;
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
Ren S.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB011212; AAN4143311; --
Hypothetical protein; Complete proteome.
SEQUENCE 336 AA; 39487 WW; F6A7E30B3FA978C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 AA; 39375 MW; 8BF091F27A4B8367 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0TN-2002 (TrEMBLrel. 21, Created)
01-UN-2002 (TrEMBLrel. 21, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Fragment).
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE-20196006; PubMed=10731132;

Adams M.D., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Adams M.D., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Adams M.D., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A dams M.D., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A dams M.D., Lewis S.E., Kichards S., Ashburner M., Henderson S.N.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A briton G.G., Wortman J.R., An Held, G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Abgayani A., An H.-J., Andrews-Ffannkoch C.R., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Boldmin D.,
Borkova D., Botchan M.R., Bourk J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahke C., Davanport L.B., Davies P.,
Cherry J.M., Cawley S., Dahke C., Davanport L.B., Davies P.,
Charry J.M., Cawley S., Dahke C., Davanport L.B., Davies P.,
Charry J.M., Cawley S., Dahke C., Perriera S., Ferriera S., Ferriera S., Peristen M.,
Challer M., Goog F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Estian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kunh M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Rammel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazquez-Boland' J.-A., Voss H., Wehland N., Cossart P.; Comparative genomics of Listeria species.";

Science 294,849-852(2001).

PIR: AB1205, AB1205.
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GO; GO:0003676; F:uncleic acid binding; IEA.
GO; GO:0003677; P:Mo-molydopterin cofactor biosynthesis; IEA.
InterPro; IPR00169; Endonuclease.
InterPro; IPR00111; MocA_C.
InterPro; IPR005111; MocA_C.
InterPro; IPR005101; MocA_N.
Pfam; PF00994; MocE_biosynth, 1.
Pfam; PF00944; MocA_C; 1.
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Neoptera, Endopterygota, Diptera; Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.4%; Score 39; DB 16; Length 407; 63.6%; Pred. No. 99; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03453; MocA_N; 1.

ProDom; PD002460; MoCF biosynth; 1.

TIGRPAMS; TIGR00177; molyb syn; 1.

PROSITE; PS01070; NUCLEASE_NON SPEC; 1.

PROSITE; PS01070; NUCLEASE_NON SPEC; 1.

SEQUENCE 407 AA; 45009 MW; CO0F642F6966ADE6 CRC64;
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Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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nes 7; Conserv
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Best Local S
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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Jalali, M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Karatiz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Milshina N.V., Mobary C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,

Relnert K., Remington K.S., Nixon K., Nusskern D.R., Pacleb J.M.,

Reinert K., Remington K.S., Sanders R.D.C., Scheeler F., Shen H.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Nillams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

Ribbs R.A., Myers E.W., Rubling Melanogaster.,

The genome sequence of Drosophila melanogaster.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0003677; F:DNA binding; IBA.
InterPro; IPR004210; BESS_motif.
InterPro; IPR006578; MADF.
Pfam: PF02944; BESS; 1.
SMART; SM00595; MADF; 1.
SEQUENCE 469 AA; 52284 MW; 03BCD580C3A4CEEF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5, 2004, 08:13:18
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EMBL, AE003708; AAF55167.1; -.
FlyBase; FBGN0038316; CG6276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.4%;
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81 LRISFRREYTNY 92
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Best Local Similarity
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model protein ĕ

5, 2004, 07:04:10 ; Search time 9.89043 Seconds (without alignments) 371.381 Million cell updates/sec October Run on:

US-09-805-290A-11 68 Title: Perfect score:

1 QVRVRFSSDYTNY 13 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* A Geneseq 29Jan04:\* 1: genesemina geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query	Length	DB	ID	Description
	69	100.0	13	4	AAE10544	Aae10544 Llama spe
N	69	100.0	130	4	AAE10557	7 HPL in
m	4, E	63.2	293	S	ABP26437	Abp26437 Streptoco
4	43	63.2	513	Ŋ	ABP30089	m
ß	42	61.8	208	ഗ	AA017579	т.
9	41	60.3	117	w	ABP33318	Abp33318 Human ORF
7	41	60.3		ᡢ	AAY81486	o
ထ	41	60.3			ABU40154	54 1
σ	40	58.8		N	AAW00456	G
10	40	58.8		•	AAB51367	Aabsi367 Japanese
11	99	57.4		4	AAG73797	Aag73797 Human col
12	39	57.4	407	Ŋ	ABB47642	
13	39	57.4		9	ABU32421	_
14	39	57.4		4	ABB62215	
15	39	57.4	84	4	ABG16347	Abg16347 Novel hum
16	39	57.4	104	4	ABB64201	Abb64201 Drosophil
17	39	57.4		4	ABG12663	
18	39	57.4	113	4	ABG07281	Abg07281 Novel hum
	38.5	56.6		4	AAM90186	Aam90186 Human imm
	38	55.9	17	ß	AAU97601	⊣
	38	55.9	51	4	ABB60770	Abb60770 Drosophil
22	37	54.4	13	4	AAE10550	20
		54.4	10	4	AAB75586	5 Human
24	37	54.4	16	4	AAG75631	1 Human
25	37	54.4	362	7	AAW00635	Aaw00635 ILTV glyc

Aaw06787 ILTV glyc	Abg31711 Infection	Aau29333 Novel mar	Aab74925 E. coli a	Abg18198 Novel hum	Abg28888 Novel hum	Aaw06417 Antiscara	Abp30755 Streptoco	Abu01997 S. pneumo	Aab19895 Neisseria	Aaw04894 Proteinas	Aaw04893 Proteinas	Aaw04891 Proteinas	Abg91063 Neisseria	Abu79079 N. mening	Aaw04892 Proteinas		Abb62469 Drosophil	Abb67105 Drosophil	Abm69430 Photorhab
2 AAW06787	5 ABG31711	4 AAU29333	4 AAB74925		4 ABG28888	2 AAW06417	5 ABP30755	6 ABU01997	4 AAB19895	2 AAW04894	2 AAW04893	2 AAW04891	5 ABG91063	6 ABU79079	2 AAW04892	6 ABP77991	4 ABB62469	4 ABB67105	6 ABM69430
362	362	479	479	1012	1012	1169	41	128	155	174	174	174	174	174	175	175	295	295	333
54.4	54.4	54.4	54.4	54.4	54.4	54.4	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9
37	37	37	37	37		37	36	36	36	36	36	36	36	36	36	36	36	36	36
26	27	28	29	30	31	32	33	34	35	36	3.7	38	ტ წ /	40	41	42	43	44	45

#### ALIGNMENTS

AAE10544 standard; peptide; 13 AA. RESULT 1 AAE10544

AAE10544;

(first entry) 10-DEC-2001

Llama species antibody VHH CDR3 #13.

Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HGL; food; human gastric lipase; HGL; cometic control; body weight; complementarity determining region 3; CDR3.

Lama sp.

EP1134231-A1.

19-SEP-2001.

20-FEB-2001; 2001EP-00200703.

14-MAR-2000; 2000EP-00200930.

(UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.

Bezemer S, Van De Burg M, WPI; 2001-572718/65.

Tareilus E;

De Haard JJW,

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Claim 4; Page 29; 37pp; English.

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HBL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region 

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Gaps

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Length 130;

100.0%; Score 68; DB 4; I 100.0%; Pred. No. 0.00017; ive 0; Mismatches 0;

ABP26437 standard; protein; 293 AA.

RESULT 3

98 OVRVRFSSDYTNY 110

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Gaps 0;

Length 13; 0; Indels

13

1 QVRVRFSSDYTNY

Conservative

Query Match Best Local Similarity Matches 13; Conserv

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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes specially human pancreatic lipses (HRL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #19 from
                                                                                                                                                                                                                                                                                                          Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Complementarity determining region 2"
98. .110
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                              HPL inhibiting VHH fragment, HPL #19 from llama species.
                         100.0%; Score 68; DB 4; I
100.0%; Pred. No. 1.2e-05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Haard JJW,
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                       AAE10557 standard; peptide; 130 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            0. .64
label= CDR2
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label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR3
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                                                                                                                                                                                                                                                 (first entry)
                                                                                    1 QVRVRFSSDYTNY 13
                                                                                                             OVRVRESSDYTNY 13
                                                      13; Conservative
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                          Query Match
Best Local Similarity
Matches 13; Conserv
Sequence 13 AA;
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                                                                                                                                                                                                                     AAE10557;
                                                                                                                                                                                                                                                                                                                                                                       Lama sp.
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Region
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5481 sequences (S1), given in the specification. The proteins have antibacterial and antihilammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and tibodies that bind (I) are used in the manifacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) is aced to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be moningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity characteraphy, immunoassays, and distinguishing/identifying
                                                                                                                                                     Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes, antibacterial, antiinflammatory, infection, vaccine, meningitis, gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.2%; Score 43; DB 5; Length 293; 70.0%; Pred. No. 16; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Masignani V, Margarit Y RosI, Grandi G,
                                                                                                                Streptococcus polypeptide SEQ ID NO 2050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 3356; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                        27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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                                                                          (first entry)
                                                                                                                                                                                                                                  Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 293 AA;
                                                                                                                                                                                                                                                                        WO200234771-A2.
                                                                          02-JUL-2002
                                                                                                                                                                                                                                                                                                               02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Telford J,
Tettelin H;
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Tareilus

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Gaps

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Best Local Similarity 70.0 Matches 7; Conservative

(camelid) species

Sequence 130 AA;

237 VRYSGDYTNF 246

VRFSSDYTNY 13

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (51), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and antibadies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is used to detecraine whether a compound binds to (1). A composition composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acids encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                       Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Telford J, Masignani V, Margarit Y Rosl, Grandi G, Fraser C, Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.2%; Score 43; DB 5; Length 513; 70.0%; Pred. No. 30; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                      Streptococcus polypeptide SEQ ID NO 9354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 4060; 4525pp; English.
                                                                                              Æ
                                                                                              ABP30089 standard; protein; 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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                                                                                                                                                                     (first entry)
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 VRYSGDYTNF 26
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                       WO200234771-A2.
                                                                                                                                                                     02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2002.
                                                                                                                                   ABP30089;
 17
                                                                          RESULT 4
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The present invention provides the protein and coding sequences of proteins from Moraxella catarrhalis. These can be used to produce vaccines which protect against M. catarrhalis infection, which can cause otitis media, respiratory infection, sinusitus, and pneumonia. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                              Moraxella, vaccine, respiratory tract infection, antiinflammatory, auditory, antibacterial, otitis media, sinusitis, pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moraxella polypeptide and polynucleotides useful as vaccine for immunizing a host e.g. humans against disease e.g. otitis media, pneumonia, caused by infection of the bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang Y;
                                                                                                                                                                                                               M catarrhalis MCA101792 protein SEQ ID NO: 38.
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                                                              AAO17579 standard; protein; 208 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0228294P.
2000US-0228295P.
2000US-0228439P.
2000US-0228439P.
2000US-0228440P.
2000US-0228441P.
2000US-0228441P.
2000US-0228442P.
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06-SEP-2000; 2000US-0230250P.
06-SEP-2000; 2000US-0230252P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AVET ) AVENTIS PASTEUR LTD
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                Moraxella catarrhalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-404555/43.
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                                                                                                                                                                                                                                                                                                                                                                                                    WO200218595-A2.
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29-AUG-2000; 2
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01-SEP-2000; 2
01-SEP-2000; 2
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                                                                                                                                                                 19-JUL-2002
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                                                                                                                AA017579;
RESULT
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Conservative

Sequence 208 AA;

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Gaps

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Gaps

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1; Indels

3; Mismatches

Score 42; DB 5; Length 208; Pred. No. 16;

61.8%; 60.0%;

Query Match
Best Local Similarity 60.00

4 VRFSSDYTNY 13

Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ Claim 10; Page 1400; 2508pp; English 24-MAY-2001; 2001WO-US017076. 24-MAY-2000; 2000US-0206690P Leach MD, Shimkets RA; (CURA-) CURAGEN CORP. WPI; 2002-106200/14. N-PSDB; ABN77344. transplantation.

Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054ABN75587 represent conding them. The invention also encompasses polypeptides at least 80% identical to the ORPT-ORR4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORPT-ORR4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX polynucleotides and polynucleotides for screening for modulators of ORFX pression or activity, and methods of screening for modulators of ORFX expression or activity, and methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX associated disorder. The ORFX protein, cell proliferation, call differentiation, immune modulation, haematopoiesis regulation, cell differentiation, immune modulation activity, thrombolyptic activity, chemokinetic activity, haemostatic activity, thrombolyptic activity, receptor/ligand, antinflammatory activity, thrombolyptic activity,

and antilinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour ORFX proteins, rucleic acids and antibodies may be used in the treatment of cancers, other proliferative disorders may be used in the treatment of cancers, other proliferative disorders may be used in the treatment of cancers, correctly and all provided the cancers of cardiovascular diseases, immune system disorders disorders related to candiovascular diseases, and infectious diseases caused by viral, bacterial, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage diseases, and infectious diseases caused by viral, bacterial, storage diseases, and infectious diseases caused by viral, bacterial, storage diseases, and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous corrected may additionally be used to produce transgenic animals necleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX protein, and in drug screening. The ORFX protein may also be used as immunogens to generate specific antibodies, which are useful in the immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases \$

0 Gaps . 5; Length 117; 1; Indels Query Match
60.3%; Score 41; DB
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0,

10 딉 2 VRVRFSSDY 3 VRVRFSGDY

AAY81486 standard; protein; 476 AA. 03-JUL-2000 (first entry) AAY81486; AAY81486 ID AAY8 

Pseudomonas putida aldehyde dehydrogenase.

Aldehyde dehydrogenase, NAD+-dependent, oxidation, 2-oxoaldehyde, hydroxypyruvaldehyde, glyceraldehyde, methylglyoxal, hydroxypyruvic acid.

Pseudomonas putida

24-AUG-1998; 29-FEB-2000.

(CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU

This sequence represents a novel aldehyde dehydrogenase from Pseudomonas putida. This catalyses reactions such as the NAD-dependent oxidation of hydroxypyruvaledhyde to hydroxypyruvic acid and reacts specifically with 2-oxoaldehydes such as hydroxypyruvaldehyde, glyceraldehyde and methylglyoxal. The protein was initially purified from a culture of P. putida, and subjected to tryptic cleavage. The fragments thus obtained were sequenced, and the sequence information used to design primers were used to amplify a aldehyde dehydrogenase PCR product. The fragment was used in the detection of a full-length DNA encoding aldehyde dehydrogenase in a genomic library.

Sequence 117 AA;

RESULT 7

JP2000060563-A.

98JP-00236691, 98JP-00236691, 24-AUG-1998;

WPI; 2000-249678/22. N-PSDB; AAA07084.

New aldehyde dehydrogenase gene - for enzymatic synthesis of serine or cysteine from glycero

Claim 2; Page 8-9; 11pp; Japanese.

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The invention relates to an isolated mucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense artisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation, or the blological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the blological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a
                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
This was amplified using primers AAA07087-A07088, and inserted into a vector for transformation of cells. Recombinantly produced Pseudomonas putida aldehyde dehydrogenase may be used for the synthesis of serine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zyskind JW;
Xu HH;
                                                                                                                                                                  Gaps
                                                                                                                                                                    .;
0
                                                                                                                                Length 476;
                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by Prokaryotic essential gene #25681.
                                                                                                                              Score 41; DB 3;
Pred. No. 64;
3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 68078; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                           A.
                                                                                                                                                                                                                                                                                                                                           ABU40154 standard; protein; 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001, 2001US-00815242.
06-SEP-2001, 2001US-0094893.
25-0CT-2001, 2001US-034223P.
08-FEB-2002, 2002US-00072851.
                                                                                                                                60.3%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAR-2002; ,2002US-0362699P
                                                                                                                                                                                                                                  99 OVEVNFTADYLDY 111
                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-2003 (first entry)
                                                                                                                                                                                                          1 QVRVRESSDYTNY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC.
                                                                                                                                                    Best Local Similarity 53.8
Matches 7; Conservative
                                                           cysteine from glycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-029926/02,
N-PSDB; ACA44024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas putida
                                                                                               Sequence 476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                              ABU40154;
                                                                                                                                  Query Match
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Wall D,
                                                                                                                                                                                                                                                                                                     RESULT 8
ABU40154
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compound's activity; (11) a culture comprising strains in which the gene product is oversypressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational required for proliferation in cells other than S. alreaus, S. typhimulium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jerusalem artichoke 1-fructan:fructan fructosyltxansferase (FFT) catalyses a polymerisation reaction involving the transfer of fructosyl units between trisaccharides, tetrasaccharides and larger fructose polymers. Its amino acid sequence was deduced from a CDNA clone (AAT31025) isolated from a Jerusalem artichoke tuber cDNA library. The enzyme can be expressed in transgenic plants to modify the fructan profile. The fructans are useful as low-calorie sweeteners or as the hydrophilic moiety in biosurfactants. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequences encoding fructan-producing enzymes - used to transform plants, for the production of low calorie sweeteners etc.
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-fructan:fructan fructosyltransferase; SST; fructan; sweetener;
surfactant; transgenic plant; Jerusalem artichoke.
                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                           Score 41; DB 6; Length 748;
Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                        .le+02;
.r 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koops AJ;
                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-Fructan:fructan fructosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW00456 standard; protein; 615 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helianthus tuberosus; cv. Colombia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 4b; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Der Meer IM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95EP-00200015.
95EP-00200762.
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                                                                                                                                                                                                                                                                                                60.3%;
                                                                                                                                                                                                                                                                                                               88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 86..
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 102 VRVRFSGDY 110
                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-333998/33.
                                                                                                                                                                                                                                                                                                                                                                   2 VRVRFSSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT31025
                                                                                                                                                                                                                                                                Sequence 748 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van Tunen AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9621023-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2003
25-SEP-1996
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AAG73797 standard; protein; 176 AA.

RESULT 11

AAG7379

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1777 IRARFSSDHT 1786

(first entry)

03-SEP-2001

AAG73797;

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The present sequence represents the Japanese yam mosaic virus (JYMV) JYMV mosaic virus. The present invention also describes: (1) a weakly toxic strain of Dioscoreaceae mesaic virus having a nucleic acid sequence which shows interference against the infection of a strongly toxic strain of Dioscoreaceae mesaic virus; (2) a Dioscoreaceae mesaic virus; strongly toxic strain of Dioscoreaceae mesaic virus; (2) a Dioscoreaceae mosaic virus; (3) a method for the cultivation of a Dioscoreaceae mosaic virus; (3) a method for the cultivation of a Dioscoreaceae mosaic virus; (3) a method for the cultivation of a Dioscoreaceae mosaic virus; is infected to the tubercle or the University toxic strain of Dioscoreaceae mosaic virus is infected to the tubercle or the University of Dioscoreaceae appoints, and (4) a method for genetic alata and the tubercle or bulbli is grown; and (4) a method for genetic diagnosis of a Dioscoreaceae mosaic virus in which a DNA fragment C muplified by using reverse transcriptese-polymerase chain reaction (RT-PCR) primers atagettacacaccecteae (AAR26999) and cacedtacattgeygaragyge (AAR32201) is treated with a restriction enzyme to distinguish the weakly to of physocoreaceae mosaic virus from the strongly toxic strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weakly toxic strain of Dioscoreaceae mosaic virus used in the genetic diagnosis of the mosaic virus infection and for the management of crops resistant to the virus.
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Japanese yam mosaic virus; JYMV; Dioscorea; resistance; JYMV-M;
                                                                          ö
                                                                                                                                                                                                                                                                                                                                                    Japanese yam mosaic virus JYMV-M protein sequence SEQ ID NO:1.
                                     Length 615;
                                 Score 40; DB 2; Length 615
Pred. No. 1.3e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                       AAB51367 standard; protein; 3132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 6-20; 22pp; Japanese.
                               58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Dioscoreaceae mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-00113671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-00113671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AICH-) AICHI KEN PREFECTURE
                                                                                                                                                                                                                                                                                                                                                                                                           Dioscoreaceae mosaic virus
                                                                                                                                                                                                                                                                                                             10-APR-2001 (first entry)
               Query Match
Best Local Similarity be...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Japanese yam mosaic virus.
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VLVYYTTDYTNY 263
                                                                                                           VRVRFSSDYTNY 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3132 AA;
Sequence 615 AA;
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                                                                                                           N
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So
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Cancer-associated nucleic acid molecules (N) and proteins (P), where the cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens in the colon cancer antigens and the colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAM37196 and AAM37708 represent sequences used in the exemplification of the present invention. N B. Pages 66 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                  Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.4%; Score 39; DB 4; Length 176; 53.8%; Pred. No. 47; 1.1ve 2; Mismatches 4; Indels
                                                                                          Human colon cancer antigen protein SEQ ID NO:4561.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 6360-6361; 9803pp; English
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ID ABB47642 standard; protein; 407 AA.
XX
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                                                                                                                                                                                                                                                                                                     28-SEP-2000; 2000WO-US026524.
                                                                                                                                                                                                                                                                                                                                           99US-0157137P.
99US-0163280P.
                                                                                                                                                                                                                                                                                                                                                                                                  HUMA-) HUMAN GENOME SCI INC
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||::|| || |
50 QVKIRFGSDPATY
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM, Barash SC,
                                                                                                                                                    colorectal carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 176 AA;
                                                                                                                                                                                                                             WO200122920-A2
                                                                                                                                                                                                                                                                                                                                         29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                           03-NOV-1999;
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                 05-APR-2001
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Gaps

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Score 40; DB 4; Length 3132; Pred. No. 8.3e+02; 2; Mismatches 1; Indels

58.8%;

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Protein encoded by Prokaryotic essential gene #17948.

19-JUN-2003 (first entry)

(first entry)

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Listeria monocytogenes protein #346.
                                                                                                   Sequence 407 AA;
                   WO200177335-A2.
                                                           polypeptides.
                      18-OCT-2001.
ABB47642;
                                                 Rose M,
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Antisense, prokaryotic essential gene, cell proliferation; drug design. New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. Claim 25; SEQ ID NO 60345; 1766pp; English 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 21-MAR-2002; 2002WO-US009107 06-MAR-2002; 2002US-0362699P 21-MAR-2001; 2001US-00815242 (ELIT-) ELITRA PHARM INC. Listeria monocytogenes Zamudio C, Trawick JD, WPI; 2003-029926/02 N-PSDB; ACA36291 40200277183-A2 03-OCT-2002 Wang L, Wall D, The present invention relates to the genome sequence of Listeria
monocytogenes EGD-e (see ABA33041). The genome sequence and fragments of
it are useful for selecting probes and primers for detecting genes in L.
conveytogenes and related organisms, and for studying genetic
monocytogenes and related organisms.

Comparisms and other genomes The present invention. Proteins
expressed from the genome sequence of the present invention. Proteins
expressed from the genome sequence of the present invention. Proteins
expressed from the genome sequence and useful for ralating specific
antibodies, identification of L. monocytogenes and related organisms, and
for biosynthesis and biodegradation, especially biosynthesis of Vitamin
B12. The genome sequence and proteins encoded by it are also useful for
selecting compounds that regulate gene expression and cell replication
and modulate L. monocytogenes-related diseases. In addition, the genome
sequence and proteins encoded by it are useful in pharmaceutical and
vaccines compositions for the treatment or prevention of infections by L.
monocytogenes and related organisms. Note: The sequence data for this
parent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garriar P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N, Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease. ftp.wipo.int/pub/published\_pct\_sequences Claim 6; SEQ ID NO 347; 192pp; French. 11-APR-2001; 2001WO-FR001118. 11-APR-2000; 2000FR-00004629. Listeria monocytogenes WPI; 2002-010914/01. (INSP ) INST PASTEUR Voss H;

or screening

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

The invention relates to an isolated nucleic acid comprising any one of the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid conditions are coll containing the vector; (3) an isolated are:

(1) a vector comprising a promoter operably linked to the nucleic acid conditions acid; (2) a host cell containing the vector; (3) an isolated antisense nucleic acid; (4) an antibody capable of specifically binding confisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) inhibiting cellular proliferation or the activity of agene in an operon required for proliferation; (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway required for proliferation or the piological pathway in which a proliferation-required gene or the biological conspands acts; (9) manufacturing an antibits proliferation of an organism acts; (9) manufacturing an antibits proliferation of an organism acts; (1) identifying the target of a compound that inhibits proliferation of an organism; or (1) identifying the target of a compound that inhibits the extent or to which each of the strains is present in a culture or collection of an organism; or (1) identifying the target of a compound that inhibits the constraints or screening for homologous nucleic acids are useful for the dense product is observed to be actived manufacturing an entisense nucleic acids actuals actuals and any dense product is organism. The antisense nucleic acids are useful for each of the recent of the recent endidated molecules for rational and dense product acids actuals and acids actuals and acids ö drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences Gaps ; 0 Length 407; 57.4%; Score 39; DB 6; Length 407 63.6%; Pred. No. 1.2e+02; iive 2; Mismatches 2; Indels Query Match
Best Local Similarity 63.69
Matches 7; Conservative Sequence 407 AA;

. 0

57.4%; Score 39; DB 5; Length 407; 63.6%; Pred. No. 1.2e+02; tive 2; Mismatches 2; Indels

ABU32421 standard; protein; 407 AA

RESULT 13 ABU32421

ABU32421;

AX H

g

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

30-MAR-2001; 2001WO-US008631.

WO200175067-A2. Homo sapiens.

11-OCT-2001.

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL3175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 13437; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.4%; Score 39; DB 4; Length 469; 50.0%; Pred. No. 1.5e+02; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 13437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers EW;
                                                                                                    ABB62215 standard; protein; 469 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PWD,
                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                   26-MAR-2002 (first entry)
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Best Local Similarity 50.05
. . 6; Conservative
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                  330 QVRAKMASDYT 340
                                                                                                                                                                                                                                                                             Drosophila melanogaster.
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OVRVRFSSDYT 11
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N-PSDB; ABL06318.
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                                                                                                                                      ABB62215;
                                                                            RESULT 14
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Tang YT;

Drmanac RT, Liu C, WPI; 2001-639362/73

N-PSDB; AAS80534.

(HYSE-) HYSEQ INC

Claim 20; SEQ ID NO 46706; 103pp; English.

biodiversity.

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed carivity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a pulppeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders or polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG3037 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
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Pred. No. 2.9e+02;
2; Mismatches 4; Indels
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159 QVKIRFGSDPATY 171
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Novel human diagnostic protein #16338.

(first entry)

18-FEB-2002

BXXXXXB

ABG16347;

ABG16347 standard; protein; 849 AA.

RESULT 15

ABG16347

81 LRISFRREYTNY

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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RESULT 1							
B90162 DNA/pantot	henate	metabo	lism f	lav	roprot	B90162 DNA/pantothenate metabolism flavoprotein (dfp) [imported] -	Sulfolobus solfataricus
C; Species: Sulfolobus solfataricus	Sulfo	lobus s	olfata	ric	ins		
C;Date: 24-May-2001 #sequence_revision	4-May-2	001 #se	quence	1,4	visio	n 24-May-2001 #text_change 15-Jun-2001	ange 15-Jun-2001
C;Accession: B90162	on: B90	162	,		,	× × × × × × × × × × × × × × × × × × ×	Jane 1 . M. veyene v. D. brell
Tong, I.:	garagn Geffr	, K.A.; jes. A.	Conta	267	ta, C.	Risne, Q.; singn, K.K.; Contaionieii, F.; Zivanovic, I.; Airte. Jong, I.: Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; T	hi-Ngoc, H.P.; Redd
arrett, R.A.; Ragan, M.A.;	A.; Ra	gan, M.	A.; Se	Sensen,	en, C.	C.W.; Van der Oost, J.	
submitted	to Gen	Bank, A	pril 2	00	_	•	
A; Description: Sulfolobus solfataricus	cion: S	ulfolob	us sol	fat	aricu	is complete genome.	
A; Referent	ce numb	er: Ayy	139				
A; Accession: Byolds	מיונט בונט	707					
A.Mologile tyme: DNA	11011	ANG					
A. Weel dies	1-41	3 KKIR>					
A; Cross-references: GB:	eferenc	es: GB:	AE0066	41	NID:	GB:AE006641; NID:g13813345; PIDN:AAK40553	53.1; GSPDB:GN00155
C; Genetics:							
A; Gene: dfp	Ęp.	•			,		
C;Superfar	nily: p	antothe	nate m	jet	abol18	;Superfamily: pantothenate metabolism rlavoprotein dip	
Query Match			Ŋ	9.68		Score 40.5; DB 2; Length	h 413;
Best Local	တ် ဝ	imilarity Conserv	7 1 1 1	ტ		Pred. No. 23; : Mismatches 0; Indel	ls 3; Gaps 1;
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Cyaccession: Scale, 2.4.4.4.

Plant Mol. Biol. 20, 809-819, 1992

Plant Mol. Biol. 20, 809-819, 1992

Plant Mol. Biol. 20, 809-819, 1992

A) Fittle: Cloning, partial sequenching and expression of a cDNA coding for branching enzyme A, Reference number: S28422; MUID:93099233; PMID:1281436

A) Reference number: S28422; MUID:93099233; PMID:1281436

A) Residues: not compared with conceptual translation

A) Molecule type: mRNA

A) Residues: 1-143;144-298;299-383 <SAL>
C; Punction: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-gl A, Dathway: glycogen/starch biosynthesis

A) Note: final step in biosynthesis of glycogen or amylopectin

C; Superfamily: 1,4-alpha-glucan branching enzyme
C; Superfamily: 1,4-alpha-glucan branching enzyme
C; Keywords: glycogen/starch biosynthesis; glycosyltransferase, hexosyltransferase 1.4-alpha-glucan branching enzyme (EC 2.4.1.18) - cassava (fragments) C;Species: Manihot esculenta (cassava) C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 07-May-1999 Accession: S28422 Query Match

58.8%; Score 40; DB 2; Length 383;

us-09-805-290a-12.rpr

167 INMAFTGDYNEY 178

2 IRRKFISEYNEY 13

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hypothetical protein [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C;Accession: C89966

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Inoue, R.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lance 357, 1225-1240, 2001

A;Tille: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Status: preliminary
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Since, Q.; Singh, R.X.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V. J.; She, Q.; Singh, R.X.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V. J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

Submitted to GenBank, April 2001

A; Description: Sulfolobus solfataricus complete genome.

A; Reference number: A99139

A; Accession: E90176
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A,Molecule type: DNA
A,Rosidues: 1-337 <KUR>
A,Residues: 1-337 <KUR>
C,Genetics: GB:AE006641; NID:g13813480; PIDN:AAK40668.1; GSPDB:GN00155
C,Genetics: A,Genetics: 
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A;Experimental source: strain N315
    R;Ennis, H.L.
submitted to the EMBL Data Library, February 1995
A;Reference number: 218851
A;Reference number: 218851
A;Accession: T18268
A;Atatus: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-280 <ENN>
A;Residues: 1-280 <ENN>
A;Cross-references: EMBL:U20608; NID:g676858; PID:g2081632; PIDN:AABS4082.1
C;Genetics:
A;Introns: 42/1
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C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision:24-May-2001 #text_change 24-May-2001
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Pred. No. 29;
5; Mismatches 1; Indels
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: DNA
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A,Gene: SA1621
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                                                                                                                                                                                                                                                                                                                                                                                                     1,4-alpha-glucan branching enzyme (EC 2.4.1.18) II - garden pea (fragment)
N;Alternate names: starch branching enzyme II
C;Species 13-Apr-1999 tisum sativum (garden pea)
C;Decies 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
C;Accession: T06494
R;Burton, R.A.; Bewley, J.D.; Smith, A.M.; Bhattacharyya, M.K.; Tatge, H.; Ring, S.; Bul plant J. 7, 3-15, 1995
A;Title: Starch branching enzymes belonging to distinct enzyme families are differential A;Reference number: Z15717; MUID:95201826; PMID:7894509
A;Reference number: Z15717; MUID:95201826; PMID:7894509
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: B90408
R;Accession: B90408
R;Accession: B90408
A;Bingh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: SBEII
C;Superfamily: 1,4-alpha-glucan branching enzyme
C;Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase
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A;Gene: SSO2370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B90408
hypothetical protein SSO2370 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Bate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-826 <BUR>
A;Cross_references: EMBL:X80010; NID:g510546; PIDN:CAA56320.1; PID:g1345571
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hypothetical protein - slime mold (Dictyostelium discoideum)
C.Species: Dictyostelium discoideum
C.Date: 15-Oct -1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T18268
                                                Gaps
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                                                Indels
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Pred. No. 58;
1; Mismatches
        Pred. No. 26;
1; Mismatches
    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.8%;
Best Local Similarity 58.3%;
Matches 7; Conservative
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421 INMAFTGDYNEY 432

2 IRRKFTSEYNEY 13

ò 셤 Query Match
Best Local Similarity 63.6
Matches 7; Conservative

A; Residues: 1-179 < KUR>

A; Molecule type: DNA

2 IRRKFISEYNE 12 :||| || :|| 80 VRRKITSVFNE 90

ò g RESULT 5

Query Match 58.8 Best Local Similarity 58.3 Matches 7; Conservative

A, Molecule type: mRNA

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Accession: A33284

Proc. Natl. Acad. Sci. U.S.A. 86, 6186-6190, 1989

A; Jung, C. Saxe III, C.L.; Kimmel, A.R.; Hammer III, J.A.

Proc. Natl. Acad. Sci. U.S.A. 86, 6186-6190, 1989

A; Reference number: A33284; MUD:89345628; PMID:2762320

A; Reference number: A33284

A; Reference number: A33284

A; Residues: 1-1111 cJUNA

A; Residues: 1-1111 cJUNA

A; Residues: 1-1111 cJUNA

A; Residues: 1-1111 cJUNA

A; Residues: 1-133 39/3

C; Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homology

C; Superfamily: Protozoan myosin heavy chain IB; myosin motor domain homology

C; Superfamily: protozoan myosin heavy chain IB; myosin motor domain nor corrected.

A; Introns: 1/3; 39/3

C; Superfamily: protozoan myosin heavy chain IB; myosin motor domain nor corrected.

F; 12c-78 Domain: myosin motor domain homology (PMOOP)

F; 12c-78 Domain: myosin motor domain predicted

F; 712-101/Region: actin binding #status predicted

F; 712-101/Region: actin binding #status predicted

F; 712-106/Domain: SH3 homology cH3>

F; 106-1106/Domain: SH3 homology cH3>

F; 108/Binding site: AFP (Lys) #status predicted

F; 332/Binding site: phosphate (Ser) (covalent) #status predicted
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A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300, MUID:98196666; PMID:9537320
A,Accession: H70484
A,Status: preliminary, nucleic acid sequence not shown; translation not shown A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2. C; Species: Aquifex aeolicus
C; Species: Aquifex aeolicus
C; Date: Ge.May-1998 #sequence_revision 08-May-1998 #text_change 03-Jun-2002
C; Accession: H70484
R; Deckert, G; Marren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
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Pred. No. 1.4e+02;
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58.3%; Pred. No. 1.8e+02;
iive 3; Mismatches 2;
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Best Local Similarity 66.7.
Best Local 8, Conservative
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nes 7; Conserv
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Best Local S
Matches 7
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                                                                                                                                                                                                 uncharacterized protein from YceG family [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: I4-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 01-Mar-2002 C; Accession: H97107 R; Molling, J.; Benter, G.N.; Koohin, E.V.; Matkarova, K.S.; Zeng, Q.; Gibson, R.; Lee, T; Dalay, M.J.; Bennett, G.N.; Koohin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A; Reference number: A96900; MUID:21359325; PMID:21359325 A; Reference number: A96900; MUID:21359325; PMID:21359325 A; Residues: 1-339 < CMR> A; Residues: GB:AE001437; PIDN:AAK79651.1; PID:G15024648; GSPDB:GN00168 A; Cross-references: GB:AE001437; PIDN:AAK79651.1; PID:G15024648; GSPDB:GN00168 A; Come: CAC1685 C; Superfamily: yceG protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Accession: C72219
A;Status: preliminary
A;Molecule type: DNA
A;Nolecule type: DNA
A;Coss-references: GB:AE001811; GB:AE000512; NID:g4982291; PIDN:AAD36785.1; PID:g498229
A;Experimental source: strain MSB8
C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Coss-references: GB:AE001811; GB:AE001811; GB:AE001812)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA mismatch repair protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: C72219
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.N.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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MyContains: myosin ATPase (EC 3.6.4.1)
N/Contains: Dictyostelium discoideum C;Species: Dictyostelium discoideum C;Species: Dictyostelium discoideum C;
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VIKRGFSSELDEY 413
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Matches 6; Conservative
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FTSDYNEF 329
                            13
                                                            49 RYTSAYNEY 57
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Best Local Similarity
Matches 7;" Conserva
                            KFTSEYNEY
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Gaps

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submitted to GenBank, June 2000

A.Authors: Ferralara, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohma, J.D.; Junqueira, W.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, J.E.; Kuramae, E.E.; Laigra chado, M.A.; Madeira, A.M.B.Y.; Matrimo, C.L.; Marques, M.V.; Martins, E.A.; A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Panieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Sa, R.G.; Santelli, R.V.; Sawasak; A.; Tsuhako, M.H.; Vallada, H.; Van Sluva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaira, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za A; Reference number: A59328
A; Aconcents: annotation
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                galacterate dehydratase, probable (garD) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001
C;Date: 24-May-2001
C;Date: 24-May-2001
C;Date: 25-May-2001
C;Date: 25-May-2001
C;Date: 25-May-2001
C;Date: 27-May-2001
C;Date: 27-May-2001
C;Date: 27-May-2001
C;Date: 27-May-2001
C;State: A. A. Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Carrettion: Sulfolobus solfataricus complete genome.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A. Molecule type: DNA
A. Residues: 1-387 < KUR>
A. Coss.references: GB: AE006641; NID: g13814453; PIDN: AAK41497.1; GSPDB: GN00155
C. Genetics:
            C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 2
Pred. No. 90;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5, 2004, 08:16:58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.87
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LIRRKFISEYNEY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 LIRKKLRSEFN 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              October
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: Octobo
Job time : 6.10648 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: garD
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A;Residues: 1-178 <AQF>
A;Cross-references: GB:AE000775; NID:g2984342; PIDN:AAC07866.1; PID:g2984346; GB:AE00065
A;Cross-references: strain VFS
C;Genetics:
C;Genetics:
C;Genetics:
C;Superfamily: CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
C;Keywords: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alternate names: hypothetical protein R015; Species Cateviside; Saccharomyces cerevisiae construction of the R015 species Saccharomyces cerevisiae construction 19-Oct-1995 #text_change 19-Apr-2002; Accession: 556199; S62281; Marrakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, Danted to the EMBL Data Library, May 1995; Pescription: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces of the number: 556186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: DNA
Residues: 1-212 <MUR>
Cross-references: EMBL:D50617; NID:g836685; PIDN:BAA09185.1; PID:g836699; MIPS:YFL056d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABSULT 14
ABSULT 14
ABSG68
molybdopterin biosynthesis protein XF1545 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: ABSG68
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Xeference number: A82515; MUD:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE003984; GB:AE003849; NID:g9106581; PIDN:AAF84354.1; GSPDB:GN001
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
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A;Residues: 1-212 <MUW>
A;Cross-references: EMBL:D44603; NID:g871957; PIDN:BAA08063.1; PID:g871970
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N;Alternate names: hypothetical protein R015
                                                                                                                                                                                                                                       Length 178
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                                                                                                                                                                                                                                                                                             3; Indels
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A;Map position: 6L
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Murakami, Y.
submitted to the EMBL Data Library, December 1994
A;Reference number: $62230
A;Accession: $62281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 2
Pred. No. 48;
4; Mismatches
                                                                                                                                                                                                                                DB
40;
                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                       Score 37;
Pred. No. 4
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                                                                                                                                                                                                                                h 54.4%;
Similarity 61.5%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        107 LIKRKFTPEPSIY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | | | | | : : | : | viatkettdykky 111
                                                                                                                                                                                                                                                                                                                                                    1 LIRRKFTSEYNEY 13
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Best Local Similarity 46.2
Matches 6; Conservative
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Best Local Similarity
Matches 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-276 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: S56199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: SGD: AAD6
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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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October 5, 2004, 07:29:35; Search time 1.16358 Seconds (without alignments) 581.749 Million cell updates/sec OM protein - protein search, using sw model Run on:

Title: Perfect score:

US-09-805-290A-12 68 1 LIRRKFTSEYNEY 13

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Q9zb21 mycoplasma		Q8rgr2 fusobacteri		_			P43547 saccharomyc	human		_						Q8rgj4 fusobacteri					-				χĮς	metha	_	มารถม		_	œ	3375
оопштите	UVB2 MYCPU	SCRK_STRMU	UVRB_FUSNN	MUTS_THEMA	MYSB_DICDI	TE80_TETTH	PGSA_AQUAE	AAD6_YEAST	VL1_HPV44	VL1_HPV55	NH35_CAEEL	UVRB_SYNY3	GLGB_SOLTU	AAD4_YEAST	AADE_YEAST	CARA_DEIRA	SYD FUSNN	UVRB THETN	SYLM SCHPO	RRB1_CANFA	YGB8_YEAST	RNH2 CHLMU	SDGF_RAT	TDP1_HUMAN	TDP1 MOUSE	REP1 KLULA	YZ07_METJA	TDP2_HUMAN	TDP2_MOUSE	LCND LACLA	CLS2_BACSU	MTC1 COREQ	RNC1_YEAST
DB	-1	Н	Н	гH	Н	Н	,	-								Н	Н	H	-	٦	Н	щ	Н	Н	Н	Н	Н	Н	٦	Н	Н	rH	Н
Length	660	293	663	793	1111	719	178	212	200	501	578	699	861	329	376	394	592	662	874	1534	184	217	243	410	410	415	415	446	446	474	482	517	617
ch rz	61.8	57.4		55.9			54.4		54.4	54.4	54.4	54.4	_:	٠.	52.9	٥.	ď	~	ď	ά.	ä	ä	ä	ä	ä	ä	i	i	ä	H	ä	i.	i.
Score	42	9	38	38	38	37.5	37	37	37	37	37	37	37	36	36	36	36	36	36	36	35	35	35	35	35	35	35	35	3	35	35	35	35
Result No.		71		4	ιΩ	ø	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P40009 saccharomyc Q928a4 listeria in	Q8y4f5 listeria mo Q971q2 clostridium	P17794 agrobacteri O9zcn6 rickettsia	P54112 staphylococ	P38811 saccharomyc	P36864 volvox cart	Q39573 chlamydomon		P96796 methanosarc
YND1_YEAST UVRB_LISIN	UVRB_LISMO UVRB_CLOAB	VIB4 AGRTS	GYRA STAEP	TRA1_YEAST	YPTS_VOLCA	YPTS CHLRE	TRIC XENLA	HDRE_METBA
		н.	٠,	Н	r-I	н	Н	ı
630	658 666	789	8 6	3744	202	206	243	263
51.5	51.5	51.5	51.5	51.5	50.0	50.0	50.0	50.0
3 3 52 52	3.35	32	n m	35	34	34	34	34
3.4 5.5	36.	80 0	J 4.	41	42	43	44	45

## ALIGNMENTS

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SEQUENCE FROM N.A.
                                                                                                                                                                                                                         NCBI_TaxID=76856;
                                                                                                                                                                                 UVRB OR FN0224
                                                                                                                                                                                                                 Fusobacterium
                                                                                                                      UVRB FUSNN
Q8RGR2;
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           Query Match
                                                                                                              UVRB_FUSNN
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                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=UALS9 / ATCC 700610 / Serotype C;
MEDLINE=22295063; PubMed=12397186;
Addic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.,
"Genome sequence of Streptococcus mutans UAl59, a cariogenic dental
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Sato Y., Yamamoto Y., Kizaki H., Kuramitsu H.K.; Isolation, characterization and sequence analysis of the scrK gene encoding fructokinase of Streptococcus mutans."; J. Gen. Microbiol. 139:921-927 (1993).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
-!- CATALYTIC ACTIVITY: ATP + D-fructose = ADP + D-fructose 6-
                                                                                                                               Score 42; DB 1; Length 660; Pred. No. 7.1;
                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                           33A5AF375705367D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase, Kinase, Complete proteome. CONFLICT 139 139 T \rightarrow A (IN REF. 1). SEQUENCE 293 AA; 31712 MW; 1089AF37B2C5B807 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphate.
SIMILARITY: BELONGS TO THE ROK (NAGC/XYLR) FAMILY
                                                                              ATP (POTENTIAL).
BETA-HAIRPIN.
                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                         Pred. No. 7.1;
1; Mismatches
                                                                                                                                                                                                                  MEDLINE=93329360; PubMed=8336109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AEO15011; AAN5946311; -.
InterPro. PRO00600; ROK.
Pfam; PF00480; ROK; PALSE_NEG.
PROSITE; PS01125; ROK; FALSE_NEG.
                                                                                                  657 U
75884 MW;
PF00271; helicase_C; 1.
                                                                                                                               61.8%;
                                                                                                                                         66.78;
                                                                                                                                                                                          569 LFKRKIQSEYNE 580
                                                                                                                                                  Conservative
                                                                                                                                                                      1 LIRRKFTSEYNE 12
                                                                                                          660 AA;
                                                                                                                                        Local Similarity
les 8; Conserv
                                                                                                           SEQUENCE
                                                                             NP BIND
DOMAIN
                                                                                                                               Query Match
                                                                                                  DOMAIN
                                                                                                                                                Matches
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A Mapatral V., Anderson I.; Ivanova N., Reznik G., Los T., Lykidis A., Rapatral V., Anderson I.; Ivanova N., Grechkin G., Zhu L., Apatracharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasal V., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M.; Kyrpides N., Overbeck R., Genome sequence and analysis of the oral bacterium Fuschart and Analysis of the oral bacterium Fuschart and Analysis of the oral bacterium complex composed of J. Bacteriol. 184:2005-2018(2002).

1. FUNCTION: The UvrABC repair system catalyzes the recognition and processing of DNA lesions. A damage recognition complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. Upon binding of the uvrA(2)B(2) complex to a putative damaged site, the DNA wraps around one uvrB monomer. DNA wrap is dependent on ATP binding by uvrB and probably causes local melting of the DNA helix, facilitating insertion of uvrB beta-hairpin between the DNA strands. Then uvrB probes one DNA strand for the presence of a lesion. If a lesion is found the uvrA subunits dissociate and the second uvrB binding the uvrA subunits dissociate and the second uvrB subsequently bound by uvrC and the uvrA subunits dissociate and the second uvrB subsequently by uvrC and the second uvrB menticial or the presence of a lesion. If a lesion of the uvrA subunits dissociate and the second uvrB subsequently by uvrC and the second uvrB menticial or the presence of a lesion. If a lesion of the uvrA subunits dissociate and the second uvrB subsequently by uvrC and the second uvrB menticial or the presence of a lesion is found the second uvrB menticial or the presence of a lesion is found the acconductor or the presence of a lesion is found the acconductor or the presence of a lesion is found the acconductor or the presence of a lesion is found the acconductor or the presence of a lesion is found the acconductor or the presence of a lesion is found the acconductor or the presence of a lesion is found the acconductor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lesion is found, the DNA wraps around the other uvrB subunit that will check the other stand for damage (By similarity). SUBUNIT: Forms a heteroterramer with uvrA during the search for lesions. Interacts with uvrC in an incision complex (By
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UvrABC system protein B (UvrB protein) (Excinuclease ABC subunit B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
-!- SUBCELLUTAR LOCATION: Cytoplasmic (By similarity).
-!- DOMAIN: The beta-hairpin motif is involved in DNA binding (By
                                                                                                                           .
0
Score 39; DB 1; Length 293;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 663 AA
                                                                                                                           2; Mismatches
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-!- SIMILARITY: Contains 1 UVR domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
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InterPro; IPR004807; UVrB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE010535; AAL94430.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001943; UvrB/C.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                        247 VREKFISLLNDY 258
                                                          Best_Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                    2 IRRKFISEYNEY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain."
                                                                                                                                                                                                                                                                                                         Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=MSB8 / DSM 3109 / ATCC 43589;

MEDINE=9287315; Dubmed=10360571;

A Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

A Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

A McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

A Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from "evidence of Thermotoga maritima.";

"Genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999).

-I FUNCTION: This protein is involved in the repair of mismatches in DNA. It is possible that it carries out the mismatch recognition step. This protein has a weak AfPase activity (By similarity).

-I SIMILARITY: Belongs to the DNA mismatch repair muts family.
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
                                                                        recombination;
                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wetmur J.G., Rosenfeld A., Wong D.M.; "Hyperthermophilic MutS proteins: isolation, characterization enhancement of PCR specificity."; enhancement of PCR specificity."; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  55.9%; Score 38; DB 1; Length 663; 63.6%; Pred. No. 38; 11ve 0; Mismatches 4; Indels
                                                                                                   40 47 ATP (POTENTIAL).
93 116 BETA-HAIRPIN.
624 659 UVR.
663 AA; 76985 MW; DEF00752C19D1389 CRC64;
Pfam; PF02151; UVR; 1.

SMART; SM00487; DEXDC; 1.

SMART; SM00490; HELICC; 1.

TIGRFAMs; TIGR00631; uvrb; 1.

R PSCSTTE; PS50151; UVR; 1.

W SOS response; Excision nuclease; DNA repair; DNA rec

NDA axxision, ATP-binding; Complete proteome.

T NP BIND 40 47 AFF (POTENTIAL).

DOWAIN

T SETA-HAIRPIN.

T AFF (24 659 UVR.)
                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                    793 AA
                                                                                                                                                                                                                                                                                                                                                                                   DNA mismatch repair protein mutS MUTS OR TM1719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF 00096; -; 1.
InterPro; IPR005748; MutS1.
InterPro; IPR00432; MutS.C.
InterPro; IPR007860; MutS.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, U71155; AAB16999.1; -. EMBL, AE001811; AAD36785.1; PIR, C72219; C72219.
                                                                                                                                                                                 Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                    572 RRKIQKEYNAY 582
                                                                                                                                                                                                                         3 RRKFTSEYNEY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxiD=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; C72215,
TIGR; TM1719; -
                                                                                                                                                                                                                                                                                                                       THEMA
                                                                                                                                DOMAIN
SEQUENCE
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                      MUTS THE P74926;
                                                                                                                                                                                                                                                                                           RESULT 4
MUTS THEMA
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Josepon.,
Josepo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myosin I heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=AX3;
MEDINDE=93315475; PubMed=8325874;
Jung G., Fukui Y., Martin B., Hammer J.A. III;
"Sequence, expression pattern, intracellular localization, and
targeted disruption of the Dictyostellum myosin ID heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
R InterPro; IPR007696; MutS_III.

R InterPro; IPR007691; MutS_IV.

R InterPro; IPR007691; MutS_IV.

R Pfam; PP01624; MutS_I; I.

R Pfam; PP01629; MutS_II; I.

R Pfam; PP01909; MutS_IV; I.

R Pfam; PP0190; MutS_II; I.

R Pfam; PP0190; MutS_IV; I.

R SWART; SW00534; MUTSac; I.

R SWART; SW00534; MUTSac; I.

R SWART; SW00539; MUTSac; I.

R PROSITE; PS00466; DNA MUTSac; I.

R PROSITE; PS00466; DNA MUSNATCH REPAIR 2; I.

R PROSITE; PS00466; DNA MUSNATCH REPAIR 2; I.

T CONFLICT 252 262 I. > W (IN REF. I).

T CONFLICT 262 262 I. > W (IN REF. I).

T CONFLICT 506 506 K. > T (IN REF. I).

T SRQUENCE 793 AA; 91065 MW; 1BCB2342E4F9B1BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 1; Length 793;
Pred. No. 46;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89345628; PubMed-2762320;
Jung G., Saxe C.L. III, Kimmel A.R., Hammer J.A. III;
"Dictyostelium discoideum contains a gene encoding a n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoldeum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 86:6186-6190(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYSB DICDI STANDARD; PRT; 1111 AA.

AC PA4502;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DF MYOB OR MYOA OR DMIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 481-490; 656-666 AND 783-798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 VIKRGFSSELDEY 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LIRRKFTSEYNEY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMEL outstation the Burepean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                         EMBL; U25641; AAC46601.1; -.
PIR; S55939; S55939.
InterPro; IPR008858; TROVE.
Pfam; PF05731; TROVE; 1.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; althe complete genome of the hyperthermophilic bacterium Aquifex aeolicus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2001 (Rel. 40, Last amnotation update)
CDP-diacylalycerol--glycerol-3-phosphate 3-phosphatidyltransferase
(EC 2.7.8.5) (Phosphatidylglycerophosphate synthase) (PGP synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- FUNCTION: This protein catalyzes the committed step to the synthesis of the acidic phospholipids (By similarity).
-1- CATALYTIC ACTIVITY: CDP-diacy101ycerol + glycerol 3-phosphate -CMP + 3-(3-phosphatidyl)-glycerol 1-phosphate.
-1- PATHMAY: Acidic phospholipids biosynthesis.
-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
-1- SIMILARITY: Belongs to the CDP-alcohol phosphatidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                    719 AA; 82351 MW; 8A945A71189CA99C CRC64;
       a 1:1:1 complex with the 159 nt telomerase RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1,
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37.5; DE Pred. No. 51; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; H70484; H70484.

PIRS, PROMOMEZ, CDP-OH P trans.

Pfam; PPOJ066; CDP-OH P transf; 1.

PROSITE; PS00379; CDP_ALCOHOL_P_TRANSF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000775; AAC07866.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                55.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 VRSKF-SEFNEY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 66.7
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 IRRKFTSEYNEY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       class-I family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                            DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGSA AQUAE
067908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGSA OR AQ
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGSA AQUAE
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       엄
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                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no wat modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=95292335; PubMed=7774009;
COllins K., Kobayashi R., Greider C.W.;
"Purification of Tetrahymena telomerase and cloning of genes encoding the two protein components of the enzyme.";
Cell 81:677-686(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i. FUNCTION: Ribonucleoprotein DNA polymerase that catalyzes the denote synthesis of telomeric simple sequence repeats. P80 binds tightly and specifically to the telomerase RNA suggesting its association with a region of RNA secondary structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetrahymena thermophila.
Bukaryota, Alveolata; Ciliophora, Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
NCBI_TaxID=5911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50002; SH3; 1.
Myosin; Actin-binding; ATP-binding; SH3 domain; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
SIMILARITY: Contains 1 myosin-like globular head domain. SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (BY SIMILARITY), W; CD6386F08DC5642F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYOSIN HEAD-LIKE.
TAIL HOWOLOGY REGION 1 (TH.1).
GLY/PRO/ALA-RICH (TH.2).
SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Telomerase component p80 (EC 2.7.7.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 65;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASN-RICH
                                                                                                                                                                                                                                                                                   HSSP, PO8799, IMND.
DictyBase; DDB002013; mycB.
DICTEPPO; IPR000048; IQ_region.
InterPro; IPR001669; mycsin_head.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0193; MYOSINHBAVY.
PROM152; SH3DOWAIN.
PRODOM; PD000035; myosin_head; 1.
ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124313 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin head; 1.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                             EMBL; M26037; AAA33229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 736 IDRKFTSDYIDF 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00242; MYSC; 1.
SMART; SM00326; SH3; 1.
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Matches 7: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemotaxis;
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SEQUENCE Query Match

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OTHER INFORMATION: nt5162-nt5242: intron
CTHER INFORMATION: nt1-nt6: SacI restriction site
NAME/KEX: misc_feature
CTHER INFORMATION: nt729-nt734, nt2811-nt2816, nt5103-nt5108: BglII restriction site
OTHER INFORMATION: nt3335-nt3340: HindIII site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1709 ATATTACGACTAATTTGCAAGACGAATCTTTTAAGCATAATTGCTCCATGATTTAACAAT 4768
                                                                                                                                                                                                                                                                                                                                                                                              4649 TIGAACAITIGAACACCIGIATAAAGIAITAAATATATACTAAAAATAATTAATTATAC 4708
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                                                                                                                                                                                                                                                                                                                                       337 TTTAATGTTTAGACACATGTATGGAGTACTAAATAT---TAATAAAAAAAATAATTACAC
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Patent No. 5859339
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Ronald, Pamela C.
APPLICANT: Ronald, Wen-Yuang
TITLE OF INVENTION: Disease Resistance in Plants
INVERSE OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Franchisco
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                                                                                                                                                                                                                  Query Match 53.9%; Score 110.2; DB 4; Length 5396; Best Local Similarity 68.6%; Pred. No. 1e-21; Matches 212; Conservative 0; Mismatches 88; Indels 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
REFERRUCE/DOCKET NUMBER: 02370-058910US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/475,891A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (415) 576-0200
(415) 576-0300
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4947 CTCTGTTCC 4955
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TELEFAX: (
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                                                                                                                                                           US-09-807-897-4
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OTHER INFORMATION: Variety: IR24
OTHER INFORMATION: Ubrary name: lambdaDASHII genomic library derived from green lea
OTHER INFORMATION: genomic DNA
OTHER INFORMATION: Clone name: RPG106 SacI-Sall 5.4 kb
NAME/KEY: misc_feature
OTHER INFORMATION: Strandedness: double - Topology: linear
OTHER INFORMATION: Molecular type: genomic DNA
OTHER INFORMATION: Feature: nlints69, nt3335-nt5108; sequences whose promoter acti
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OTHER INFORMATION: nt4964-nt4969: TATA box like sequence
OTHER INFORMATION: nt49964-nt4969: TATA box like sequence
OTHER INFORMATION: nt49964-nt4997: transcription initiation points of RPC213 gen
OTHER INFORMATION: nt5016-nt5018: the first ATG of RPC213 gene
NAME/KRY: nisc_feature
OTHER INFORMATION: nt5128-nt5130: the second ATG of RPC213 gene
OTHER INFORMATION: nt5370-nt5372: the third ATG of RPC213 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 TACAGTAAACATTTGCTAATGACAGATTAATTAAGGCTTAATAAATTCGTCTCACAGTTTA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 GIGIAAATIGCGAGAIAAAICTITIIAAGCCIAATIGCICCAIGA----ACAAIGIGGIGI 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 CTTGAAATTTACGAGACAAATCTTTTAAGCCTAATTGCGCCATGATTTGACAATTTGGTGC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: IWAMOTO, MASAO
TITLE OF INVENTION: PROMOTOR SEQUENCE WHICH IS EXPRESSED IN ANTHERS AND IN
TITLE OF INVENTION: POLLEN
FILE REPERENCE: YAM 2 0006 US / AR010
CURRENT APPLICATION NUMBER: US/09/100,971
CURRENT APPLICATION NUMBER: 2000-12-08
NUMBER OF SIG ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEC ID NO 2.
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APPLICANT: TAKAKURA, Yoshimiteu
TITLE OF INVENTION: NOVEL DNA FRAGMENT ENHANCING GENE EXPRESSION LEVEL
FILE REFERENCE: 0230-0156P
CURRENT APPLICATION NUMBER: US/09/807,897
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: PCT/JP00/05539
PRIOR FILING DATE: 2000-08-18
NUMBER OF EXQ ID NOS: 25
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.6%; Score 124.6; DB 4; Length 4670; Best Local Similarity 82.8%; Pred. No. 5.4e-26; Matches 168; Conservative 0; Mismatches 29; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517 CAGGTGAATATGTAATTTATTT 539
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Patent No. 6660851
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ORGANISM: Oryza sativa
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LENGTH: 5396
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Sequence 1336, Ap
Sequence 1338, Ap
Sequence 13, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 2, Appli
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US-09-700-971-1

Sequence 1, Application US/09700971

Sequence 1, Application US/09700971

GENERAL INFORMATION:

APPLICANT: HAMOTO, KENICHI

APPLICANT: HAMOTO, MASAO

TITLE OF INVENTION: PROMOTOR SEQUENCE WHICH IS EXPRESSED IN ANTHERS AND IN

TITLE OF INVENTION: PROMOTOR SEQUENCE WHICH IS EXPRESSED IN ANTHERS AND IN

TITLE OF INVENTION: PROMOTOR SEQUENCE WHICH IS EXPRESSED IN ANTHERS AND IN

CURRENT APPLICATION NUMBER: US/09/700,971

CURRENT APPLICATION NUMBER: US/09/700,971

CURRENT FILLE OF INC. 2.0
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                       Seguence
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US-09-575-574-3
US-08-446-794A-5
US-08-750-007-4
US-09-313-294A-1336
US-09-313-294A-1338
US-09-313-294A-1338
US-09-310-390-8
US-09-105-390-8
US-09-105-390-8
US-09-105-390-8
US-09-105-390-8
US-09-105-390-8
US-08-446-794A-5
US-08-567-891A-1
US-08-567-375-1
US-08-567-375-1
US-08-567-375-1
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update
Putative aryl-alcohol dehydrogenase AAD6 (EAAD6 OR FFL056C.
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ACT_SITE 151
SEQUENCE 212
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Murakami Y., Naitou M., Hagiwara H., Shibata T.,
Sasanuma M., Tsuchiya Y., Soeda
Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromoso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD6_YE
P43547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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InterPro; IPRO01395; Aldo/ket_red.
Pfam; PF00248; aldo ket_red; 1.
ProDom; PD000288; Aldo/ket_red; 1.
                                                                                                                                                                                                                                                                                                                                                     EMBL; D50617; BAA09185.1; -. PIR; S56199; S56199.
                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
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SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE
TO THE N-TERMINUS OF YEAST AAD14.
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                                                                                         Conservative
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23918 MW;
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                                                                                       Score 37; DB:
Pred. No. 17;
4; Mismatches
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                                                                                                                                                                              HYDROGEN-BOND DONOR (PROBABLE)
; C3FF042B12C91580 CRC64;
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                                                                                                                                 Length 212,
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RESULT 9 VL1\_HPV44

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SON DESCRIPTION OF THE PROPERTY OF THE PROPERT
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Best Local S
Matches 6
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P50816; Q80919;
01-OCT-1996 (Rel. 34, C
15-JUL-1998 (Rel. 36, L
15-JUL-1998 (Rel. 36, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 312-462 FROM N.A.

MEDLINE=95052821; PubMed="963696;

Bernard H.U., Chan S.Y., Manos M.M., Ong C.K., Villa L.L.,

Delius H., Peyton C.L., Bauer H.M., Wheeler C.M.;

"Identification and assessment of known and novel human papillomaviruses by polymerase chain reaction amplification, restriction fragment length polymorphisms, nucleotide sequence, phylogenetic algorithms.";

phylogenetic algorithms.";

J. Infect. Dis. 170:1077-1085 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
Delius H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR002210; PV_capsid_L1.
Interpro; IPR008975; Viral_cap_coat.
Pfam; PF00500; late_protein_L1; 1.
PRINTS; PR00865; HPVCAPSIDL1.
ProDom; PD000544; PV_capsid_L1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Papillomavirus.
NCBI_TaxID=10592;
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                                                                                        SEQUENCE
Delius H.
                                                                                                                                                                               Human papillomavirus ty
Viruses; dsDNA viruses,
Papillomavirus.
                                                                                                                                                                                                                                                                                              P50820; Q80940;
01-OCT-1996 (Rel. 34, Creat
15-JUL-1998 (Rel. 36, Last
15-JUL-1998 (Rel. 36, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coat protein; Late SEQUENCE 500 AA;
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                                                                                                                                                                                                                                                                               Major
SEQUENCE OF 312-462 FROM N.A. MEDLINE=95052821; PubMed=7963696;
                                                                  Submitted (OCT-1995)
                                                                                                                                                           NCBI_TaxID=37114;
                                                                                                                                                                                                                                                                                                                                                                                                 HPV55
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55849 MW;
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RNA
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277A44B7CAA421F9 CRC64;
                                                                                                                                                                                                               stage;
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                                                                                                                                                                                                               Papillomaviridae,
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Best Local
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EMBL; U12494; AAA67238.1; -.
InterPro; IPR002210; PV capsid L1.
InterPro; IPR008975; Viral cap coat.
Pfam; PF00500; late protein L1; 1.
PRINTS; PR00865; HPVCAPSIDLI.
ProDom; PD000544; PV capsid L1; 1.
Coat protein; Late protein.
Coat protein; Late protein.
Coat protein; Aate Protein.
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                                                                                                                                                                         Bogan A., Maina C.V., Yamamoto K., Cohen F., Sluder A.E.; "Caenorhabditis elegans nuclear receptor sequences exhibit biophysical compatibility with the ligand-binding domain fold."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                              Waterston R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Bristol N2; Geisel C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NH35_CAEEL STANDARD; PRT; 578 AA. Q17771; Q9GTH7; 15-DEC-1998 (Rel. 37, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nuclear hormone receptor family member nhr-35, NHR-35, OR C07A12.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the EMropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                   -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
                                                                                                                                                                                                                                                    SEQUENCE OF 35-578 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAEEL
                                                                                                                                                                                                                                                                                                                       REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phylogenetic algorithms.";
J. Infect. Dis. 170:1077-1085(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bernard H.U., Chan S.Y., Manos M.M., Ong C.K., Villa L.L., Delius H., Peyron C.L., Bauer H.M., Wheeler C.M.; Telentification and assessment of known and novel human papillomaviruses by polymerase chain reaction amplification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                            FUNCTION: Orphan nuclear receptor.
SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 448 LREKESSELDOY 459
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ODBC4D47E552E968 CRC64;
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RESULT 12
UVRB_SYNY3
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Best Local 9
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Q55170;
15-JUL-1998
15-JUL-1998
28-FEB-2003
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Pfam; PF00105; zf-C4; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STRDIDENKONER.
PRINTS; PR00047; STROIDEINGER.
PRODOM; PD000035; Znf_C4steroid;
SMART; SM00430; HOLI; 1.
SMART; SM00339; ZnF_C4; 1.
                                     processing of DNA lesions. A damage recognition complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. Upon binding of the uvrA(2)B(2) complex to a gutative damaged site, the DNA wraps around one uvrB monomer. DNA wrap is dependent on ATP binding by uvrB and probably causes local melting of the DNA helix, facilitating insertion of uvrB beta-hairpin between the DNA strands. Then uvrB probes one DNA strand for the presence of a lesion. If a lesion is found the uvrA subunits dissociate and the uvrB-DNA preincision complex is formed. This complex is subsequently bound by uvrC and the second uvrB subunit that will check the other stand for damage (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                    UVTABC system protein B (UVTB protein)
UVRB OR SILU459.
System protein B (UVTB protein)
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ZN_FING
ZN_FING
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome."; pna Res. 2:153-166 (1955).

The UVCTION: The UVCABC repair system catalyzes the recognition and
                                                                                                                                                                                                                                                                            Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium "Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
                                                                                                                                                                                                                                                                                                         MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima
Sugiura M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                               Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00031; NUCLEAR RECEPTOR; Receptor; Transcription regulation;
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR008946; Str_ncl_receptor.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WormPep; C07A12.
               lesions. Ir similarity)
SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          566 FISSYNOY 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P19793; 2NLL.
en: C07A12.3; CE29071.
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(Rel.
(Rel.
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                             Interacts with uvrC in an incision complex
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36, Last sequence update)
41, Last annotation updat
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97 C
137 C
302 M
65256 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.4%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR RECEPTOR-TYPE C4-TYPE. C4-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9868FD24FBCEE8C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches

    DNA-binding; Nuclear protein;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          (Excinuclease ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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Best Local (
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InterPro; IPR001410; DEAD.

InterPro; IPR00150; Helicase_C.

InterPro; IPR004807; UVrB/C.

InterPro; IPR001943; UVrB/C.

Pfam; PF00271; helicase_C; 1.

Pfam; PF00271; UVR; 1.

SMART; SM00480; HELICC; 1.

SMART; SM00490; HELICC; 1.

TIGRPAMS; TIGR00631; UVrb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P30924;
01-JUL-1993
01-NCV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D64001; BAA103(
PIR; S74391; S74391.
HSSP; Q56243; 1C40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Solanum tuberosum (Potato).

Bukaryota; Viridiplantae; Streptophyta; Embryospermacophyta; Magnoliophyta; eudicotyledons; Lamiids; Solanales; Solanaceae; Solanum.

NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                         SEQUENCE OF 279-527 FROM N.A.
STRAIN-CV. Desiree, TISSUE-Tuber;
MEDLINE=92079917; PubMed=1745241;
KOSSMann J., Visser R.G.F., Mueller-Roeber
                                                                                                                                                                                                                                     MEDLINE=94105324; PubMed=8278528; Poulsen P., Kreiberg J.D.; Poulsen P., Kreiberg J.D.; Rreich branching enzyme cDNA from Plant Physiol. 102:1053-1054(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SBE1 OR SBE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Creat
01-NOV-1995 (Rel. 32, Last
10-OCT-2003 (Rel. 42, Last
1,4-alpha-glucan branching
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
   "Cloning and expression and
branching enzyme: evidence
                                                       Sonnewald U
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similarity).
SIMILARITY: Belongs to the uvrB family.
SIMILARITY: Contains 1 UVR domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Q-enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRKFTSEYNE 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     669 AA;
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                                                                                                                                                                                                                                                                                                                                                        Dianella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580
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70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
         analysis of a potato
nce for co-expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
annotation updat
enzyme (EC 2.4.1
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                                                                                                                                                                                                                                                                    Solanum tuberosum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
2.4.1.18) (Starch branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Embryophyta; Tracheophyta; edons; core eudicots; aster
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         of starch
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                                                                                                Willmitzer
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biosynthetic
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Best Local S
Matches 7
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Mol. Gen.
-!- FUNCT
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AAD4_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X69805; CAA49463.1; -. PIR; S34730; S34730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Starch biosynthesis; Transferase; Glycosyltransferase; Amyloplast;
use by non-profit modified and this st entities requires a
  This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                         Alt-Moerbe J., Schneider C., Moro M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the aldo/keto reductase 2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00128; alpha-amylase;
Pfam; PF02922; isoamylase_N; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR004193; Glyco_hydro_13N.
                                                                                                                                 SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic linkages in glycogen by scission of a 1,4-alpha-linked oligosaccharide from growing alpha-1,4-glucan chains and the subsequent attachment of the oligosaccharide to the alpha-1,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Starch biosynthesis; third step.
SUBUNIT: Monomer.
SUBCELLULAR LOCATION: Chloroplast; amyloplast.
SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                position.
CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages
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                                                                                                                                                                                                                                                                                                                                                       441
                                                                                                                                                           TaxID=4932;
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3550
427
5534
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355
427
484
553
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                                                                                                                                                                                                                                                                                           329
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                                                                                                                                                                                        Saccharomycetes;
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AADE_YEAST
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                            SGD; S0005275; AAD14.
InterPro; IPR001395; Aldo/ket red.
Pfam; PF00248; aldo ket red; I.
ProDom; PD000288; Aldo/ket_red; 1.
                                                                                                                                                                                                                         EMBL; X83226; CAA58227.1; -.
EMBL; Z71607; CAA96264.1; -.
PIR; S51335; S51335.
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
Obermaler B., Piravandi E., Rinke M.;
Obermaler B., Piravandi E., Rinke M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-1996) to THE ALDO/KETO REDUCTASE 2 FAMILY. STRONG,
                                                                                                                       Oxidoreductase.
ACT_SITE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase.
ACT_SITE 105
SEQUENCE 329 AA;
                                                                                                         SEQUENCE
                                                                                                                                                                                                        GermOnline; 143337; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=S288c / FY1679;
van Dyck L., Pascual-Ahuir A., Goffeau A.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGD; S0002402; AAD4.
InterPro; IPR001395; Aldo/ket_red.
Pfam; PF00248; aldo ket_red; 1.
ProDom; PD000288; Aldo/ket_red; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P42884;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
Putative aryl-alcohol dehydrogenase AAD14 (EC 1.1.1.-).
AAD14 OR YML331C OR NO300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z74291; CAA98823.1; PIR; S67807; S67807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GermOnline; 140486; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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1 LIRRKFTSEYNEY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 VIATKFTGDYKKY 65
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                                                                                                      151
376 AA;
                                            Conservative
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                                                                                                      151 F
41991 MW;
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                                                          52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.9%; Score 36; 46.2%; Pred. No.
                                             ω
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                                                          Score 36; DB 1; Length 376; Pred. No. 47;
                                                                                                    HYDROGEN-BOND DONOR (POTENTIAL).; 2265406386938313 CRC64;
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                                             Mismatches
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Search completed: October 5, 2004, 08:01:43
Job time: 3.16358 secs

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
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1: Sp archea:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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	39	40	40	40	40	40	40	40	40	40	40.5	41	42	43	45	46	Score
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*	Q97w67 sulfolobus	Q8iju3 plasmodium	Q81ev1 bacillus ce	Q08131 manihot esc	Q41059 pisum sativ	Q8t021 drosophila	Q9vuz6 drosophila	Q88tf9 lactobacill	Q7v0x5 prochloroco	Q08130 manihot esc	Q980s0 sulfolobus	Q86bj7 drosophila	Q86bj8 drosophila	Q86bk0 drosophila	Q8xin5 clostridium	Q9w017 drosophila	Description

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## ALIGNMENTS

RESULT 1

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobary L., Muzny D.M., McShrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stepleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskas R., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
      Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; ARE03469; AAF27426.2;

EMBL; AY122170; AAM52682.1;

R FlyBase; FBgn0052479; CG32479;
R GO; GO:0004197; F: cysteine-type endopeptidase activity; IE;
R GO; GO:0004217; F: ubiquitin thiolesterase activity; IE;
R GO; GO:0004211; P: ubiquitin thiolesterase activity; IE;
R GO; GO:0006511; P: ubiquitin-dependent protein catabolism;
R GO; GO:0007511; P: ubiquitin dependent protein catabolism;
R GO:0007511; P: ubiquitin dependent protein catabolism;
R GO:0007511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.", "Annotation of Drosophila melanogaster genome.", "Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M.D.
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01-JUN-2003 (
01-JUN-2003 (
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MEDILINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B. Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G
                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=13 / Type A;
MEDLINE=21664973; Phibmed=11792842;
MEDLINE=21664973; Phibmed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shimizu T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
                                                                                                                                                                       CG9614-PJ
                                                                                                                                                                                                                                                                                                                                                                                                                         flesh-eater.";

Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

EMBL; AP003192; BAB81786.1; -.

GO; GO:0004559; F:alpha-mannosidase activity; IE;

GO; GO:0005975; P:carbohydrate metabolism; IEA.
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Pfam; PF01074; Glyco_hydro_38; 1.
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Bacteria; Firmicutes; Clostridia;
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolinakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J. M., Cawley S., Dahlke C., Davemport L. B., Davies P.,
RA Cherry J. M., Cawley S., Dahlke C., Davemport L. B., Davies P.,
RA Cherry J. M., Cawley S., Dahlke C., Davemport L. B., Davies P.,
RA Dodson K., Doup L. B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K. Dabrielian A. E., Garg N. S., Celbart W. M., Glasser K.,
RA Glodek A., Gong F., Gorrell J. H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibeyawan C.,
RA Hostin D., Houston K.A., Howland T. J., Wei M.H., Ibeyawan C.,
RA Kimmel B. E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J. Moshrefi A.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J. Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Spier E., Sjendling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun H.,
RA Williams S.M., WoodageT, Worley S., Wang A.H., Wang X.,
RA Williams S.M., WoodageT, Worley K., Sun S., Yang S., Yao Q., Xeeng L.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
"The genome sequence of Drosophila melanogaster.";
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                             Query Match
01-JUN-2003
01-JUN-2003
01-OCT-2003
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InterPro; 1...
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PRO5040; H.
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Ballew R.
Beeson K.
                                                           Q86BJ8;
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                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2003) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Cempbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E., Clamp M.B., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J., Clamp M.B., Drysdale R.A., Emmert B., Millburn G.H., Richter J., Harris N.L., Kronmiller B., Marshall B., Millburn G.H., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Russo S., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Annotation of Drosophila melanogaster genome. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
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, Basu A., Baxendale J., Bayraktaroglu L., E
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Pred. No. 16;
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                                                                              PRT;
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Beasley E.M.,
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                     RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Holt R.A., W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wottman J.R., Yandell N.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wottman J.R., Yandell N.D., Zhang Q., Chen L.X.,
RA Abril J.F., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Rayendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Burtis K.C., Blacos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Blasam D.A., butler H., Caddeu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Devies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Codson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibseyam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibseyam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibseyam C.,
RA Kimmel B.E., Kodira C.D., Kraff C., Kravitz S., Kulp D. Lai Z.,
RA Jalaii M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraff C., Kravitz S., Kulp D. Lai Z.,
RA Melson D.R., Nelson K.A., Nixon K., Nusseern D.R., Wocherson D.,
RA Merkalov G., Milshina N.V., Mobarry C., Morris J., Mosheefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusseern D.R., Sheel H.,
RA Shue B.C., Siden-Kiamos I., Singson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Shan M., Slang G., Zhao Q., Ye J.,
RA Sheng X.H., Wang X., Zhan M., Zhang K., Zhu X., Smith H.O.,
RA Science S. R., Roddaget, Worler J.C.,
Ra Science S. Shan M., Scon K., Shin H., Wang X.,
Ra S
                 Submitted (JAN-2003) to the EMBL; AE003517; AA041227.1; InterPro; IPR007734; HS2ST. Pfam; PF05040; HS2ST; 1. SEQUENCE 405 AA; 47803 MW
                                                                                                                                                                                                                                                                                               Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E., Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J., Harris N.L., Kronmiller B., Marshall B., Millburn G.H., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Millshurn G.H., Richter J., Whitefield F. T. Abbrer W. M. Bubbin M. Millshurn G.H.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                     5807FC09A5CA264C CRC64;
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Length 405

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RESULT 5
ID 86847
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Doyle C., Baxter E.G., Helt G., Welson C.R., Gabor G.L.,
RA Abril J.F., Aphayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Besson K.Y., Bennss P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouke J., Bayraktaroglu L., Beasley E.M.,
RA Gheson K.Y., Benns P.D., Dahlke C., Davepoert L.B., Davies P.,
RA Borkova D., Botchar A., Dong Z., Mays A.D., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davepoert L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Bavenpoert L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Borriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Houck J.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Heiman T.J., Heiman W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Heim M.H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lang Y., Lin X.,
RA Hostin D., Houston K.A., Nixon K., Musskern D.R., Melson D.L.,
RA Mchulto G., Milshina N.V., Mobarry C., Morris J., Moshefi A.,
RA Mchulto G., Milshina N.V., Mobarry C., Morris J., Moshefi A.,
RA Mchulto G., Milshina N.V., Mobarry C., Morris J., Moshefi A.,
RA Mount S.M., Welson K.A., Saunders R.D., Scheeler P., Shan H.,
RA Spies E.W., Rainstock G.M., Weissenbach J.,
RA Spies E.W., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spies S.M., Moodage T., Worley K.C., Mu D., Zhou S., Zhu X., Smith H.O.,
RA Spies S.M., Moodage T., Worley K.C., Mu D., Zho
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                    Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E., Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J., Harris N.L., Krommiller B., Marshall B., Millburn G.H., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Mungall C.J

RESULT Q08130

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RESULT QUESCOSO ID PROPERTY OF STATE OF
                                                                                                                                                                                                                                                                                                                            ARALIN=ATCC 35092 / DSM 1617 / P2;

RX MEDLINE=21332266; PubMed=11427726;

RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard (
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.

RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

RA Heikamp-de Jong I., Jeffrises A.C., Kozera C.J., Medina N.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstr

RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

The complete genome of the crenarchaeon Sulfolobus solfata:

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

R PIR; B90162; B90162.
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InterPro; IRR005352; Cons hypo
InterPro; IRR007085; Dfp_C.
InterPro; IRR003382; Flavoprot
Pfam; PF04127; dfp; 1.
Pfam; PF04441; Flavoprotein; 1
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Complete proteome.
SEQUENCE 413 AA;
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Archaea; Crenarchaeota;
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"hmitted (MAR-2000) to the
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phosphoribosyl transferase (EC 2.4.2.7).
APT OR PMM1122.
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MEDLINE=93099233; FubMed=1281436;

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Ahlgren N.A., Arellano A., Coleman M., Farella W., Shah
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.,
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
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Q9VUZG 10
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RX MEDILINE-20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Baster B., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baster B., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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Best Local
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proc. Natl Acad. Sci. U.S.A. 100:1990-1995(2003).
EMBL; AL935260; CAD65187.1; -.
GO; GO:0003677; F.DNA binding; IEA.
InterPro; IPR001387; HTH_3;
Pffam; PF01381; HTH_3; 1.
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Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbr
Piers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Brobr
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries
De Vos W.M., Siezen R.J.;
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
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SEQUENCE 273 AA; 30562 MW;
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STRAIN=NCIMB 8826 / WCFS1;
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Pred. No. 38;
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Sandbrink H.M.,
L., Bron P.A.,
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Allali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhong G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhong G., Zhao Q., Zheng L.,
RA Zheng K.H., Zhong F.N., Zhong M., Zhong G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhong S., Yao Q., Zheng L.,
RA Zheng S.R., Wyers B.W., Rubin G.M., Venter J.C.,
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EMBL, AE003528, AAR49526.1, -
DR FINERFPO, WD40, 6.
DR FRAM, PF00400, WD40, 6.
DR FRAM, PF00400, WD40, 6.
DR FRAM, PF00404, WD—REPEATS_REGION, 2.
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Repeat; WD repeat.
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                                                                                                                                                                                                                                                                                                                          Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guartin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY069620; AAL39765.1; FlyBase; FBgn0036578; CG5018. InterPro; IPR001080; WD40. Pfam; PF00400; WD40. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS
Repeat; WD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8T021
    Local Similarity hes 8; Conserv
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                                                                                                                                                                                                                                                                                               SM00320; WD40;
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8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat.
             Conservative
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                                       58.8%;
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                                           Score 40;
Pred. No.
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Pred. No. 1e+02;
                                                                                                                                                                 1A832C915A2E88E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6654706B927D7D26 CRC64;
        Mismatches
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                                           1e+02;
                                                                                  DB 5;
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era; Muscomorpha;
    4.
                                                                              Length 696;
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    Indels
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RESULT 12
Q4105
Q4105
D7 Q4105
D7 01-NO
D7 01-NO
D7 01-JU
D8 Starc
GN SBEII
GS Pisum
OC Eukar
OC Eukar
OC Eukar
OC Sperm
OC Holl
RN HEDLI
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RN HEDLI
RA Buxto
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Best Local S
Matches 7
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Q41059;
01-NOV-1996 (TrEMBLTel. 0
01-NOV-1996 (TrEMBLTel. 0
01-JUN-2003 (TrEMBLTel. 2
                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Manihoteae;
SEQUENCE FROM N.A.
STRAIN=cv. M.COL 22; TISSUE=Tuberous root;
Salehuzzaman Snim., Jacobsen E., Visser R.G.F.;
Salehuzzaman Snim. to the EMBL/GenBank/DDBJ c
                                                                                                                                                                                                                                                          Manihot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSIT
CHAIN
                                                                                                                       NCBI_TaxID=3983;
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InterPro; IPR004193; Glyco_hydro_13N.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .;
GO; GO:0005975; P:carbohydrate metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burton R.A., Bewley J.D., Smith A.M., Bhattacharyya M.K., Tatge Ring S., Bull V., Hamilton W.D.O., Martin C., "Starch branching enzymes belonging to distinct enzyme families differentially expressed during pea embryo development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pisum sativum (Garden pea).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid.

eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
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01-NOV-1996 (TrEMBLrel. 21, Last sequ
01-JUN-2003 (TrEMBLrel. 24, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=95201826; PubMed=7894509;
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94191 MW;
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Last annotation updat
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Pred. No. 1.2e+02;
1; Mismatches 4
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POTENTIAL.
; 46B9D1965CB5EC9C CRC64;
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  databases
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Best Loc Matches Query Match

Similarity 8; Conserv

Conservative

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58.88

Score 40; DB Pred. No. 1.5e 0; Mismatches

DB 16; 1.5e+02;

Length 1028; Indels

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Matches 7
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SEQUENCE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q81EV1;
Q81EV1;
01-JUN-2003
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GO; GO:0004556; F:alpha-amylace activity; IEA.
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl...
GO; GO:0016757; F:transferase activity, transferring glycosyl...
GO; GO:0015975; P:carbohydrate metabolism; IEA.
GO; GO:0019252; P:starch biosynthesis; IEA.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR004193; Glyco hydro 13N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            branching enzyme in cassava.";
Plant Mol. Biol. 20:809-819(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salehuzzaman S.N., Jacobsen E., Visser R.G.; "Cloning, partial sequencing and expression of a cDNA coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00128; alpha-amylase; Pfam; PF02922; isoamylase_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X77012; CAA54308.1; -. EMBL; X69714; CAA49372.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: AMYLOPLAST.
-!- SIMILARITY: BELONGS TO FAMILY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      +
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GLYCOGEN.
-!- PATHWAY: THIRD STEP IN STARCH BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                  MEDIINE=22608415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapic
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transit peptide.
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycosyltransferase; Starch biosynthesis; Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003
01-OCT-2003
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                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                            Grechkin Y., Pusch G., Ha
Overbeek R., Kyrpides N.;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                         Bacillus anthracis.";
Nature 423:87-91(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=226900;
                                            PROSITE; PS50051; MCM_2; 1.
                                                                                                                                                                                                                                                      "Genome sequence of Bacillus cereus and
                                                                  InterPro;
                                                                              JUN-2003 (TrEMBLrel. 24,
JUN-2003 (TrEMBLrel. 24,
OCT-2003 (TrEMBLrel. 25,
Ocmain family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNOWN AS THE ALPHA-AMYLASE FAMILY.
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7; Conservative
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  proteome.
1028 AA
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                                                                       )6270; P:DNA replication 
IPR001208; MCM.
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1,4-ALPHA-GLUCAN BRANCHING ENZYME; 1FBAE6E3B6674CA5 CRC64;
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    90C134CA8E0FBC4D CRC64;
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Q8IJU3;
01-MAR-2003
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MEDINING-2255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.G., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.,
                                                                                                                                                                                                                                                                             Nature 419:498-511(2002).
EMBL; AE014830; AAN35297.1;
Hypothetical protein.
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Eukaryota; Alveolata;
NCBI_TaxID=36329;
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371.381 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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### ALIGNMENTS

AAE10545 standard; peptide; 13 AA.

AAE10545;

10-DEC-2001 (first entry)

Llama species antibody VHH CDR3 #14.

Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.

Lama sp.

EP1134231-A1.

19-SEP-2001.

20-FEB-2001; 2001EP-00200703.

14-MAR-2000; 2000EP-00200930

(UNIL ) UNILEVER NV.

Bezemer S, Van De Burg M, De Haard JJW, Tareilus Ħ

WPI; 2001-572718/65

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Claim 4; Page 29; 37pp; English

RESULT 1
RESULT 1
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ID AAEI
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XX The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HFL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region

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RESULT 2
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                    The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #18 from llama (camelid) species
                                                                                                                                                                              New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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Region
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Sequence 130 AA

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIG176-ABIG1751), expressed DNA sequences (ABIG1840-ABIG1815) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directlem wiffor at ftp.wipo.int/pub/published_pct_sequences
AAE10550;
                                                AAE10550
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1003 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 33078; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABL12865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUL-2000;
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                                                                                                                                                                                   179
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                                                                                                                                                                                                                                                                                         Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                             standard; peptide; 13 AA
                                                                                                                                                                                   VRRKYSSEYNHH 190
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                                                                                                                                                                                                                                                                                         Conservative
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2000US-00614150.
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                                                                                                                                                                                                                                                                                                                   58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                   Score 46; DB Pred. No. 30;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HFL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1134231-A1
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                                                          WO200171042-A2
                                                                                                              Drosophila melanogaster
                                                                                                                                                                   pharmaceutical.
                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 10356
                                                                                                                                                                                                                                                                                                      26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                               ABB61188 standard; protein; 696 AA
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UNILEVER PLC.
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Pred. No. 2.4;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
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genes from Drosophila and
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11-UUL-2000; 2000US-00614150.
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                      Wang
Wall
                                                                           21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923F.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                               Streptococcus mutans
                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #30030.
                                                                                                                                                                                                                                                                                                         ABU44503;
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                                                                                                                                             21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                    03-OCT-2002
                                                                                                                                                                                          WO200277183-A2
                                                                                                                                                                                                                                    Antisense; prokaryotic essential
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                                                       (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to an isolated nucleic acid detection reagent
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8; Conserv
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                                                        ELITRA PHARM
                                                                                                                                                                                                                                                                                                                             standard; protein;
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                     Zamudio
Trawick
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                      Malone
Carr G
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Pred. No. 2.3e+02;
1; Mismatches 4
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                       Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                      gene; cell proliferation; drug design.
                         Ohlsen
Forsyth
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WPI; 2003-029926/02

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 7
                                                                                                                                                                                                               Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine; reagents; non-B; non-C; non-D; non-E; clone; tamarin; infected plasma;
                                                                                                                                                                                                                                                                                         Hepatitis GB
                                                                                                                                                                                                                                                                                                                                    27-AUG-2003
02-JUL-1996
                                                                                        Misc-difference
                                                                                                                                                        Hepatitis G virus
                                                                                                                                                                                                                                                                                                                                                                                                      AAR82067;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR82067 standard; protein; 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                     lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1) a vector comprising a promoter operably linked to the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25; SEQ ID NO 72427; 1766pp; English.
                                                                                                                                                                                                 phage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 58. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACA48373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VREKFTSLLNDY 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRRKFTSEYNEY 13
                                                                                                                                                                                                                                                                                         virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                   cDNA library
                                                                                 Location/Qualifiers
1. .1422
                                             AAT00052"
                                                             note= "others correspond to degenerate or STOP codons
                                                                                                                                                                                                                                                                                         (HGBV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.3%;
                                                                                                                                                                                                                                                                                      clone protein prod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB
Pred. No. 1.4e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 6; Lex.
; 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  °;
                                                                                                                                                                                                                                           non-A;
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ACC NOT DEPTH OF THE PROPERTY 
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AAB09037
ID AAB0
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Best Local S
Matches 5
                        14-FEB-1994;
13-MAY-1994;
29-JUL-1994;
23-NOV-1994;
                                                                                                                                                                                                                                                                                                                             Hepatitis G detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Double stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV infected tamarin plasma, using standard procedures, was used to prepare a lambde phage HGBV cDNA library. The cDNA clone AAR00052, which encodes the proteins AAR82066-71 (the 6 possible reading frames), was rescued from the lambda phage, searched against a sequence database and found to be unique HGBV sequence. Reagents which comprise the HGBV DNA, or its protein prods. can be used for the diagnosis, therapy or in a vaccine t prevent HGBV infection. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                      US6051374-A
                                                                                                                                                                                                                                                                                Hepatitis GB
                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-2003
30-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB09037 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-A, non-B, non-C, r diagnosis and therapy
                                                                                                                                                                                          18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB09037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT00052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 240-244; 661pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-293123/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-NOV-1994;
27-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-1994;
13-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1994;
23-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9521922-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1222 MVRRKLVNDYNRF 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΤP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LIRRKFTSEYNEY 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                        g
G
                                                                                                                                                                                                                                                                                                                                characterisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pilot-Matias Muerhoff AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                           virus; HGBV;
                                                                                                                                                                                                                                                                                                                                                                                                   virus protein sequence SEQ ID NO:82
                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
94US-00196030.
94US-00242654.
94US-00283314.
94US-00344185.
94US-00344190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt non-C}, {\tt non-D}, {\tt non-E} Hepatitis virus reagents - useful for therapy of hepatitis GB virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-00196030.
94US-00243654.
94US-00283314.
94US-00344185.
94US-00344190.
95US-00344557.
                                                                                                                                             95US-00488445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-US002118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                diagnosis; therapeutic; immunogenic; infection;
on; hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erker JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB
Pred. No. 7.1e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dawson GJ, Schlauder GG,
r JC, Buijk SL, Mushahwan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.1e+02;
3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mushahwar IK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desai SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a lambda
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describe a method for detecting target hepatitis GB virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of containing HGBV. The method involves reacting (T) with a HGBV polynuclectide probe (I) containing 15 contiguous nuclectides, and which selectively hybridises to the HGBV genome or its full complement, and detecting the complex that contains THN, indicating the presence of target HGBV. The method is used for detecting target HGBV nucleic acid in the test sample suspected of containing HGBV and for characterisation of newly ascertained etiological agent of non-A, non-B, non-C, non-D and non-E hepatitis causing agents collectively tremed as hepatitis GB virus.

AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and protein sequences used in the exemplification of the present invention. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting suspected
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Mushahwar IK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Col 215-224; 369pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-338307/29.
                                                                                                                                                                                                                                                                  Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; cardiac infection; central nervous system; kidney infection; urinary tract infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1422 AA;
                                                                                                                                                                                                                                                                                                                                         Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                     30-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                             AAW77533 standard; protein;
               Black MT, H
Burnham MKR,
                                                      (SMIK )
                                                                                                                            24-SEP-1997;
                                                                                                                                                       13-MAY-1998
                                                                                                                                                                                    EP841394-A2
                                                                                                                                                                                                              Staphylococcus
                                                                                                                                                                                                                                          therapy.
                                                                                                                                                                                                                                                         antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
5; Conserv
                                                       SMITHKLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MVRRKLVNDYNRF 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIRRKFTSEYNEY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     target hepatitis GB virus nucleic acid in a test sample of containing HGBV comprises reacting the test sample the otide probe and detecting the complex that contains target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leary TP,
[K, Simons
                Hodgson JE,
R, Pratt JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                        compound
                                                                                                                                                                                                                                                                                                                                         aureus protein of unknown function.
                                                                                                   96US-0027032P.
                                                                                                                              97EP-00307485
                                                       BEECHAM CORP
BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muerhoff AS,
JN, Desai SM,
                                                                                                                                                                                                                                                           identification; broad spectrum antibiotic
                Knowles DJC,
Rosenberg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     υ
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 3; L
Pred. No. 7.1e+02;
5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pilot-Matias
Erker JC, (
                Reichard RW, Nicho
Ward JM, Lonetto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s TJ, Buijk SL;
Schlauder GG;
                                 Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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RESULT 10
AAG82630
ID AAG82
XX AAG82
XX Staph
TO 03-SE
XX Staph
KW endoc
XX Staph
XX W0200
XX
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a Staphylococcus aureus protein of unknown function, and is encoded by a DNA sequence of the invention. The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response by Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, especially respiratory, cardiac, bonces and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-252940/23.
N-PSDB; AAV53334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 236; 390pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid sequences from Staphylococcus aureus WCHU29 - useful vaccines and for treatment of bacterial infections of e.g. respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S. epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200134809-A2
                                                                                                                                                                                            Nucleic acids encoding polypeptides from Staphylococcus epidermidis. useful for vaccinating against infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                WPI; 2001-316495/33.
N-PSDB; AAH53480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-NOV-2000; 2000WO-US030782.
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                                                                                                                                                                                                                                                                                                                                                                       Kimmerly WJ
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             GLAXO
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                                                                                                                                                                                                                                                                                                                                                                                                                                GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    open reading frame protein sequence SEQ ID NO:2354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0164258P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epidermidis SR1 strain; infection;
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Pred. No. 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; vaccination;
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis, and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S.

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Claim 18; Page 623;

2188pp; English

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RESULT 11
ADC23861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cepidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to CAAH55090 represent specifically claimed S. epidermidis genomic DNA coplynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention consecutions all the polynucleotide sequences given in the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present volume.
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                21-JUN-2001;
30-JUL-2001;
22-JAN-2002;
                                                                                                       Novel nitrilase polypeptide, useful for making (R)- or (S)-ethyl-4-cyano-3-hydroxybutyric acid or (R)- or (S)-mandelic acid or (S)- or (R)-phenyl lactic acid derivative and for producing pharmaceutical composition, and
                                                                                                                                                                                                                                            (DIVE-)
(MADD/)
                                                                                                                                                                                                       Short
                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                  Madden
                                                                                                                                                                                                                                                                                                                                     15-MAY-2002; 2002WO-US015983
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                                                                                                                                                                                                                                                                                                                                                                                       WO2003000840-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            enantiomer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        enzyme;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC23861 standard; protein; 334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 133
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                                                                                                                                                                ADC23860
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MADDEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                          nitrilase;
mer; chiral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence (SeqID 128) exhibiting nitrilase activity.
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Burk M;
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2001US-0309006P
2002US-0351336P
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                                                                                                                                                                                                                                                                                                                                                                                                                                          nitrile;
medicine.
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Pred. No.
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89;
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This invention relates to nitrilases and the nucleic acids that encethese enzymes thereof. Specifically, it refers to polypeptides that exhibit nitrilase activity, i.e. the ability to directly hydrolyse nitriles or cyanohyrdins into their corresponding carboxylic acids:

Claim

40:

SEQ ID

NO 128; 560pp;

English

additive

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AAU07861
ID AAU
XX
The present invention relates to the isolation of novel mammalian and CC human reproductive-specific proteins (AMU07859-AMU07899), and the nucleic acids encoding them. The nucleic acids encoding reproductive-specific CC contesins are useful for diagnosing infertility which is a result of CC reduced sperm count, reduced sperm motility, malformed sperm or CC combinations of these. The sequences of the invention are useful as CC markers for spermatogonial cells, for identifying genes or proteins CC characteristic of male infertility, diagnosing or aiding in the diagnosis CC characteristic of male infertility, diagnosing or aiding in the diagnosis CC of infertility in men, and for contraception in which sperm production or sperm count is reduced or defective sperm is produced. Antibodies to CC these proteins in a sample obtained from a man being assessed for these proteins in a sample obtained from a man being assessed for contracepticity, for identifying the expression of genes in particular cell type or particular developmental stage, for studies of spermatogenesis, and for immunofluorescence of germ cells or in Western blots for
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                                                                                                                                                                                                                                                                                                Claim 22;
                                                                                                                                                                                                                                                                                                                                             Novel reproduction-specific protein, useful for treating discreduced sperm count, enhancing/increasing sperm count and/or
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-570774/64.
N-PSDB; AAS13625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the synthesis of enantiomerically pure aromatic and aliphatic amino acids, as well as hydroxy acids, which are important for the development of chiral medicines. Furthermore, the present invention describes isolated from mesophilic microorganisms, that have improved activity and stability at increased pH and temperature. They are also inexpensive, efficient catalysts, have broad substrate specificity and are capable of chiral differentiation. This polypeptide is a protein sequence that exhibits nitrilase activity of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAR-2000;
12-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200166752-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spermatogenesis; sperm count
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU07861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU07861 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ammonia. Nitrilases have commercial utility as biocatalysts for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                            Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reproductive-specific protein; male infertility; resis; sperm count disorder; anti infertility; re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
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2001US-0261557P.
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                                                                                                                                                                                                                                                                                              6; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for mammalian Spg3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          685 AA
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Pred. No.
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assessing the presence of the protein the antibody binds. The sequences of the invention are also useful for treating disorders of reduced sperm count, and for increasing sperm count and/or sperm activity. The nucleic acids of the invention are useful in gene therapy. AAU07859-AAU07882 represent the mammalian reproduction-specific proteins of the present

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2 IRRKFTSEYNEY 13

206

VONKFTSEQMEY 217

Query Match Best Local S Matches 7

Similarity

58.3%;

Score 38; Pred. No.

4.9e+02; DB 4;

Length 685;

0

Gaps

0

Mismatches

Conservative

Sequence 685

AA;

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AAWO1602
ID AAWO1
XX AAWO1
XX 16-AP
XX 16-AP
XX Muss;
KW Polym
XX Muss;
KW Polym
XX Therm
XX Mo963
XX 12-DE
XX 06-JU
XX 06-JU
XX 06-JU
XX 12-DE
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                                                                     Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                     The Thermotoga maritima thermostable protein, MutS (AAW01602), binds specifically to bulge loops in a heteroduplex nucleic acid. Recombinant MutS can be produced in transformed host cells using an isolated gene sequence (AAT58228). MutS proteins (see also AAW01601) are useful in methods for reducing DNA misincorporation in amplification reactions such as PCR and LCR, in methods for detecting and amplifying nucleic acids contg. specific sequences, and in methods for selecting against a nucleic acid comprising a specific sequence. These methods enable detection of partic. sequences associated with infectious diseases, genetic disorders or cellular disorders such as cancer, e.g. oncogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermostable protein, MutS, and corresponding coding amplification methods to detect particular sequences genetic diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MusS; thermostable protein; bulge loop; heteroduplex; amplification; polymerase chain reaction; PCR; ligase chain reaction; LCR; mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-043147/04.
N-PSDB; AAT58228.
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                                                                                                                                                                                              Sequence 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Fig 4; 93pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA misincorporation; genetic disease; cancer;
                                                                     Similarity 7; Conser
          LIRRKFTSEYNEY
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                                                                                                       55.9%;
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                                                                        Score 38; DB 2;
Pred. No. 5.8e+02;
4; Mismatches 2
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RESULT 15
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DE SBL/I
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                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
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17-DEC-2001
                                                                                                                                                                                                                                                        The protein is encoded by the third reading frame of HIV-2 SBL/ISY, a proviral clone of HIV-2. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 2.
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                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 5; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   Complete human immuno-deficiency type 2 pro-viral clone generate animal model for function studies of HIV genes
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Deduced sequence encoded by bottom reading frame of cDNA clone HIV-2 {\tt SBL/ISY} of HIV related retrovirus strain.
                                 25-MAR-2003
07-NOV-1990
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                                                                                                                                                VRRKLRLIRLLHQTSEYNEW 2005
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                                                                                                                                             CC Synthetically produced proteins and peptides, characterised in that the CC AA sequence is derived from the primary nucleotide sequence of HIV-2 CSBL/ISY or a part thereof, or a degenerate thereof are claimed. HIV-2 CC SBL/ISY represents the complete genome of the virus SBL-6699 (=SBL-6699-685). The proviral DNA was obtd. from a genomic library constructed from CC DNA of HUT-78 cells infected with SBL-669-85 using the lambda-phage vector EMBL-3. SBL-669-85 was isolated from lymphocytes of a West CC African woman. Protection is requested for the entire genome disclosed in CC n80890 and for parts thereof, and corresp. to various genes such as the CC gag gene (corresp. to nucleotides 547 to 2105), the pol gene (nucleotides 547 to 2105), the pol gene (nucleotides 61827-4931) and the env gene (nucleotides 6144 to 8682), the corresp. AC Sequences and parts thereof and various products derived therefrom, or use thereof, such as clones prepd. by recombinant vector method, HIV test CC devices and methods. X corresponds to the translation of a stop codon.
                                                                      Query Match
Best Local S
Matches 9
                                                                                                                                               Sequence 3210 AA;
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N-PSDB; AAN80890.
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(STAT-) STATENS BAKTERIOLOGISKA LAB.
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                                                                  Score 38; DB 1; Length 321
Pred. No. 2.5e+03;
2; Mismatches 1; Indels
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Search completed: October 5, 2004, 07:59:48 Job time: 14.8904 secs

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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2: pir2:*
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ALIGNMENTS

### C;Accession: T33515 R;Jones, K.; Graves, T.; Antoniou, B. submitted to the EMBL Data Library, October 1998 A;Description: The sequence of C. elegans cosmid F5. A;Reference number: Z21362 A;Accession: T33515 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA hypothetical protein F59H5.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 21-Jul-2000 A;Map position: 2 A;Introns: 38/2; 168/3; 182/1; 232/3 C;Superfamily: Caenorhabditis elegans hypothetical C;Genetics: A;Gene: CESP:F59H5.3 A,Cross-references: EMBL:AF098991; PIDN:AAC67450.1; GSPDB:GN00020; CESP:F59H5.3 A,Experimental source: strain Bristol N2; clone F59H5 A;Residues: 1-272 <JON> Query Match Score 47; ВB 2 F59H5 protein F52C6.7; Length 272; POZ domain homology

A;Title: Genomic sequence of a Lyme disease spirochaete, Borrella burgdorferi. A;Reference number: A70100; MUID:98065943; PMID:9403685 A;Accession: E70101 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-199 <kile> A;Cross-references: GB:AE001115; GB:AE000783; NID:92687879; PIDN:AAC66401.1; PID:92687890 A;Experimental source: strain B31</kile>	RESULT 2  RESULT 2  RESULT 2  RYPOTHETICAL protein BB0013 - Lyme disease spirochete hypothetical protein BB0013 - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Accession: E70101  C;Accession: E70101  R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997  Nature 390, 580-586, 1997  A;Authors: Smith, H.O.; Venter, J.C.	Best Local Similarity 77.8%; Pred. No. 1.2;  Best Local Similarity 77.8%; Pred. No. 1.2;  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  Mismatches 1; Mismatches 1; Indels 0; Gaps 0; Gaps 0;  Mismatches 1; Mismatches 1; Mismatches 1; Indels 0; Gaps 0; Mismatches 1; Mis

hypothetical prote

Query Match

64.2%; Score 43;

DB 2;

Length 199;

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A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617199
A;Accession: A85042
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:NC_001268; NID:g7270201; PIDN:CAB77816.1; GSPDB:GN00140
C;Genetics:
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S33758
                flavin-containing monooxygenase 1 - rat
C;Species: Rattus norvegicus (Norway rai
C;Date: 06.Jan.1995 #sequence_revision o
C;Accession: S33758
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C; Superfamily:
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A85042
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Nature 402, 769-777,
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C;Accession: D84129

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Mucleic Acids Res. 28, 4317-4331, 2000

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: D84129
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Gene: AT4g03310
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     Yokoi,
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85.7%;
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Query Match
Best Local Similarity
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...._unange 03-Aug-2001
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G95057
                                                  A; Molecule type: DNA
A; Residues: 1-1659 < KUR>
A; Cross-references: GB: AB005672; PIDN: AAK74656.1;
A; Experimental source: strain TIGR4
A;Gene:
                                                                                                                                                                                                                  A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Title: Complete Genome Sequence of a virilent isolate of Streptococcus A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision
C;Accession: G95057
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Yardhes 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
H97926
                                                                                                                                                                                    A; Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-1659 <KUR>
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A; Residues: 1-532 < ITO>
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A; Status: preliminary
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A;Title: Rat liver flavin-containing monooxygenase (FMO): cDNA cloning
A;Reference number: 833758; MUID:93277949; PMID:8504165
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5; Conser
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llarity 50.0%;
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Pred. No. 42;
5; Mismatches
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Pred. No. 1
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1.5e+02;
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                                                                                   PID:g14971970;
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59.7%; 75.0%;

Score Pred.

40;

DB 2; 1.5e+02

Length 1659

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probable dihydrolipoamide S-succinyltransferase C;Species: Streptomyces coelicolor C;Date: 20-Apr-2000 "-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucose inhibited division protein B (gidB) RP057 - Rickettsia prowazekii C;Species: Rickettsia prowazekii
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                                                                                                                                                                                                                                                                                                                C;Accession: T35297
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parki submitted to the EMBL Data Library, July 1999
A;Reference number: Z21574
A;Accession: T35297
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Nature 396, 133-140, 1998
                                                                                                            A;Status: translated from GB/EMBI/DDBJ
A;Molecule type: DNA
A;Residues: 1-590 <SEE>
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A;Experimental source: strain Madrid E
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A; Residues: 1-191 < AND>
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A;Cross-references: EMBL:AL096872; PIDN:CAB51265.1; GSPDB:GN00070; SCOEDB:SC5F7
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6; Conser
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                                                        Similarity 7; Conserv
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21;
                                                                                     DB 1; Length 590;
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RESULT 10 F83843

hypothetical

protein

BH1550

[imported]

Bacillus halodurans

(strain

C-125)

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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwir B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwir n, J.; Ennolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter Crescentus.
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A;Cross-references: GB:Ap001512; GB:BA000004; NID:g10174030; PIDN:BAB05269.1; GSPDB:GN001
A:Experimental source: strain C-125
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                                                                                                                                                                                                 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4833-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325, A;Accession: B97116
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1191 < KUR>
A;Cross-references: GB:AE001437; PIDN:AAK79717.1;
A;Experimental source: Clostridium acetobutylicum
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                             chromosome segregation SMC protein, ATPase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: B97116
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A; Residues: 1-851 <STO>
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A;Accession: D87252
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DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No.
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Pred. No.
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                                            PID:g15024720; GSPDB:GN00168
ATCC824
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L.; Venter,
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N-acetylglutamate gamma-semialdehyde dehydrogenases homolog argC [imported] - ()Species: Listeria innocua ()Species: Listeria innocua ()Species: Disteria innocua ()Specie
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R;Ogata, H; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001

A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893

A;Accession: E97710
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submitted to the EMBL Data Library, March 1995
s;Reference number: 562757
A;Accession: $62751
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E97710
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A;Molecule type: DNA
A;Residues: 1-172 <VIE>
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Matches
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;Molecule type: DNA
;Residues: 1-192 <KUR>
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Pred. No. 31;
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Pred. No.
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Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
27;
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      A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 172
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      Baquero,
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                                                                                                                                    Listeria
          Bloecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7)
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.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1636
Search completed: October Job time : 5.94444 secs
                                                                                        밁
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                                                                                                                                                                                                                                                          A;Gene: argC C;Superfamily: N-acetyl-gamma-glutamyl-phosphate reductase
                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA,
A;Residues: 1-343 <GLA,
A;Cross-references: GB:AL592022; PIDN:CAC96864.1; PID:g16414120; GSPDB:GN00178
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                               Matches
                                                                                                                                                                                                  Query Match
Best Local |
                                                                                                                                                                                                  Local Similarity
                                                                                    216 LTKWDKSI 223
                                                                                                                                2 ITRWDKSV 9
                                                                                                                                                                               Conservative
                                                                                                                                                                                               56.7%;
                     ຸທ
                       2004,
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Pred. No. 58;
                       08:17:02
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Gapop 10.0 ,
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67
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      SwissProt_42:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyright
      2004, 07:29:35 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version (c) 1993 - 2004
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YO13 BORBU
FMO1 RAT
GIDB RICPT
GIDB RICPT
GIDB RICRN
YH62 FUSUN
YH63 FUSUN
YH64 FUSUN
YH64 FUSUN
YH65 FUSUN
YH66 YEAST
SMF0 YEAST
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p36365 rattus norv
g9ze89 rickettsia
p10676 drosophila
p20491 rickettsia
g9zbb7 listeria in
p22490 staphylococ
g00099 ictalurid h
g9ket5 bacillus ha
p47281 mycoplasma
g07935 rhodobacter
p38140 saccharomyc
p78562 homo sapien
      p10041 drosophila
Q0980 schizosacch
P16355 trypanosoma
p43340 escherichia
O05826 wycobacteri
P40505 saccharomyc
Q29409 staphylococ
Q81w34 staphylococ
Q81w34 staphylococ
Q91b6 campylobact
P40024 saccharomyc
P32802 saccharomyc
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P32802 saccharomyc
P32802 buran immun
P19551 human immun
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P19551 human immun
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P78562 homo sapien
P70669 mus musculu
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Y013 May
Polity
AC 0511
AC 0511
AC 0511
AC 0511
DT 15---

           RESULT 2
FMO1_RAT
ID FMO1_RAT
AC P36365;
DT 01-JUN-1994
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28 STRAINATIC 35210 / B31;

29 STRAINATIC 35210 / B31;

20 STRAINATIC 35210 / B31;

21 STRAINATIC 35210 / B31;

22 STRAINATIC 35210 / B31;

23 STRAINATIC 35210 / B31;

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26 STRAINATIC 35210 / B31;

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20 STRAINA
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Best Local S
Matches 7
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15-DEC-1998 (Rel. 37, Last sequence up.
16-OCT-2001 (Rel. 40, Last annotation Hypothetical protein BB0013.
BB0013.
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051046;
15-DEC-1998
15-DEC-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                     EMBL; AB001115; AAC66401.1; -.
PIR; E70101; E70101.
TIGR; BB0013; -.
Hypothetical protein; Complete
SEQUENCE 199 AA; 23301 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BORBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                    101 IITKWCKSINIY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LITRWDKSVNDY 12
                                                                                                                                                                                                                                                    Similarity 58...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   il protein; Complete proteome.
199 AA; 23301 MW; C645D1603EDEF610 CRC64;
                (Rel. 29, Created)
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                                                                                                                                                                                                                                                                           64.2%;
58.3%;
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ENV HV1H3
ENV HV1H9
ENV HV1PV
ENV HV1PV
ENV HV1PP
VA5 DOLAR
ENGB ZYMMO
NPD HELPY
NPD HELPY
NPD HELPY
VSPZ VIPLE
YQCC BACSU
                                                                                                                                                                                                                                                          Score 43; DB Pred. No. 2.4; 3; Mismatches
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P04624
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Result No.

Searched:

Maximum

DB

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RESULT 3
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Best Local
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   30-MAY-2000 (Rel. 30-MAY-2000 (Rel. 28-FEB-2003 (Rel. Methyltransferase protein B).
                                                                                 GIDB_RI
Q9ZE89;
                                                                                                                                                                                                                                                                                                   NP BIND
                                                                                                                                                                                                                                                                                                                 PRINTS; PR00370; FMOXYGENASE.

PRINTS; PR00370; FMOXYGENASE; NADP; Flavoprotein; FAD; Microsome;

Oxidoreductase; Monooxygenase; NADP; Flavoprotein; FAD; Microsome;

Transmembrane; Multigene family.

FAD (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endoplasmic reticulum and Golgi apparatus in mammalian cells."; Cell 89:149-158(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDLINE=97248495; PubMed=9094723;
Hay J.C., Chao D.S., Kuo C.S., Scheller R.H.;
"Protein interactions regulating vesicle transport between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Sprague-Dawley; TISSUE-Liver; MEDLINE-93277949; PubMed-8504165; MEDLINE-93277949; PubMed-8504165; Kamataki Itoh K., Kimura T., Yokoi T., Itoh S., Kamataki "Rat liver flavin-containing monooxygenase (FMO) expression in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000960; Flav cont mnoxgn Pfam; PF00743; FMO-like; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M84719; AAA41165.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 34-42 AND 52-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FMO1 OR FMO-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dimethylaniline monooxygenase [N-oxide forming] 1
(Hepatic flavin-containing monooxygenase 1) (FMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Microsomal.
TISSUE SPECIFICITY: Liver.
SIMILARITY: Belongs to the FMO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: This protein is involved in the oxidative metabolis: a variety of xenobiotics such as drugs and pesticides. Form I catalyzes the N-oxygenation of secondary and tertiary amines. CATALYTIC ACTIVITY: N,N-dimethylaniline + NADPH + O(2) = N,N-dimethylaniline N-oxide + NADP(+) + H(2)O.
                                                                                                  RICPR
                                                                                                                                                                                                                                                                                                                                                                                                                          833758; 833758.
                                                                                                                                                                          488 ILTOWDRTVN 497
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                                                                                                                                                                                                                                     Similarity
5; Conserv
                                                                                                                                                                                                       LITRWDKSVN
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                                                                                                                                                                                                                                                                                                 191
532 AA;
                                                                                                                                                                                                                                     59.7%;
ilarity 50.0%;
Conservative
                (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 41, Last annotation updat
ferase gidB (EC 2.1.-.-) (Glucos
                                                                                                STANDARD;
                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                               59781 MW;
                                                                                                                                                                                                                                     Score 40; DB
Pred. No. 22;
5; Mismatches
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                                                                                                PRT;
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Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                               A8193C1E9733DF92 CRC64;
                   on update)
(Glucose
                                                                                                191
                                                                                                                                                                                                                                                                  DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ataki T.;
(FMO): cDNA cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muridae;
                   inhibited division
                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                Length 532;
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Dimethylaniline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metabolism
                                                                                                                                                                                                                                     0;
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RESULT 4
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Best Local :
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HAMAD; MF 00074; -; 1.
InterPro; IPR003682; GidB.
Pfam; PF02527; GidB; 1.
ProDom; PD004441; GidB; 1.
TIGRFAMS; TIGR00138; gidB; 1.
TIGRFAMS; TIGR00138; GidB; 1.
SEQUENCE 191 AA; 21830 MW; 7A:
                                          -i- 1
                                                                                                                                                                                                                                             NINC DROME STANDARD; PRT; 1501 AA. P10676; P10677; 01-OCT-1989 (Rel. 12, Created) 01-OCT-1989 (Rel. 12, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Neither inactivation nor afterpotential protein
                                                                                "The Drosophila ninaC proteins with domains
                                                                                                                                                                           Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexa
                                       heavy chain head.";
Cell 52:757-772(1988).
-!- FUNCTION: Required for
                                                                                                            Montell C., Rubin
                                                                                                                        SEQUENCE FROM N.A., MEDLINE=88151067; P
                                                                                                                                                                 NCBI_TaxID=7227;
                                                                                                                                                                                                                                      NINAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondria.";
Nature 396:133.140(1998).
-i- FUNCTION: Probable S-adenosyl-L-methionine dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99039499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia prowazekii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ235270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
-!- SIMILARITY: Belongs to the gidB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Madrid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
 proteins combines putative myosin activities.
CATALYTIC ACTIVITY: ATP + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methyltransferase specific
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                                                                                                                                                                                                                                                                                                                                                                                          LIKKWNKSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAA14528.1;
                                                                                                              ດ.×.;
                                                                                                                         FubMed=2449973;
                                                                                                                                                                                                                                                                                                                                                                                          26
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                                                                                locus encodes homologous to
ATP + a protein
                                         photoreceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB
Pred. No. 11;
                          serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
7A15026A16C2D6C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for a sterol
                                                                                                                                                                                                          Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                      ALTERNATIVE
                                                                                two photoreceptor cell specific protein kinases and the myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family
  П
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                                          cell function.
 ADP
                                                                                                                                                                                                          Insecta;
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+
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                                                                                                                                                                                           Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 191;
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phosphoprotein
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                                                                                                                                                                                                        Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     origin
                           kinase
                                          The ninac
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SUBCELLULAR LOCATION: Cytoskeleton ALTERNATIVE PRODUCTS: Event-Alternative splicing; Named Name=Long;

splicing; Named isoforms=2;

use by non-profit institutions as long as modified and this statement is not removed. But entities requires a license agreement (See htt or send an email to license@isb-sib.ch).

noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/ There are no restrictions ong as its content is in

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way its

the European Bioinformatics Institute.

SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -

SUPERFAMILY.
SIMILARITY: Contains 1 IQ domain.

SIMILARITY: IN THE N-TERMINAL SECTION; FAMILY OF PROTEIN KINASES.
SIMILARITY: IN THE C-TERMINAL SECTION;

BELONGS TO THE MYOSIN

VSP\_004941; BELONGS TO

THE

SER/THR

IsoId=P10676-2; Sequence=VSP\_004940, MILARITY: IN THE N-TERMINAL SECTION; MILY OF PROTEIN KINASES.

This

between

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Name=Short;

IsoId=P10676-1; Sequence=Displayed;

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DR Pfam; PF00612; IQ; 2.

DR Pfam; PF00612; myosin head; 1.

DR Pfam; PF00063; myosin head; 1.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00193; MYOSINHEAVY.

DR PRODOM; PD000001; Prot_kinase; 1.

DR PRODOM; PD000001; Prot_kinase; 1.

DR SMART; SM00024; MYSG; 1.

DR SMART; SM00220; S_TKC; 1.

DR SMART; SM00220; S_TKC; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_ATP; FALSE_NEG.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00101; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00101; PROTEIN_KINASE_DMM; 1.

DR PROSITE; PS00101; PROTEIN_KINASE_DMM; 1.

CYCOSKeleton; Actin-binding; ATP-binding; Myosin; Transferase; Vision; Crima/threonine-procain kinase; Alternative splicing.
EMBL; J03131; AAA28719.1; -.
EMBL; J03131; AAA2879.1; -.
EMBL; M20230; AAA28721.1; -.
EMBL; M20231; AAA28720.1; -.
EMBL; M20231; AAA28720.1; -.
EMBL; M20813; A29813.
PIR; B29813; B29813.
HSSP; P08799; IMND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0002938; ninaC.

G0; G0:0005737; C:cytoplasm; IDA.

G0; G0:0042385; C:myosin III, NAS.

G0; G0:0016028; C:rhabdomere; IDA.

G0; G0:0016028; C:rhabdomere; IDA.

G0; G0:0006516; F:calmodulin binding; IMP.

G0; G0:0004674; F:pyrotein serine/threonine kinase activity; IDA.

G0; G0:0004674; P:pyrotein serine/threonine mediated signaling; IMP.

G0; G0:0016062; P:adaptation of rhodopsin mediated signaling; IMP.

G0; G0:0007603; P:phototransduction, visible light; IMP.

G0; G0:0008104; P:protein localization; IMP.
                                                                                          DOMAIN
NP BIND
BINDING
ACT SITE
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
InterPro; IPR000719; Prot kinase.
InterPro; IPR0002290; Ser_Thr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS.
                                                                            ACT SITE
                                                                                                                                            DOMAIN
 VARSPLIC
                                                              VARSPLIC
 1136
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1036
1066
22
 1501
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1035
1065
1501
                                                               145
934
1135
                                                                                          ATP
ATP
BY (
                                                 BY SIMILARITY
ACTIN-BINDING (BY SIMILARITY).
AFRGFRDFVELPFLYNEXSGCUNENTADFIRDFAKKWREKS
IFQVLLHYRAARF -> GKKTQVDRLREYDEBHIDISETPS
                                                                                             IQ.

NON ALPHA-HELICAL, C-TERMINAL ATP (BY SIMILARITY).

ATP (BY SIMILARITY).
Missing (In isoform Short)
              isoform SI
/FTId=VSP
                                       EAEEMFLEARMDEALAAVRIAKIEQASAEE
                          Short
               004940.
                                                                                                                                 DOMAIN
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RESULT 6
YH62 FUSNN
ID YH62 FI
AC Q8RI57

YH62\_FUSNN Q8RI57;

STANDARD;

PRT;

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RESULT 5

GIDB GIDB GO 92077

AC 092077

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Best Local S
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Best Local S
Matches 5
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28-FEB-2003 (Rel. 41, La
28-FEB-2003 (Rel. 41, La
Methyltransferase gidB (
protein m)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
SEQUENCE
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Q92JT2;
28-FEB-2003
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiff
Samson D., Roux V., Cossart P., We
Raoult D.;
                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                          TIGRFAMS; TIC
Transferase;
                                                                                                                                                                                                                                                    HAMAP; MF 00074; -; 1.
InterPro; IPR003682; GidB.
Pfam; PF02527; GidB; 1.
ProDom; PD004441; GidB; 1.
                                                                                                                                                                                                                                                                                                                                                  EMBL; AE008575; AAL02623.1; PIR; E97710; E97710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mechanisms of evolution in Science 293:2093-2098(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIDB OR RC0085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Probable S-adenosyl-L-methionine dependent methyltransferase specific for a sterol and/or lipid substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SIMILARITY: Belongs to the gidB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249
  18
                                                                                      Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 5; Conserv
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LVKKWNKSIN
                                            LITRWDKSVN 10
                                                                                                                                                                                                     TIGR00138; gidB; 1.
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1089
1501
                                                                                                                                                                                      192 AA;
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Cossart P., Weissenbach
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  27
                                                                                                            56.7%;
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Last annotation update)
B (EC 2.1.-.-) (Glucose
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K -> Q (IN REF. 1; AAA28720/AAA28721).
P -> R (IN REF. 1; AAA28771).
MW; D167EABC82A3933A CRC64;
                                                                                           Score 38; DB Pred. No. 17; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fournier P.-E.,
ch J., Claverie
                                                                                                                                       1; Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibited
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RESULT
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Best Local .
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SERAIN-CLIP 11262 / Serovar 6a;

MEDLINE=21537279; PubMed=11679669;

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Covve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Gautier L., Goebel W., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Jones L., M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
                                                                                                                                                                                                                                                                                                                         Q92BB7;
28-FEB-2003
28-FEB-2003
10-OCT-2003
                                                                                                                                                                                                                                                                             acetyl
                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
N-acetyl-gamma-glutamyl-phosphate reductase ()
acetyl-glutamate semialdehyde dehydrogenase)
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                                                                                                                                                                                                                                          Listeria innocua.
Bacteria; Firmicutes;
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SEQUENCE FROM N.A.
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10-OCT-2003 (Rel. 42,
10-OCT-2003 (Rel. 42,
Hypothetical UPF0246)
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Kapatral V., Anderson I., Ivanova N.,
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Fusobacteria;
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protein FN1762.
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Pred. No. 22;
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8A0D699131C5CDBF CRC64;
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(CSTRAIN-MU50 / ATCC 700699, and N315;

RX MEDLINE=21311952; PubMed=11418146;

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshimo C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
ALE REPARANTE DE LA COMPANIA DEL COMPANIA DE
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Matches
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HAMAP; MF 00150; -; I.

InterPro; IPR000706; AGPR act_site.

InterPro; IPR000706; Semialdh_dh.

Pfam; PF01118; Semialdhyde_dh; 1.

Pfam; PF02774; Semialdhyde_dhC; 1.

ProDom; PF02774; Semialdhyde_dhC; 1.

PROSITE; PS01224; AGPR act_site; 1.

PROSITE; PS01224; ARGC; 1.
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NCBI_TaxID=158878, 158
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-i-SUBCELIJULAR LOCATION: Cytoplasmic (Probable).
-i-SIMILARITY: Belongs to the NAGSA dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Comparative genomics of Listeria species.";
Science 294:849-852(2001).
-i- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL596169; CAC96864.1; PIR; AH1636; AH1636.
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Vazquez-Boland J.-A., Voss H., Wehland J., Cossart
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid 17:83-85(1987).

-!- FUNCTION: THE INTERACTION OF THE RSA SITE AND THE PRE PROTEIN ME
-!- FUNCTION: THE PROTEIN ME
-!- FUNCTION IN PLASMID MAINTENANCE, BUT MAY ALSO
CONTRIBUTES TO THE DISTRIBUTION OF SMALL ANTIBIOTIC RESISTANCE
PLASMIDS AMONG GRAM-POSITIVE BACTERIA.

-!- MISCELLANEOUS? PRE PROTEINS CONTAIN CONSERVED POSITIVELY CHARGEE
-!- MISCELLANEOUS? PRE PROTEINS CONTAIN CONSERVED POSITIVELY CHARGEE
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                                                                                                                                                                                                                                                                                                                                         Pfam; PF01076; Mob Pre; 1.

Plasmid; DNA-binding; Complete proteome.
BINDING 44 44 DNA (POTENTIAL).
BINDING 114 114 DNA (DOTENTIAL).
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EMBL; AP003139; BAB41247.1; -.
EMBL; M37273; AAA98212.1; -.
EMBL; M19465; AAA88859.1; -.
PIR; T44132; T44132.
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MCKenzie T., Hoshino T., Tanaka T., Sueoka N.;
"Correction. A revision of the nucleotide sequence and functional map of pUB110.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=86206447; PubMed=3010356; MCKenzie T., Hoshino T., Tanaka T., "The nucleotide sequence of pUBLIO: to replication and its regulation.";
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                                           Hypothetical 56.
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Ictalurid herpesvirus 1 (Channel catf:
Viruses; dsDNA viruses, no RNA stage;
Ictalurid Herpes-like viruses.
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THE RAS SITE.
SIMILARITY: TO OTHER PRE PROTEINS (FROM PLASMIDS PUBLIO,
PEL94, PT181, PTB913), IN THEIR N-TERMINAL ONLY.
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                                                                                                                                                                                                                                                                  Similarity 6; Conserv
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1 gene
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                                                          protein.
                                                                         Last sequence up
                               (Channel catfish virus)
                                                                                                                                                                                                                                                                                                                            MW;
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Pred. No. 38;
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                                                                                                               "Complete genome sequence of the alkaliphilic bacterium Bacillus RT "Complete genome sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331 (2000).

"Interior Acids Res. 28:4317-4331 (2000).

"Complete Res. 28:4317-431 (2000).

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SEQUENCE FROM N.A.
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STRAIN=C-125 / JCM 9153;
STRAIN=C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132;
MEDLINE-20512582; PubMed=11058132; PubMed=11058132; PubMed=11058132; PubMed=11058132; PubMed=11058132; PubMed=11058132; PubMed=11058132; PubMed=11058125; PubMed=11058125; PubMed=11058125; PubMed=11058125; PubMed=11058125; PubMed=11058125;
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10-OCT-2003 (Rel. 42, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
3-oxoacyl-[acyl-carrier-protein] synthase III 1)
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MEDLINE=92087490; PubMed=1727613;
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                                              SIMILARITY:
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Ogasawara N.,
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RESULT 11
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R HSSP; P24249; HNK.

R HAMSP; MF 01815; -; 1.

R InterPro; IPR004655; FabH.

R InterPro; IPR004677; fabH; 1.

R TICREAMS; TICR00747; fabH; 1.

H ACT SITE 115 115 BY SIMILARITY.

FT ACT SITE 252 BY SIMILARITY.

FT ACT SITE 282 282 BY SIMILARITY.

FT SITE 253 257 ACP-BINDING (BY SIMILARITY)

TOTOTIFNCE 332 AA; 36264 MW; D0D70C10F8B69C6D CRC64;
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RMEDINE-96026346; PubMed=7569993;

RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Prischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Rritchmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Rritchmann J.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Romb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270.397-403(1995)

C -i- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +

Gibnosphate + L-histidyl-tRNA(His).

C -i- SUBLINIT: Homodimer (By similarity).

C -i- SUBCELLULAR LOCATION: Cytoplasmic

-i- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
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Best Local S
Matches 7
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01-FEB-1996
01-FEB-1996
28-FEB-2003
              EMBL; U39683; AAC71251.1;
PIR; H64203; H64203.
HSSP; O32422; 1QE0.
                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no rest the European Bioinformatics Institute. There are no restrained by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma genitalium.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Pred. No. 44;
3; Mismatches
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D0D70C10F8B69C6D CRC64;
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44;
                                                                                            http://www.isb-sib.ch/announce/
                                                                                                               Usage
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"Characterization of anf genes specific for the alternative
nitrogenase and identification of nif genes required for both
nitrogenases in Rhodobaccer capsulatus.";

LMOL MICROBIOL 8:673-684(1993)

LMOL MICROBIOL 8:873-684(1993)

LMOL MICROBIOL BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
CCATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
IRON PROTEIN (COMPONENT 2) AND A COMPONENT WHICH IS EITHER A
MICROBIOL HONOR FORTEIN A VANABULW-IRON, OR AN IRON-IRON PROTEIN.

CC MOLYBDENUM-IRON PROTEIN A VANABULW-IRON, OR AN IRON-IRON PROTEIN.

C-!- CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATP

C--- CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATP

C--- SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO DELTA CHAINS.

C-!- SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO DELTA CHAINS.
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Best Local
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HSDF; P11347; IMIO.
InterPro; IPR000318; Nitrognse_compl.
InterPro; IPR000510; Oxred_nitrognsel.
Pfam; PF00148; oxidored_nitro; 1.
PROSITE; PS00699; NITROGENASE 1 1; 1.
PROSITE; PS00090; NITROGENASE 1 2; 1.
Oxidoreductase; Nitrogen fixation; Iron-sulfur.
Oxidoreductase; Nitrogen fixation; Iron-sulfur.
Oxidoreductase; Nitrogen fixation; Iron-sulfur.
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Q07935;
Q1-FEB-1995
Q1-FEB-1995
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the It the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                              EMBL; X70033; CAA49627.1; PIR; S34947; S34947.
                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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HAMAP; MF 00127; -; 1.

InterPro; IPR004516; Hiss.

InterPro; IPR004516; trNA-synt_2b.

InterPro; IPR002314; trNA-synt_2b.

InterPro; IPR006195; trNA ligase_II.

Pfam; PF00887; trNA-synt_2b; 1.

PIGRRAMS; TIGR00442; his5; 1.

PROSITE; P850862; AA TRNA LIGASE_II; 1.

AMIDGACY1-TRNA SYNThetase; Protein biosynthesis; Ligase;

Complete proteome.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhod
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ANFK.
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NCBI_TaxID=1061;
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159 (Rel. 31, Last sequence
19 (Rel. 38, Last annotatic
19 in iron protein beta c
1) (Dinitrogenase 3 beta s
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Last annotation updat
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Pred. No.
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chain (EC 1.18.6.1)
subunit).
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                        CRC64;
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TRESULT 13
TYB9 YEAST
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TO 1.-OCT-1994 (Rel. 30, Created)
DT 01.-OCT-1994 (Rel. 30, Last sequence update)
DT 01.-OCT-1994 (Rel. 30, Last sequence update)
DT 01.-OCT-2001 (Rel. 40, Last annotation regulatory pro
DE putative 60.3 kDa transcriptional regulatory pro
DE putative 60.3 kDa transcriptional regulatory pro
DE putative 60.3 kDa transcription regulatory
DE putative 60.3 kDa transcription regulatory
DE putative 60.3 kDa transcription regulation;
DR PROSITE; PSO01 entry 10. Last annotation pro
CC -1. SUMILARITY: Contains 1 PAS (PER-ARMT-SMM)
CC -1. SIMILARITY: Contains 1 PAS (PER-ARM
                                RESULT 14
PEX_HUMAN
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Best Local S
Matches 6
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InterPro; IPR001014; PAS_domain.

Pfam; pF00172; Zn_clus; 1.

SMART; SM0006; GAL4; 1.

SMART; SM00091; PAS; 1.

R PROSITE; PS00463; ZN2_CY6_FUNGAL_1; 1.

R PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.

R PROSITE; PS50148; ZN2_CY6_FUNGAL_2; 1.

R PROSITE; PS50112; PAS; 1.
                                                                                                                                                                             Query Match
Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288c; Pohl F.M., Pohl T.M.; Aljinovic G., Pohl F.M., Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
P78562; 000678;
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                                                                                                                                           WDKSVNDY
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                   STANDARD;
 Q13646;
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 Q93032; Q99827;
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                    749 AA
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                                                                                                                                                                                                                 Length 529;
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       SEQUENCE
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Karaplis A.C.
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                                                                                                                SEQUENCE OF
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MEDLINE=97343325; PubMed=919930; Francis F., Strom T.M., Hennig S., Boe Brandau O., Mohnike K.L., Cagnoli M., Borzym K., Pohl T., Oudet C.L., Econs Meitinger T., Lehrach H.; "Genomic organization of the human PEX dominant hypophosphatemic rickets."; Genome Res. 7:573-585(1997).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phosphate regulating neutral endopeptidase (EC 3.4.24.-)
(Metalloendopeptidase homolog PEX) (X-linked hypophosphatemia
''''' /vitamin D-resistant hypophosphatemic rickets protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=97232252; PubMed=9077527;

MEDLINE=97232252; PubMed=9077527;

Beck L., Soumounou Y., Martel J., Krishnamurthy G., Gauth Goodyer C.G., Tenenhouse H.S.;

Goodyer C.G., Tenenhouse H.S.;

"Pex/PEX tissue distribution and evidence for a deletion region of the Pex gene in X-linked hypophosphatemic mice. Clin. Invest. 99:1200-1209(1997).
                                                                                                                                                                                                                                         Prancis F., Hennig S., Korn B., Reinhardt R., de Jong P., P
Lehrach H., Rowe P.S.N., Goulding J.N., Summerfield T., Mou
Read A.P., Popowska E., Pronicka E., Davies K.E., Orioddan
Econs M.J., Nesbitt T., Drezner M.K., Oudet C.L., Pannetier
Hanauer A., Strom T.M., Meindl A., Lorenz B., Cagnoli M.,
Mohnike K.L., Murken J., Meitinger T.,
Watth homologies to endopeptidases is mutated
patients with X-linked hypophosphatemic rickets. The HYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guo R., Quarles L.D.; "Cloning and sequencing of human PEX from a bone cDNA library: evidence for its developmental stage-specific regulation in
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MEDLINE=97343325;
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Grieff M., Mumm S., Waeltz P., Mazzarella R.,
Thakker R.V., Schlessinger D.;
"Expression and cloning of the human X-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 4-641 FROM N.A. MEDLINE=96024647; PubMed=7550339;
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Lipman M.L., Panda
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MEDLINE=97343443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=97260404; Pu
Holm I.A., Huang X.,
                                                  VARIANTS HYP TYR-85; CYS-166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bone Miner.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (JAN-1997) to
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                                                                                                                                               1-116 FROM N.A.
                                                                                                                                                                                                    11:130-136(1995).
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     PubMed=9106524;
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Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12:1009-1017(1997)
                                                                                                  to the EMBL/GenBank/DDBJ databases
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                                                     SER-252;
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li M., Steffens C., Klages
Econs M.J., Rowe P.S.N., 1
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                                                       ILE-253
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                                                     AND VAL-579
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VARIANTS HYP ARG-160 AND ASN-444 INS. MEDLINE=20461419; PubMed=11004247;
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"Distribution of mutations in the PEX gene in families with X-linked hypophosphataemic rickets (HYP).",
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                                                                                                                                                                                                                                                                                                                                                                                                                                      patients with
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MEDLINE=98439610; PubMed=9768674;
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15:383-384(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    responsible for adult-onset vitamin emic osteomalacia: evidence that the disorder from x-linked hypophosphatemic rickets."; ab. 83:3459-3462(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .N., Speer M.C.,
Ninomiya J.T., 1
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Smith C., Tau
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Lee B.E.,
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RESULT 15
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        p70669, p97439;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Metalloendopeptidase homolog PEX (EC 3.4.24.-) (Phosphate regulating neutral endopeptidase) (X-linked Nypophosphatemia protein) (HYP)
(Vitamin D-resistant hypophosphatemic rickets protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 include skeletal deformities, growth failure, craniosynostosis, paravertebral calcifications, pseudofractures in lower excremities, and muscular hypotonia with onset in early childhe X-linked hypophosphatemic rickets is the most common form of hypophosphatemia with an incidence of 1 in 20000.

SIMILARITY: Belongs to peptidase family M13.

DATABASE: NAME=PHEXdb; www="http://data.mch.mcgill.ca/phexdb/".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U82970; AAC22487

U87284; AAB47562

Y0811; CAA63326

1; Y08112; CAA63326

1; Y08113; CAA63326

1; Y08114; CAA63326
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U75645; AAB47749.1;
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  PEX OR HYP
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Pred. No. 1e+02;
2; Mismatches
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EMBL; U49908; AAC36502.1; -.
EMBL; U73910; AAC25962.1; -.
EMBL; U73912; AAC25965.1; -.
EMBL; U73913; AAC25965.1; -.
EMBL; U73914; AAC25966.1; -.
EMBL; U73914; AAC25967.1; -.
EMBL; U73915; AAC25967.1; -.
EMBL; U73915; AAC25967.1; -.
EMBL; U75646; AAB47750.1; -.
EMBL; U75646; AAB47750.1; -.
HSSP; P08473; IDMT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   renal phosphate reabsorption.
-:- COPACTOR: Binds 1 zinc ion per subunit (By s
-:- SUBCELIULAR LOCATION: Type II membrane prote
-:- TISSUE SPECIFICITY: Bone.
-:- SIMILARITY: Belongs to peptidase family Mi3.
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STRAIN-C57BL/6J;
MEDLINE-97232252; PubMed-9077527;
Beck L., Soumounou Y., Martel J., Krishnamurthy
Goodyer C.G., Tenenhouse H.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINGE FROM N.A.
MEDLINE=97217775; PubMed=9063736;
Strom T.M., Francis F., Lorenz B., Boeddrich A., Econs M.J.,
Lehrach H., Meitinger T.;
Lehrach H., Meitinger T.;
"pex gene deletions in Gy and Hyp mice provide mouse models for
X-linked hypophosphatemia.";
X-linked hypophosphatemia.";
Hum. Mol. Genet. 6:165-171(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=96411643; PubMed=8812412;
Du L., Desbarats M., Viel J., Glorieux F.H., Cawthorn C., Ecarot "CDNA cloning of the murine Pex gene implicated in X-linked hypophosphatemia and evidence for expression in bone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
DOMAIN
METAL
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CARBOHYD
                                                                                                                                                                    InterPro; IPR00602; Pept M 2n BS.
InterPro; IPR000718; Peptidase M13.
InterPro; IPR000753; Peptidase M13.
InterPro; IPR000753; Peptidase M13.
Pfam; PF01431; Peptidase M13; I.
Pfam; PF05649; Peptidase M13; I.
PRINTS; PR00786; NEPRITYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Biomineralization; Hydrolase; Metalloprotease; Zinc; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "PEX/PEX tissue distribution and evidence for a deletion in the 3' region of the Pex gene in X-linked hypophosphatemic mice.";
J. Clin. Invest. 99:1200-1209(1997).
-i- FUNCTION: Probably involved in bone and dentin mineralization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 36:22-28(1996).
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                                                                                                                                             Transmembrane;
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MGD; MGI:107489; Phex.
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Rodentia;
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                 EXTRACELLULAR (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
PROTON DONOR (POTENTIAL).
                                                                                                                CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
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2; Mismatches
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Copyright (c) 1993 - 2004 Compugen Ltd.
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# SUMMARIES

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## ALIGNMENTS

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SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-Bristol N2; Jones K., Graves T., Antoniou B.; "The sequence of C. elegans cosmid F59H5."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases. [3] SEQUENCE FROM N.A. STRAIN-Bristol N2;	SEQUENCE FROM N.A. STRAIN-Bristol NZ; WEDLINE-94150718; PubMed=7906398; WEDLINE-94150718; PubMed=7906398; Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Wilson R., Ainscough R., Connell M., Copsey T., Cooper J., Coulson A., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Jones M., Kershaw J., Xirsten J., Laister N., Jatreille P., Jones M., Kershaw J., Xirsten J., Haillier I., Jier M., Johnston L., Johnson J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P., "2.2 M. of contiguous nucleotide sequence from chromosome III of C. elegans.", Nature 368:32-38(1994).	T 1  OPTZI3 PRELIMINARY; PRT; 272 AA.  OPTZI3;  O1-MAY-2000 (TrEMBLrel. 13, Created)  O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)  O1-CCT-2003 (TrEMBLrel. 25, Last annotation update)  F59H5.3 protein.  F59H5.3.  Caenorhabditis elegans.  Caenorhabditis elegans.  Caenorhabditidae; Peloderinae; Chromadorea; Rhabditidae; Rhabditoidea;  NCBI_TaxID=6239;  [1]

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REMBL; AY005472; AAG32538.1; -

RGO; GO:0016021; C:integral to membrane; IEA.

RGO; GO:0005524; F:ATP binding; IEA.

RGO; GO:0004009; F:ATP-binding cassette (ABC) transport; IEA.

RGO; GO:0004009; F:ATP-binding cassette (ABC) transport; IEA.

RGO; GO:0006233; F:peptidase activity; IEA.

RGO; GO:0006508; P:proteolysis and peptidolysis; IEA.

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GO; GO:0005515; F:protein binding; If InterPro; IPR000210; BTB POZ.
InterPro; IPR002083; MATH:
InterPro; IPR002083; MATH:
InterPro; IPR008974; Traf_dom.
Pfam; PF00651; BTB; 1.
Pfam; PF00651; MATH; 1.
Prodom; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
PROSTIE; PS00211; ABC_TRANSPORTER_1;
PROSTIE; PS50893; ABC_TRANSPORTER_2;
                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-21289078; PubMed-11395456; Upton M., Tagg J.R., Wescombe P., Jenkinson H.F.; Upton M. Tagg J.R., Wescombe P., Jenkinson H.F.; "Intra- and Interspecies Signaling between Streptococcus salivarius and Streptococcus pyogenes Mediated by SalA and SalA1 Lantibiotic Peptides."; J. Bacteriol. 183:3931-3938(2001).
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Q9F445;
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Ross K.F., Ronson C.W., Tagg J.R.;
"Isolation and characterization of the lantibiotic salivaricin A and
its structural gene salA from Streptococcus salivarius 20p3.";
Appl. Environ. Microbiol. 59:2014-2021(1993).
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           Mycobacteriophage Bxz2.
Viruses; dsDNA viruses,
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
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01-MAY-1999
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glyco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Foley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C-96BW16B01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99214383; PubMed=10196340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding; Transport. SEQUENCE 722 AA; 83364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Essex M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novitsky V.A., Montano M.A., McLane M.F., Rei
Foley B.T., Ndung'u T.P., Rahman M., Makhema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRAIN=C-96BW16B01;
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                                                                                                                                                                                                                                                                      TOWDREINNY
                                                                                                                                                                                                                                                                                                              TRWDKSVNDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
858 AA;
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                                                                           (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    Conservative
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50.0%;
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Last annotation updat
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Pred. No. 13;
3; Mismatches
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Pred. No. 1.2e+02;
i; Mismatches 1
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             Caudovirales; Siphoviridae.
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ema M.J., Marlink R.,
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q82K72
Q82K72;
01-JUN-2003
01-JUN-2003
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22592660; PubMed=12705866;
Pedulla M.L., Ford M.E., Houtz J.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomycineae; Streptomycetaceae; Streptomyces NCBI TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Origins of highly mosaic mycobacteriophage genomes."; Cell 13:171-182(2003). EMBL; AY129332; AAN01831.1; -. SEQUENCE 77 AA; 8809 MW; B8D295DB02C82ED6 CRC64;
Q9K693;
Q9K693;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence and comparative microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003). EMBL, APO05031; BAC70243.1; -...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takaha Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Stre avermitilis: deducing the ability of producing secor metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL MEDLINE=21477403; PubMed=11572948; Omura S., Ikeda H., Ishikawa J., Hanamoto A., Ta) Shinose M., Takahashi Y., Horikawa H., Nakazawa H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces avermitilis. Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical SAV2532.
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MEDLINE=22608306; PubMed=12692562;
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                                                                                                                                                                                                                                                                                                                protein;
9 AA; 105
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                                            PRELIMINARY;
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577 MW; 8
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Last annotation update)
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Pred. No.
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Pred. No. 16;
1; Mismatches
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Q9ZR00

Q9ZR00;

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Q1-MAY-1999 (TrEMBLrel 10, Created)

DT 01-MAY-1999 (TrEMBLrel 10, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel 25, Last annotation update)

DT 01
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STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132;
MEDLINE-20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno
Fuji F., Hirama C., Nakamura Y., Ogasawar
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus halodurans.
Bacteria; Firmicutes
NCBI_TaxID=86665;
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GO; GO:0016491; F: exidoreductase

InterPro; IPR004925; HpaB.

Pfam; PF03241; HpaB; 1.

Complete proteome.

SEQUENCE 479 AA; 54604 MW; CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the alkaliphilic halodurans and genomic sequence comparison wit Nucleic Acids Res. 28:4317-4331(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.
Spiegel L.A., Huang E.N., Shah R., O'Shaughnessy A., Rodriguez M.,
Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
Shekher M., Schutz K., Saer K.F.X.;
Mewes H.W., Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP001520;
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50.0%;
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Ogasawara N
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th Bacillus subtilis.";
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RESULT 8
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AC Q90Q
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DT 01-J
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DT 01-J
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OS Huma
OC Viru
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RN SEQI
RC STRJ
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Matches 6
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Best Local
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                                                     Methanosarcina acetivorans.
Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databatemBL, AF286249; AAX88673.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.
             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00516; GP120; Pfam; PF00517; GP41; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gao F., Vidal N., Li Y., Ti Kim J., Choe K., Oh M.-D.,
                                                                                                                                  Predicted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hahn B.H., Peeters M.; "Evidence for two distinct sub-subtypes within the HIV-1 subtype A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=94CY042-10e;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; Retroid viruses; NCBI_TaxID=11676;
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8MÖ06Ö
                                           NCBI_TaxID=2214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           radiation."
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
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Pfam; PF03004; Transposase 24; 1.
PROSITE; PS00761; SPASE_I_3; 1.
Hypothetical protein.
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         FROM N.A
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                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           97687 MW;
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85.7%;
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                                                                                                                                                Last sequence update)
Last annotation update)
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Pred. No. 1.8e+02;
2; Mismatches 1
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M., Robertson D.L., Shaw (
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1e+02;
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RESULT 11
Q9YRU2
ID Q9YRU
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Q9YRS3
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A Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh
A Jones J., Ward J.;
T "Surveillance of Central African Nationals living in the Uni
reveals multiple subtypes of HIV-1 Group M and Group O.";
I Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF096343, AAD04418.1; -.
R GO; GO:0015021; C:integral to membrane; IEA.
R GO; GO:0015031; C:viral envelope; IEA.
R GO; GO:0005198; F:structural molecule activity; IEA.
R InterPro; IPR000328; Env_GP41.
R Transmembrane
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Best Local S
Matches 5
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Best Local
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NON_TER 117

NON_TER 117

SEQUENCE 117
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Q9YRS3;
01-MAY-1999
01-MAY-1999
01-JUN-2003
Q9YRU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; Retroid 'NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Edmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Leigh J.A., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Epigh J.A., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Fritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Whetcalf W.W., Birren B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metcalf W.W., Birren B.;
"The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";
Genome Res. 12:532-542(2002).
EMBL; AE011115; AAM07379.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=96USNG62;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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MEDLINE=21929760; PubMed=11932238;
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5; Conserv
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117 AA;
PRELIMINARY;
                                                                                                                                                                        Conservative
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41.7%;
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Pred. No.
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Pred. No. 17;
4; Mismatches
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PRT;
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117
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RESULT 12
Q9E5R4
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Best Local S
Matches
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Fonjungo P.N., Mpoudi E
Ngengasong J.N., Gao F.
Lal R.B.;
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Q9E5R4;
01-MAR-2001
01-MAR-2001
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones J., Ward J.;
"Surveillance of Central African Nationals living in the "Surveillance of Central African Nationals living in the reveals multiple subtypes of HIV-1 Group M and Group O.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF096323; AAD04398.1; -
GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
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01-JUN-2003
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01-MAY-1999
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Robbins K., Lal R., Storck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=96USCF92,
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                                                                                                                                                                                                                                                                                                                               MEDLINE=20414627; PubMed=10957729;
Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.
"Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
Variants in Cameroon.";
             Submitted (APR-2000) to the EMBL/GenBank/DDB-EMBL; AF252107; AAG14316.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005198; C:istructural envelope; IEA.

GO; GO:006198; F:structural molecule activinterPro; IPR000328; Env_GP41.

Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CAM170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Envelope
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2003 (TrEMBLrel. 2
e glycoprotein (Fi
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5; Conserv
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117
117 AA;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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117
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55.6%;
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corck C., Schable
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C.A., Wise
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H., Tetteh
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RESULT
Q90DQ4
ID Q9
AC Q

Viruses; Retroid NCBI\_TaxID=11676;

Human immunodeficiency virus

viruses;

Retroviridae;

Q90DQ4 PRELIMINARY
Q90DQ4;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
Envelope glycoprotein (

(TrEMBLrel. (TrEMBLrel.)

(Fragment) 19, 19, 24,

Last

sequence update) annotation updat

update)

Created)

PRELIMINARY;

PRT;

122

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Matches 5
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Q9E5Q8;
01-MAR-2001
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SEQUENCE
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01-JUN-2003 (TrEMBLrel
Envelope glycoprotein
                                                                                                                                                                    SEQUENCE
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Ngengasong J.N., Gao F.,
Lal R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20414627; PubMed=10957729;
Peter F.N., Eitel M.N., Judith T.N., George A.A., L
John N.N., Feng G., Mark R., Thomas F.M., Danuta P.
"Presence of Diverse Human Immunodeficiency Virus T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CAM203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variants in Cameroon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CAM203
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                                                                                                                                                                                                                                   Transmembrane.
                                                                                                                                                                                                                                                     Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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5; Conserva
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5; Conservative
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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## ALIGNMENTS

#### RESULT 1 AABIO546 ID AABIO546 AABIO546 AABIO546 AACTO Llama species antibody VHH CDR3 #15 10-DEC-2001 AAE10546; AAE10546 standard; peptide; 12 (first entry) A

Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.

Lama ds.

EP1134231-A1

19-SEP-2001.

20-FEB-2001; 2001EP-00200703

14-MAR-2000; 2000EP-00200930

(UNIL ) UNILEVER NV.

Bezemer S, Van De Burg M, De Haard JJW, Tareilus

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WPI; 2001-572718/65

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Claim 4; Page 29; 37pp; English.

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region

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RESULT 2
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                     The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #13 from llama (camelid) species
                                                                                                                                            Example 2;
                                                                                                                                                                     of light chains.
                                                                                                                                                                          New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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Pred. No. 9.6e-05;
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Best Local Similarity
dorrigocin, lactimidomycin and related chemical structures via chemical engineering of the enzymes involved in the biosynthesis of dorrigocin and lactimidomycin. They are useful for introducing chemical modifications normally inert positions that permit subsequence chemical modifications and facilitate the development of polyketides. The genes and proteins of the invention can also be used to generate a focused library of analogues around a polyketide lead candidate to fine-tune the compound for optimal properties. They are useful for generating antibodies specific for the polyketide biosynthesis. The present sequence is Streptomyces platensis
                                                                                                                                                                                                                 The invention relates to novel proteins involved in the biosynthesis polyketide dorrigocin (DORR) or lactimidomycin (LACT) biosynthesis by microorganisms. Sequences of the invention allow direct manipulation
                                                                                                                                                                                                                                                                                                                                                        Novel isolated or purified polypeptide involved in biosynthesis polyketide dorrigocin or polyketide lactimidomycin, useful for portigocin or lactimidomycin.
                                                                                                                                                                                                                                                                                                          Claim 13; Page 182-188; 312pp; English.
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                   CC ANYZEGO TEXTESSENT CONSENSUS SEQUENCES OF VARIOUS SECTIONS OF THE 2014 ANYZEGO TEXTESSENT CONSENSUS SEQUENCES OF VARIOUS SECTIONS OF THE 2014 ANYZEGO TEXTESSENT CONSENSUS SEQUENCES OF THE INVENTION. THE CONSTRAINED HEIGHT CONSTRAINED HEIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production of constrained helical peptide(s) by linking side chains on termini of octa:peptide - derived from human immunodeficiency virus gp. protein, useful in vaccines for treatment and prevention of infection.
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16-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus (HIV). Specifically, AAY22810-Y22910 are derived from 9D41 proteins of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY2288 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-1997;
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Pred. No. 1.6e
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RESULT 5
ABG68347
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                        The invention relates to cyclic peptides (A) with a constrained helical conformation, derived from gp41 (glycoprotein 41, a viral envelope CC protein) protein of human immunodeficiency virus (HIV). The cyclic peptides have formulas given in the specification part of which are CC derived from a consensus sequence of gp41 derived from HIV clades A, B, CC, D, E or O. The peptides are used to cause induction of a specific CC immune response, resulting in antibodies that prevent virus-induced CC membrane fusion. The peptides are used to treat subjects with, or at risk of, HIV infection, either as antifusion/anti-infection agents or, CC preferably where associated with a carrier, as an immunogen (including as vaccine) to raise antibodies. The antibodies may be used for diagnosis or prevention/treatment of HIV infection (i.e. acquired immunodeficiency syndrome, AIDS), e.g. prevention of mother-to-child transmission or in CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in CC syndrome, and the care accidents. The peptides can be based on specific HIV strains, e.g. breakthrough isolates of HIV that have developed during convection. The present sequence is gp41 protein from a particular HIV clade used to derive a consensus sequence of gp41. (Updated on 29-AUG-2003 to standardise OS field)
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16-JUN-1997;
16-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV; glycoprotein; gp41; antigen; helical conformation; virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS; viral envelope protein; vaccine; virucide; anti-HIV.
                                                                                                                                                                                                                                                                                                                                                                                           New cyclic peptides from treatment or prevention chelical conformation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 1; clade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Envelope protein gp41 from HIV clade A strain
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07-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                          Disclosure; Col 227-230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Braisted AC,
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5; Conserv
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97US-0049787P.
97US-00876698.
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                                                                                                                                                                                                                                                                                                                                                                                                           m human immune deficiency virus gp41, useful for of HIV infection, are constrained to have alpha
                                                                                                                                                                                                                                                                                                                                                            175pp;
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Mismatches
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     CC The invention describes a constrained helical peptide compound (I) CC comprising a first constrained helical peptide comprising a sequence of 8 cmino acids (a.as) having a first and second terminal residue both CC flanking an internal sequence of 6 a.as, where the terminal residues have can side chain that are linked to each other forming a locking group to CC attached to a carrier, for use as an immunogen to raise antibodies that prevent viral membrane fusion, as haptens, preferably cantiached to a carrier, for use as an immunogen to raise antibodies that the composition of treatment of patients at risk of corried and administration of the composition of the combinatorial constrained helical peptide CC intraries that are useful in chemical selection systems, to isolate the CC libraries that are useful in chemical selection systems, to isolate the binding determinants from alpha-helical binding domains of known protein can serve as a structural model continuing domain of a known protein can serve as a structural model for the design of peptideminetics, to replace intact binding proteins or protein binding domains in the affinity purification of ligands, to mimic epitopes in proteins to selectively raise polyclonal or monoclonal antibodies against such individual epitopes for isolating synthetic cantibodies against such individual epitopes for isolating synthetic.
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16-JUN-1997;
16-JUN-1997;
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viral
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(STAR/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunodeficiency virus.
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membrane fusion;
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JUDICE J K.

MCDOWELL R S.

PHELAN J C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 16; 180pp;
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55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide compound useful for prophylactically or mammal at risk for or infected with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcdowell RS,
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Pred. No. 1.2e
3; Mismatches
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The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also CC claimed are a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a CC that increases or decreases the expression of the polynucleotide sequence CC that is differentially expressed in neuronal tissue of a first animal CC that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates the expression of the polynucleotide sequence CC the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound to that regulates the activity in an animal of one or more of the polynucleosides given in the activity in an animal of one or more of the polyneptides given in the activity in an animal of one or more of the polyneptides given in the sequence specification, a method for identifying a compound useful in treating
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Matches 5
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01-NOV-2001;
26-NOV-2001;
                                                                                                                                                                                                                                                                                                   Claim 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                  New composition comprising preparing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                   GENBANK;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Woolf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             combinatorial libraries, to provide conformationally stable variant peptides or proteins which exhibit floppy or unstable alpha-helical secondary structure at one or more sites in unrestrained form under conditions of interest. This is the amino acid sequence of an HIV envelope protein gp41, fragments of which are used in the creation locked helix peptides
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2001US-0346382P.
2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002WO-US025765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Befort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 injury;
                                                                                                                                                                                                                                                                                                                                  treating
                                                                                                                                                                                                                                                                                                                                                    two or
                                                                                                                                                                                                                                                                                                                                                                                                                                  ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; spinal segmental nerve injury;
; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4012
                                                                                                                                                                                                                                                                                                                                                                                                                                Costigan
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                                                                                                                                                                                                                                                                                                                                more isolated polypeptides, useful for ng pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6;
1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 268,
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RESULT 8
AAB69351
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Best Local S
Matches 5
Query Match
Best Local Similarity 55.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polypuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 532 AA;
                                                                                                                             The present in invention provides the protein and coding sequences number of human immunodeficiency virus (HIV) type I non-subtype B isolates. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, rev and nef proteins. These can be used to detect the presence of H in a sample and to produce antibodies against non-subtype B HIV-1 These antibodies can be used in vaccines to prevent and treat HIV infection. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV-1 non-subtype B clone 94CY032-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vif; vpr; tat; rev; nef; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV-1; human
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20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                  Novel genomic nucleic acids of non-subtype B human immunodeficiency virus type 1 useful for detecting and treating AIDS comprises a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-1999;
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                                                                                       Sequence 855
                                                                                                                                                                                                                                                                                                                                   Claim 41; Fig 21; 131pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-365651/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UABR-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shaw GM,
                                                                                                                                                                                                                                                                                                                                                                             sequence.
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(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunodeficiency virus; non-subtype B; gag; pol; env; vpu;
                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-00184418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US024837.
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                       59.7%;
                                                                                                                                                                                                                                                                                                                                     English
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  Score 40; DB 3;
pred. No. 4.4e+02;
3; Mismatches 1
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Pred. No.
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2.6e+02;
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                                               Length 855
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The invention relates to a protein comprising or having at least 50% cc identity to any of the 2469 amino acid sequences, identified in the cspecification (available on a computer readable format), or its fragment, ce expressed from 2469 of 2489 identified DNA codding regions from the cc streptococcus pneumoniae type 4 strain genomic sequence appearing as composition), a kit comprising first and second primers, which are the composition a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the target sequence complementarity define the termini of the target sequence contained within a Streptococcus nucleic acid sequence to be amplified, assay comprising contacting a test compound with the correction, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bactering a test compound with the caroding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus sequence and multibotics. The methods are useful for identifying cimmunodominant proteins. The present sequence is one of the 2469 proteins componed the sequence data for this patent did not form part of the printed componed data for this patent did not format directly from WIPo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae;
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11-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media of the streptococcus bacteria, such as pneumonia, sepsis, otitis media of the streptococcus bacteria, such as pneumonia, sepsis, otitis media of the streptococcus bacteria, such as pneumonia, sepsis, otitis media of the streptococcus bacteria, such as pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-2001; 2001GB-00007658
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antiinflammatory; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU00861 standard; protein; 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 858; 56pp; English.
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(first entry)
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immunostimulant; auditory; respiratory;
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ABP81332
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Best Local Similarity
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Matches
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                                                                                                                   The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of a Streptococcus pneumoniae genomic sequence, a fragment or degenerate variant of the polynucleotide or a nucleic acid sequence 95% identical to one of the polynucleotides. The S. pneumoniae polynucleotides and encoded polypeptides (ABP81299-ABP81674) are useful for treating or preventing S. pneumoniae infections or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. These are also useful for detecting S. pneumoniae in a biological sample or diagnosing S. pneumoniae in a subject. The polynucleotides have antibacterial activity and are useful in gene therapy
                                                                                                                                                                                                                                                                                       New Streptococcus pneumoniae polynucleotides, useful for treating of preventing S. pneumoniae infections, or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae.
                                                                                                  Sequence 1659 AA;
                                                                                                                                                                                                                                                                 Claim 42; Page 412-419; 1091pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    Zagursky RJ,
Wooters JL;
                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-093010/08
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18-APR-2001; 2001US-0284443P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae; diagnosis; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                        (AMCY ) AMERICAN CYANAMID CO
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WDKAKNDY 421
                       WDKSVNDY 12
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                                                                                                                                                                                                                                                                                                                                                                                               AW,
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                                                           59.7%;
75.0%;
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75.0%;
                                                                                                                                                                                                                                                                                                                                                                                              Green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection; otitis media; antibacterial;
                                               Score 40; DB 6; L
Pred. No. 9.3e+02;
1; Mismatches 1;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                               BA,
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9.3e+02;
                                                                      Length 1659;
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RESULT 11
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Best Local S
Matches 6
SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                              27-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid genes from Drosophila and
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11-JUL-2000; 2000US-00614150.
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RESULT 13
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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                                          Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                                                                             20-OCT-2003
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, Jen S, Carter D;
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Pred. No. 42;
2; Mismatches
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RESULT 14
ABBO8079
ABBO8
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AC
AC
ABBO8
XX
DT
10-SE
XX
DE
Maize

ABB08079 standard; protein; 527

10-SEP-2002 ABB08079

(first entry)

Maize cytochrome P450, CYP72A1

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9 N

VTRWNSSVN ITRWDKSVN 10 Query Match Best Local S Matches

Similarity 6; Conserv

Conservative

2;

58.2%;

Score 39; DB Pred. No. 42; Mismatches

φ,

Length 74

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Sequence 74 AA;

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composition and repaired protein. The invention and so relates to comprehensing a propionibatterium acmes protein. The invention also relates to comprehension of proteins of p. acmes polypeptides. The invention and to companie fragments of p. acmes polypeptides. The invention companies of the invention and host cells comprising a polypeptide of the invention; an invention; an invention; an invention; an invention; an invention; an invention; a comprising a polypeptide of the invention; a comprising proteins comprising polypeptide of the invention; a complex comprehension of the invention; a complex comprehension of polypeptide and an isolated T cell population comprising T cells prepared contigen-presenting cells that express the polypeptides, or comprehension of p. acmes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations, or comprehension of p. acmes in a companient; and a method for inhibiting the development of P. acmes in a companient; and a method for inhibiting the development of P. acmes in a companient, the p. acmes in a comprehens, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acme composition. The polymucleotides can also be used as probes or primers for mucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acmes in a complex companient of the primers for the stimulation of an immune response against p. acmes of the companient of the composition is useful for the stimulation of an immune response against p. acmes of the companient of the companie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitcham JL, Skeiky YAW, Ferb
Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-2001; 2001US-00978825.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID NO 5170; 1481pp; English.
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DB; ACF64450.
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Lodes MJ,
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Benson DR,
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Jones R, Carter D;
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Maize; cytochrome P450; CYP72A1; CYP92A1; plant; gene therapy; antidote

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RESULT 15
ABU24124
ID ABU24
XX ABU24
XX ABU24
XX ID-JU
DT 19-JU
DE Prote
XX Antis
XX
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Best Local
                                                        03-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acids may be used in genetic engineering protocols to transform plants and other eukaryotes e.g. yeast, maize (especially), soybean, beet, tobacco, wheat, barley, poppy, rape, sunflower, alfalfa, sorghum, rose, carnation, gerbera, carrot, tomato, lettuce, chicory, pepper, melc and cabbage. They may be used in this way to confer protection against heterocyclic herbicides, sulfonylurea herbicides, substituted urea herbicides and/or organophosphate insecticides. The present sequence represents the Z. mays CYP72A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules encoding a Zea mays cytochrome P450 CYP72A1, useful for the production of plants resistant to heterocyclic, sulfonylurea and substituted urea herbicides and organophosphate insecticides e.g. Classic and Pursuit.
                                                                                                                                                                                                                                                                                                                                                                                            ABU24124;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU24124 standard; protein; 1191 AA
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Peptide
                                                                                                           WO200277183-A2
                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                        Protein encoded by Prokaryotic essential gene #9651.
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)B; ABL60758.
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sequence indicated in
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200. .527
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Pred. No. 3.8e+02;
3; Mismatches 1
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Search completed: October Job time: 13,1296 secs

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LIEEWEKSIKQY

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1 LITRWDKSVNDY Similarity 6; Conser

Conservative

50.0%;

Score 39; Pred. No.

Mismatches

0

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9.4e+02; DB 6;

Length 1191; Indels

Query Match Best Local Matches

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression to fit the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid concluded acid concluded acid; (2) a host cell containing the vector; (3) an isolated concluded acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense concluded acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, (7) identifying a gene in an operon required for required for proliferation, or that has an activity against a biological pathway in which a proliferation-required gene or its gene product that has an activity against a proliferation of compound's activity; (11) a culture compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational cory discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, S. present did not form part of the printed specification, but was obtained content did not form part of the printed specification, but was obtained content directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID NO 52048; 1766pp; English.
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  1191
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Trawick
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
  AA
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Carr GJ,
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Forsyth
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Xu HH;
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Minimum DB
Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                               40.5
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seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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72
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1: pir1:*
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                                                  GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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                                        JC4393
AE2132
                                                             D70559
H87081
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T35743
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C71338	A55718	T03530	A61500	S51641	JQ0337	F64454	S21864	S12247	A39832	\$40048	AJECN	T46865	D69675	AH1381	S57837	
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#### ALIGNMENTS

RESULT 1

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RESULT 2
S55091
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Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0952
R;Martin, T;, Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0952
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F;15-98/Domain: immunoglobulin homology <IMM>F;35-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
A;Gene: MIPS:YMR209c
A;Cross-references: (
A;Map position: 13R
                                                                 A;Molecule type: DNA
A;Residues: 1-457 < ADD)
A;Cross-references: EMBL:Z49809; NID:g854459; PID:g854461; GSPDB:GN00013; MIPS:YMR209c
A;Experimental source: strain AB972
C;Genetics:
                                                                                                                                                                            C;Accession: S55091
R;Dedman, K.; Brown, D.; Bowman, S. submitted to the EMBL Data Library, A;Reference number: S55089
A;Accession: S55091
                                                                                                                                                                                                                                                                                  probable membrane protein YMR209c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM8261.03c
C;Species: Saccharomyces cerevisiae
C;Date: 08-701-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGGNYDYIWGSY 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                              SGD:S0004822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 42; DB 2; Pred. No. 8.6; 0; Mismatches
                                                                                                                                                                                                                             June 1995
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RESULT
S30313
                                                                                                                                                                                                                                                                                                                                       Gene 122, 53-62, 1992
A;Title: Cloning and sequencing of the genes encoding glyceraldehyde-3-phosphate dehydr comparison with corresponding sequences from thermophilic Bacillus stearothermophilus.
A;Reference number: JQ1952; MUID:93083995; PMID:1452037
A;Accession: PQ0538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
PQ0538
hypothetical protein 8 - Methanobacterium thermoformicicum C;Species: Methanobacterium thermoformicicum
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A87679
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                                                                                                                                                                                                                                             A;Cross-references: GB:M87647; NID:g143315; PIDN:AAA73205.1; PID:g143320
A;Experimental source: strain DSM319
C;Superimily: cofactor-independent phosphoglycerate mutase
C;Keywords: intramolecular transferase; isomerase
                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-232 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S. 4136-411, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87679
                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable phosphoglycerate mutase (EC 5.4.2.1), 2,3-diphosphoglycerate-independent
C;Species: Bacillus megaterium
C;Date: 31-Dec-193 #sequence_revision 31-Dec-1993 #text_change 27-Oct-2003
C;Accession: PQ0538
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A;Molecule type: DNA
A;Residues: 1-152 <STO>
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R;Nierman, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein CC3467 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-20: C;Accession: A87679
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                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Schlaepfer,
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A;Title: The complete genome sequence of the murine respiratory A;Reference number: A99512; MUID:21267165; PMID:11353084 A;Accession: D90571
                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein MYPU_4760 [imported] - Mycoplasma pulmonis (strain C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
                                                                            A; Genetic code:
                                                                                                                              A;Cross-references: GB:AL445566; PID:g14089890; PIDN:CAC13649.1; A;Experimental source: strain UAB CTIP
                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-560 < KUR>
                                                                                                                                                                                                                                                                               R; Chambaud, I.; Hei
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                         C; Accession: D90571
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A;Molecule type: DNA
A;Residues: 1-415 <KANA
A;Cross-references: EMBL;AB009866; NID:d1204727; PIDN:BAA31880.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Biosci. Biotchenl. Biochem. 61, 1960-1962, 1997
A;Title: Panton-Valentine leukoidin genes in a phage-like A;Reference number: Z14119; MUID:98067870; PMID:9404084
A;Accession: T00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 22-Oct-1999 C;Accession: S30313 R;Noelling, J.; van Eeden, F.J.M.; Eggen, R.I.L.; de Vos, W.M. Nucleic Acids Res. 20, 6501-6507, 1992 Nucleic Acids Res. 20, 6501-6507, 1992 N.Title: Modular organization of related Archaeal plasmids encoding different restriction A;Reference number: S30302; MUID:33126090; PMID:336177 A;Accession: S30313
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A;Genome: plasmid pFV1
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A; Residues: 1-361 < NOE>
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation not
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Similarity 50. 6; Conservative
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alanyl-tRNA synthetase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2003
C;Accession: F75289
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Do, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalv
S.; Smith, H.O.; Venter, J.C.; France, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U00030; NID:g458927; PID:g458928; GSPDB:GN00008; MIPS:YHR202w
C;Comment: This sequence has motifs characteristic of a variety of phosphoesterases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, February 1994 A;Description: The sequence of S. cerevisiae cosmid 9998
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A; Residues: 1-602 < MAC>
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A;Molecule type: DNA
A;Residues: 1-890 <WHI>
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C; Superfamily: alanyl-tRNA ligase
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D83230
hypothetical
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                                                                                                                                                                                                                                                                                                  A;Gene: DR2300
                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE002062;
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A75250;
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Best Local S
Matches 5
                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: Saccharomyces cerevisiae probable phosphoesterase; Keywords: hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Saccharomyces cerevisiae;
Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 19-Apr-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
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    protein PA3318 [imported]
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45.5%;
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Pred. No. 5
                                                                                                                                                                                                      Score 40.5;
Pred. No. 1
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      Pseudomonas aeruginosa
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57;
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1e+02;
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    yeast (Saccharomyces cerev)

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        (strain PAO1)
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T.; Zalewski,
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C.; Ma
        A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-341 <MON>
A,Cross-references: EMB
                                                                                     A;Reference number: Z24471
A;Accession: T47653
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R; Monfort, A.; Casacuber submitted to the Protein

Casacuberta,

Sequence Database,

E.; Puigdomenech,

h, P.; Mewes, H.W.; Lemcke, K.; Mayer, February 2000

K.F.X.;

EMBL:AL132954

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A;ACCESSION. PERIADRAY
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-166 <STO>
A;Cross-references: GB:AE004754; GB:AE004091; NID:g9949446; PIDN:AAG06706.1; GSPDB:GN001:
A;Cross-references: GB:AE004754; GB:AE004091; NID:g9949446; PIDN:AAG06706.1; GSPDB:GN001:
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R;Stover; C:K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual A;Reference number: A81455; MUID:99178987; PMID:10077609
A;Accession: A81455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: D83230
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C;Date: 15-Sep_2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 1
G;Superfamily: Leishmania major probable membrane
G;Keywords: transmembrane protein
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pectate lyase-like protein - Arabidopsis thaliana
N;Alternate names: protein T26112.20
G;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 24-Mar-1999 #sequence revision 24-Mar-1999 #text_change 19-May-2000 C;Accession: A81455; T02789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable membrane protein L549.1 [imported] - Leishmania major (strain Friedlin)
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T02789
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                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: L549.1
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Best Local
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Pred. No.
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Pred. No. 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:g2978450;
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A.; Larbig,
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K.; Lim,
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302 NFDRGWNEY 310

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                             R;Su, Z.H.; Tominaga, O.; Ohama, T.; Kajiwara, E.; Ishikawa, R.; Okada, T.S.; Nakamura,
J. Mol. Evol. 43, 662-671, 1996
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A;Vartiety: isolate I-7
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
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A;Experimental source: ssp. takiharensis; isolate I-7; adult, thorax muscle
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A; Introns: 43/1; :
A; Note: T26I12.20
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                                                                                                                                                                                                                                                                                                                                             . Mol. Evol. 43, 662-671, 1996
.Title: Parallel evolution in radiation of Chomopterus ground beetles inferred from mi.Reference number: Z17791; MUID:97149035; PMID:8995063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Accession: T14117; Su, Z.H.; Tominaga, O.; Ohama, T.; Kajiwara, E.; Ishikawa, R.; Okada, T.S.; Nakamura, Mol. Evol. 43, 662-671, 1996; Title: Parallel evolution in radiation of Ohomopterus ground beetles inferred from mi;Reference number: Z17791; MUID:97149035; PMID:8995063; Accession: T14117
                                                                                                                                                                                                                               Residues: 1-355 <SUZ>
Cross-references: EMBL:D50728; NID:g1001020; PIDN:BAA09359.1;
Experimental source: adult; thorax muscle
                                                                                                                                      Superfamily: NADH dehydrogenase (ubiquinone) chain 5 Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                  Genome: mitochondrion
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;Residues: 1-355 <SUZ>
                                                                    Matches
                                                                                         Query Match
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                                                                  Similarity 5; Conserved
NYDRSWGDY 12
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                                                             Score 40; DB
Pred. No. 50;
2; Mismatches
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Pred. No. 48;
2; Mismatches
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Pred. No. 50;
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                                                                                                        DB 2;
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C;Accession: T14125
R;Su, Z.H.; Tominaga, O.; Ohama, T.; Kajiwara, E.; Ishikawa, R.; Okada, T.S.; Nakamura, F. J. Mol. Evol. 43, 662-671, 1996
A;Title: Parallel evolution in radiation of Ohomopterus ground beetles inferred from mitch A;Reference number: Z17791; MUID:97149035; PMID:8995063
                                                                                                                                                                                              C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5 C;Keywords: membrane-associated complex; mitochondrion;
                                                                                                                                                                                                                                                                               A; Experimental source: ssp. C; Genetics:
                                                                                                                                                                                                                                                                                                                                               A,Status: preliminary, translated A,Molecule type: DNA A,Residues: 1-355 <SUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: mitochondrion Ohe
A;Variety: isolate Mie (Y-3)
C;Date: 20-Sep-1999 #sequenc
                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:D50731; PIDN:BAA09362.1
A;Experimental source: ssp. cupidicornis; isolate Mie (Y-3); adult; thorax muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Ohomopterus yaconinus mitochondriC_iSpecies: mitochondrion Ohomopterus yaconinus
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PBS167; Q986F5;
01-FEB-1994 (Rel. 28, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
2,3-bisphosphoglycerate-independent phosphoglycerate mutase
2,3-bisphosphoglyceromutase) (BPG-independent PGAM) (iPGM).
                                            Schlaepfer B.S., Zuber H.;
"Cloning and sequencing of the genes encoding glyceraldehyde-3-
phosphate dehydrogenase, phosphoglycerate kinase and triosephosphate
isomerase (gap operon) from mesophilic Bacillus megaterium: comparisc
with corresponding sequences from thermophilic Bacillus
stearothermophilis.";
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIR-ATCC 12872 / QMRDC B1551;
Chander M., SetLow P., Lamani E., Jedrzejas M.J.;
Chander M., SetLow P., Lamani E., Jedrzejas M.J.;
"Structural studies on a 2,3-diphosphoglycerate independent
phosphoglycerate mutase from Bacillus stearothermophilus.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=93126090; PubMed=1336177;
Noelling J. van Beden F.J.M., Eggen R.I.L., de Vos Welling J., van Beden F.J.M., Eggen R.I.L., de Vos Welling J., van Beden F.J.M., Eggen R.I.L., de Vos Welling J., van Beden F.J.M., Eggen R.I.L., de Vos Welling J., van Beden F.J.M., Eggen R.I.L., de Vos Welling J., van Beden F.J.M., Eggen R.I.L., de Vos Welling J., van Jenes J., de Vos Welling J., de Vos We
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thermoformicicum.";
7. "Anida Res. 20:6501-6507(1992)
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Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                 MEDLINE=93083995; PubMed=1452037;
                                                                                                                                                                                                                                                                        SEQUENCE OF 1-232
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51 AA; 40667 MW;
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Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirst-
Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., V.
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R
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MEDLINE=94378003; PubMed=8091229;
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Saccharomycetales;
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EMBL; M87647; AAA73205.1; -.
EMBL; M87648; AAA73208.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ram;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP;
                                                                                                                          EQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roDom; PD004429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-phosphoglycerate (By similarity).

CAPALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.

COFACTOR: Binds 2 manganese ions per subunit (By similarity).

PATHWAY: Glycolysis.

SUBUNIT: Monomer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Monomer (By similarity). SIMILARITY: Belongs to the BPG-independent family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQ0538; PQ0538.

p; MF 01038; -; 1.

rPro; IPR005124; Metalloenzyme.

rPro; IPR005995; Pgm_bpd_ind.

pr01676; Metalloenzyme; 1.
                                                                                                                                                                                                                                                                          YEAST
                                                                                                                                                                                                                                                                                                                                        29
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                                                                                                                                                                                                                                                                                                                                                                                      Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                               RRSNYDRSWGDY
   nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR013:07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          equires a license agreement (S email to license@isb-sib.ch).
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62
403
407
444
445
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                                                                                                                                                                                      cerevisiae (Baker's
                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                             Ascomycota; Saccharomycotina; Saccharomycetaceae; Saccharomycetaceae;
                                                                                                                                                                                                              31,
31,
42,
kDa
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07; pgm_bpd_ind; 1.
ysis; Metal-binding;
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62
403
407
444
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41.7%;
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Last
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                                                                                                                                                                                                              protein
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                                                                                                                                                                                                                           sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                Albinding; Manganese.

PHOSPHOSERINE INTERMEDIATE
BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                   Score 41;
Pred. No.
   of Saccharomyces
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                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  -> E (IN REF. 2).
7D3FAB449983E6C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                       yeast).
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17;
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                                                                                                                                                                                                              intergenic region
     cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                      Vaughan
   chromosome
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- outstation
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Matches 5
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;

MEDLINE=20036896; PubMed=10567266;

White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,

Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,

Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Shen M.,

Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,

Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,

Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,

Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,

Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYA DEIRA
Q9RS27;
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U00030; AAB68354.1; -. PIR; S46676; S46676.
                                                                               This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatist the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for comment entitles requires a license agreement (See http://www.isb-sib.ch/annot or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
-!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP + diphosphate + L-alany1-trNA(Ala).
-!- SUBCELULUAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-II aminoacy1-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Germonline; 139520; -. SGD; S0001245; YHR202W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 265:2077-2082(1994).
                              EMBL; AE002062; AAF11848.1;
PIR; F75289; F75289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALAS OR DR2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deinococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 602 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004843; M-ppestrase.
Pfam; PF00149; Metallophos; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CBI_TaxID=1299;
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5; Conserv
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(Rel. 41, Last sequence update)
(Rel. 41, Last sequence update)
synthetase (SC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 21;
4; Mismatches
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                                                                                                    noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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TIGR; DR2300; HAMAP; MF\_000

RESULT 7
RS1\_MYCLE
ID RS1\_M
AC P4683
DT 01-NC
DT 16-OC

RS1\_MYCLE P46836; 01-NOV-1995 16-OCT-2001

(Rel. 32, (Rel. 40,

Created) Last sequ

sequence

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STANDARD;

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Best Local
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                                                     Matches
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InterPro; IPR003218; tRNA-Synt;
InterPro; IPR006193; tRNA-Synt;
InterPro; IPR006193; tRNA-Synt
Pfam; PF02272; DHHA1; 1.
Pfam; PF01411; tRNA-Synt 2c; 1.
PRINTS; PR00980; TRNASYNTHALA.
                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the In the Buropean Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAINADSM 3720 / Z-245;
MEDLINE-93126090; PubMed-1336177;
Noelling J. van Beden F.J.M., Egg
"Modular organization of related;
restriction-modification systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequenc)
01-APR-1993 (Rel. 25, Last annotat)
Hypothetical 40.6 kDa protein (ORR
Methanobacterium thermoformicicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPZ8 ME
                                                                                                        Hypothetical SEQUENCE 3
                                                                                                          PIR; S30325; S30325.
Hypothetical protein; Plasmid.
SEQUENCE 361 AA; 40565 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGREAMs; TIGR00344; alas; 1.
PROSITE; PS50860; AA TRNA_LIGASE_II_ALA; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase;
                                                                                                                                                 EMBL; X68367; CAA48439.1;
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 20:6501-6507(1992).
-!- SIMILARITY: TO THE CORRESPONDING ORF IN PFV1.
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=145262;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota;
Methanobacteriaceae; Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pFZ1.
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 RRDGLPRSWGPY 292
                          RRSNYDRSWGDY
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.2%;
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                                                                  58.3%;
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in (ORF8')
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Pred. No. 37;
                                                                  Score 40; DB
Pred. No. 18;
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Ala.
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ed Archaeal plasmids encodi
ms in Methanobacterium
                                                                                                           5787C9D090A6384F CRC64;
                                                        Mismatches
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                                                                                Length 361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- FUNCTION: BINDS MRNA; THUS FACILITATING RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkiri J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=96059637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacte Corynebacterineae; Mycobacteriaceae; CORJ TaxID=1769;
                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR008994; Nucleic_acid_OB.
InterPro; IPR000110; Ribosomal_S1.
InterPro; IPR003029; S1.
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Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The Mycobacterium leprae genome: systematic sequence analysis identifies key catabolic enzymes, ATP-dependent transport syste a novel polA locus associated with genomic variability."; Mol. Microbiol. 16:909-919(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reproma; ML1382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: BINDS MRNA; THUS FACILITATING RECOGNITION OF THE INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
SIMILARITY: Belongs to the S1P family of ribosomal proteins.
SIMILARITY: Contains 4 S1 motif domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H87081; H87081.
S77660; S77660.
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                                                                                                                                                                                                                                                                                                                                                                          SM00316; S1;
                                          Similarity 5; Conser
RRSNYDRSWG
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PS50126; S1; 4.
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S1.
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S1 MOTIF 1.
S1 MOTIF 2.
S1 MOTIF 3.
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                                                                                                                                                       SI MOTIF 1.
SI MOTIF 2.
SI MOTIF 3.
SI MOTIF 4.
AFVDL -> CVCRS (IN REF. 1).
AFVDL -> CVCRS (IN REF. 1).
RGVRPGKVRYGPTATTSRATTSSL (IN REF.
                                                                   Score 40;
Pred. No.
                                                                                                                                        4F955F6D8EA8E09B
                                          Mismatches
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THE SECOND DESCRIPTION OF THE SECOND DESCRIP
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006147;
                                                       PROSITE; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Golde S.T., Brosch R., Parkill J., Garnier T., Churcher C., Harris Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                        EMBL; Z95554; CAB08883.1; -.
EMBL; AE007030; AAK45936.1;
EIR; D70559; D70559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
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30-MAY-2000
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Pfam; PF00575; S1;
PRINTS; PR00681; R
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TIGR; MT1666; -.
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MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D.; Eisen J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CDC 1551 /
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30-MAY-2000 (Rel. 39, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
30S ribosomal protein S1.
RPSA OR RV1630 OR MT1666 OR MTCY01B2.2
                                                                                                                                                                                          InterPro; IPR008994; Nucleic acid OB. InterPro; IPR000110; Ribosomal S1.
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                                NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Bacteriol. 184:5479-5490(2002).

1- FUNCTION: BINDS MRNA; THUS FACILITATING RECOGNITION OF THE INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHOR'S SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).

1- SIMILARITY: Belongs to the S1P family of ribosomal proteins.

1- SIMILARITY: Contains 4 S1 motif domains.
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                                                                      PS50126; S1; 4.
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RNA-binding; Complete S1 MOTIF 1. S1 MOTIF 2.
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P59989;
15-MAR-2004
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MEDLINB=22709107; PubMed=12788972;

Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,

Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S.,

Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,

Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,

Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;

"The complete genome sequence of Mycobacterium bovis.";

Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

-!- FUNCTION: May be a sulfotransferase involved in the formation of thosquifate (By similarity).

-!- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.

-!- SIMILARITY: Contains 2 rhodanese domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    мусво
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynobacterineae; Mycobacteriaceae; Mycobacterium. NCBI_TaxID=1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BX248336; CAD93700.1; -.
PROSITE; PS00380; RHODANESE 2; 1.
PROSITE; PS00683; RHODANESE 2; 1.
PROSITE; PS50206; RHODANESE 3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein 1).
CYSA1 OR MB0838C
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5; Conservative
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154
233
277 AA;
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(Rel. 43, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat;
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                          STANDARD;
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274 R
233 B
31014 MW;
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25 RHODANESE 1.
74 RHODANESE 2.
33 BY SIMILARITY.
31014 MW; AC37B715D99565A9 CRC64;
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1; Mismatches
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Pred. No. 24;
4; Mismatches
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                          PRT;
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Interpro; IPR001307; Rhodanese.
Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
PROSITE; PS00380; RHODANESE_1; 1.
PROSITE; PS00683; RHODANESE_2; 1.
PROSITE; PS00683; RHODANESE_3; 2.
PROSITE; PS50206; RHODANESE_3; 2.
Transferase; Complete proteome; Repeat.
DOMAIN
18 125 RHODANESE 1.
DOMAIN
18 125 RHODANESE 2.
ACT_SITE 233 233
SEQUENCE 277 AA; 31094 MW; 527E05C9FE93
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Smith D.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- FUNCTION: May be a sulfotransferase involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-WAR-2094 (Rel. 43, Last annotation update)
Putdelive thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese-like
  005793;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U15182; AAA62982.1; -.
EMBL; AL583924; CAC31153.1;
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CYSA OR CYSA3 OR ML2198.
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Leproma; ML2198; -.
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6; Conserva
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  36, Created)
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Pred. No. 20;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        me, Repeat.
RHODANESE 1.
RHODANESE 2.
BY SIMILARITY.
527E05C9FE93969D CRC64;
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Query Match
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TIGR; MT0837;
TIGR; MT3199;
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                               DOMAIN
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                          EMBL; Z95150; CAB08374.1; --
EMBL; AL022004; CAAL7621.1; --
EMBL; AL00206973; AAX45079.1; --
EMBL; AB007136; AAX47539.1; --
EMBL; AB007136; G70809.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22206494; PubMed=12218036; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Enchar A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; [100,000]
                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=H37RV;
MEDLINE=98295987;
                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (or send an email to license@isb-sib.ch)
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-!- EUNCTION: May be a sulfotransferase involved
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(CYSA1 OR CYSA OR
RV0815C OR MT0837
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Corynebacterineae; Mycoba
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                                                                                                                                                               Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
                                                                                                                                                                                              TubercuList; Rv0815c; -.
InterPro; IPR001763; Rhodanese-like
InterPro; IPR001307; Rhodanese.
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15-MAR-2004 (Rel.
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PS00683;
PS50206;
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                                31014 MW;
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sulfurtransferase (EC 2.
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                             POTHEOME 1.

RHODANESE 1.

RHODANESE 2.

BY SIMILARITY.

AC37B715D99565A9 CRC64;
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Length 277;
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RESULT 13
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P16385;
01-AUG-1990
01-AUG-1990
28-FEB-2003
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ACT_SITE
SEQUENCE
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InterPro; IPR001307; Rhodanese.
Pfam; PF00581; Rhodanese; 2.
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Donadio S., Shafiee A., Hutchinson C
"Disruption of a rhodaneselike gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein).
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01-AUG-1990 (Rel. 15, Last sequence upo
28-FEB-2003 (Rel. 41, Last annotation u
Putative thiosulfate sulfurtransferase
                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00380; RHODANESE 1; PROSITE; PS00683; RHODANESE 2; PROSITE; PS50206; RHODANESE 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharopolyspora erythraea.";
J. Bacteriol. 172:350-360(1990)
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Pseudonocardineae; Pseudon
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- SIMILARITY: Contains 2 rhodanese domains.
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fibringgen-like protein 1 precursor (Hepatocyte-derived related protein 1) (HFREP-1) (Hepassocin) (HP-041).
FGL1 OR HFREP1.
Homo sapiens (Human)
                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
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"Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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h M., Sasaki H.,
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MBUDANT Disanto J.P., Certaun Disanto J.P., Certaun Prischer A., de Saint Basile "The murine interleukin-2 re"
"The murine interleukin-2 re"
                                                                                                                                                                                                                                                                                           MEDIINE=93366191; PubMed=8359699;
Kobayashi N., Nakagawa S., Minami Y., Taniguchi T.,
"Cloning and sequencing of the cDNA encoding a mous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93277575; PubMed=8503926;
Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., U
"Cloning of the mouse interleukin 2 receptor gamma chain:
demonstration of functional differences between the mouse
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Pfam; PF00147; fibrinogen_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93391374; PubMed=8378320; Cao X., Kozak C.A., Liu Y.J., Noguchi M., "Characterization of cDNAs encoding the m (IL-2R) gamma chain: chromosomal mapping
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Noguchi M., O'Connell E., Leonard ...
Noguchi M., O'Connell E., Leonard ...
Noding the murine interleukin 2 receptor
Noding '-- and tissue specificity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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I -> D (IN REF. 1).
I -> V (IN REF. 1).
P -> L (IN REF. 2).
26BC82124E6660C2 C
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                                                                                                                     Macdonald
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mma chain)
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                            gene:
                                                                                                                     H.R.,
                                                                                                                                                                                                                                                                                                        mouse
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                            organization, thymus.";
                                                                                                                     Avner
                                                                                                                                                                                                                                                                                                        IL-2
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Salivary gland;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Milahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
EMBL; D13821; BAA02974.1; -...
EMBL; U21795; AAA64279.1; -...
EMBL; U21795; AAA64279.1; -...
EMBL; D13565; BAA02760.1; -...
EMBL; S75844; AAA39286.1; -...
EMBL; S75845; AAB32904.1; JOINI
EMBL; S75846; AAB32904.1; JOINI
EMBL; S75847; AAB32904.1; JOINI
EMBL; S75848; AAB32904.1; JOINI
EMBL; S75848; AAB32904.1; JOINI
EMBL; S75848; AAB32904.1; JOINI
EMBL; S75869; AAB32904.1; JOINI
EMBL; S75861; AAB32904.1; JOINI
EMBL; S75865; AAB32904.1; JOINI
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[5]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
MGD; MGI:96551; I12rg.
InterPro; IPR002996; CR1A.
InterPro; IPR003957; FN_III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR0033961; Femili.
InterPro; IPR003391; Hemitopoptn_S_F1
Pfam; PF00041; fn3; 1.
                                                                                              PIR; 149280; 149280.
HSSP; P31785; 11LM.
MGD; MGI:96551; 112r
                                                                                                                                                        EMBL; BC014720; AAH14720.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Subfamily 5.
-!- SIMILARITY: Contains 1 fibronectin type III domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dougherty G.J.; "Molecular mechanisms regulating the hyaluronan binding activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interleukins.
-!- SUBUNIT: The gamma chain is common to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chiu R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96341745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probably also the IL13 receptors.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Belongs to the type I cytokine family of receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Common subunit for the receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               institutions as long as atement is not removed. I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the IL2,
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RESULT 15
IRF4 MOUSE
ID TAFA MOUSE
AC 064287; Q60802;
DT 01-NOV-1997 (Rel.
DT 01-NOV-1997 (RE
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                         MEDLINE-5531464; And 129/SvJ; TISSUE-Spleen; MEDLINE-5531464; PubMed-7541907; MESSUE-Spleen; Mattruecker H.-W. Kiefer F., Kawakami T., Richardson C.n Mak T.W.;
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DISULFID
CARBOHYD
                                                                                                                                                                                                                                                               "Molecular cloning of LSIRF, a lymphoid-specific member of the interferon regulatory factor family that binds the interferonstimulated response element (ISRE).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
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                                                                                                                                Stimulated response element (ISRE).";
Nucleic Acids Res. 23:2127-2136(1995).";
Nucleic Acids Res. 23:2127-2136(1995).
-i- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INTERFERON-
STIMULATED RESPONSE ELEMENT (ISRE) OF THE MHC CLASS I PROMOTER
BINDS THE IMMUNOGLOBULIN LAMBDA LIGHT CHAIN ENHANCER, TOGETHER
WITH PU1. PROBABLY PLAYS A ROLE IN ISRE-TARGETED SIGNAL
TRANSDUCTION MECHANISMS SPECIFIC TO LYMPHOID CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eisenbeis C.F., Singh H., Storb U.;
"Pip, a novel IRF family member, is a lymphoid-specific,
"U.1-dependent transcriptional activator.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95317607; PubMed=7797077; Eisenbeis C.F., Singh H., Storb U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Interferon regulatory factory factor (IFF-4) (Lymphocyte specific interferon regulatory factor) (ISIRF) (NF-EMS) (PU.1 interaction partner)
(Transcriptional activator PIP).
IRF4 OR SPIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01355; HEMATOPO REC S F1; 1.

Receptor; Transmembrane; Glycoprotein;
SIGNAL 1 22 BY SIMILAR
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                                                                                         SUBCELLULAR LOCATION: Nuclear ALTERNATIVE PRODUCTS:
                                                                       Event=Alternative
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                           IsoId=Q64287-1;
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Rodentia;
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                           Sequence=Displayed
                                                                     splicing; Named isoforms=2
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Pred. No.
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CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
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SIMILARITY.
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DR EMBL; U11692; AAA75309.1; -.

DR EMBL; U20949; AAA75317.1; -.

DR EMBL; U20949; AAA75317.1; -.

DR HSSP; P23906; ZIRF.

DR HSSP; P23906; ZIRF.

DR HSSP; P23906; ZIRF.

DR HSSP; P23906; ZIRF.

DR HRSP; P20605; IRF.

DR HRSP; P20605; IRF; 1.

PR MGD; MGI:096873; IRF, 1.

DR PFAM; PF00605; IRF; 1.

DR PFAM; PF00605; IRF; 1.

DR PRINTS; PR00267; INTERNREGECT.

DR PRINTS; PR00267; IRF; 1.

DR PROSITE; P800601; IRF; 1.

DR ALTERNATIS SM00348; IRF; 1.

DR PROSITE; P800601; IRF; 1.

                                                                                                                                                                                                                                                                                  Ouery Match 54.2%; Score 39; DB 1; Length 450; Best Local Similarity 75.0%; Pred. No. 33; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOId=Q64287-2; Sequence=VSP 002756;
-1- TISSUE SPECIFICITY: LYMPHOID CELLS.
-1- INDUCTION: Not induced by interferons.
-1- SIMILARITY: Belongs to the IRF family.
                                                                                                                                              174 HDRSWRDY 181
                                                                                                                                                                                                            5 YDRSWGDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                        450 AA; 51577 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform 2).
/FTId=VSP_002756.
; 5FD94CA6C453869C CRC64;
                                                                                                                                                                                                                                                                                                 0
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
                                                                                                                                                                                                                                                                                                                                    SPTREMBL 25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_fungan:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1017041 segs, 315518202 residues
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Gapop 10.0 , Gapext 0.5
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72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     October 5, 2004, 07:34:11; Search time 6.35185 Seconds (without alignments) 596.081 Million cell updates/sec
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Query
Match Length
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sp_rodent:*
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Q94H68	Q8LNE3	Q9VX04	Q7XQV1	Q8IQZ3	Q87UR0	Q812W2	Q8A3Y6	063409	Q8F7U3	Q97TN7	QBPLM6	Q8 P 9 U 7	Q8G5L7	Q7XF61	Q8SB49	10
Q94n68 Oryza sactv		Q9vx04 drosophila	Q7xqv1 oryza sativ	Q8iqz3 drosophila	Q87ur0 pseudomonas	Q8i2w2 plasmodium	Q8a3y6 bacteroides	Q63409 rattus norv	Q8f7u3 leptospira	Q97tn7 clostridium	Q8plm6 xanthomonas	Q8p9u7 xanthomonas	Q8g517 bifidobacte	Q7xf61 oryza sativ	Q8sb49 oryza sativ	1101101111000

## ALIGNMENTS

RESULT Q7XF61 ID Q AC Q DT 0	음 성	Z B O	SON	무막	2222	28888 88888	8888	DT DT AC	RESULT QBSB49 ID Q
ULT 2 F61 Q7XF61 PRBLIMINARY; PRT; 332 AA. Q7XF61; 01-OCT-2003 (TrEMBLrel. 25, Created)	1 RRSNYDRSWGDY 12                   98 RSKNFDRWWGDW 109	Query Match 63.9%; Score 46; DB 10; Length 332; Best Local Similarity 58.3%; Pred. No. 13; Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	₹	"Rice Genomic Sequence."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL: AC091732: AALT7159.1;	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  Wing R.A., Yu Y., Soderlund C., Chen M., Kim HR., Rambo T.,  Saski C., Henry D., Oates R., Simmons J.;	Spermatorbyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatorbyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Shrhartoideae; Oryzeae; Oryza.  NCBI TaxID-4530;	Putative polyprotein.  CSJNBB0091009.10.  Oryza Sativa (Rice).  Oryza Sativa (Rice).	Q8SB49; 01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)	JLT 1 349 Q8SB49 PRELIMINARY; PRT; 332 AA.

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RESULT

1086SLT

1086SLT

1086SLT

1096SLT

1097SLT

1097
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                                                                                                                                                To the human gastrointestinal tract.";

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

EMBL; AE01472; AAN24800.1; --.

R GO; GO:0005840; C:ribosome; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003735; F:structural constituent of ribosome; IEA.

R GO; GO:0006412; P:protein biosynthesis; IEA.

R InterPro; IPR008994; Nucleic acid OB.

R InterPro; IPR000110; Ribosomal_S1.

R InterPro; IPR003029; S1.

R Pfam; PF00575; S1; 4.

R PSNNTS; PR00681; RIBOSOMALS1.

R SMART; SM00316; S1; 4.
Query Match
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Best Local :
                                                                                                 PROSITE; PS50126; S1; 4. Ribosomal protein; Compl
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Bifidobacteriaceae: Bifid
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Buell C.R., Wing R.A., McCombie W.R., Messing
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ
EMBL; AE017088; AAP53497.1; -.
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STRAIN=CV. Nipponbare;
The Rice Chromosome 10 Sequencing Consortium;
The Rice Chromosome for sequencing Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schell M.A., Karmirantzou
Pessi G., Zwahlen M.-C., I
Pridmore R.D., Arigoni F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=NCC 2705;
MEDLINE=22294977; PubMed=12381787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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01-MAR-2003
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Bukaryota; Viridiplancae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=216816;
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                                                                    Complete proteome 54633 MW; 604AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       teria; Actinobacteridae; Bifidobacteriales; Bifidobacterium.
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   Score 46;
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., Bork P., Delley
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Length 491;
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RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighteri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Meddanis J., Menck C.F.M., Miyaki C.V., Moon D.H.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.V., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Moreira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Texeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Sceubal J.C., Kitajima J.P.;
"Comparison of the genomes of two Xanthomonas pathogens with differing Not specificities.",
Nature 417:459-463(2002)
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                      Query Match
Best Local :
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Matches 6; Conser
                                         01-OCT-2002
01-OCT-2002
01-JUN-2003
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01-OCT-2002
01-JUN-2003
                                                                                  Q8PLM6;
                                                                                                                                                                                                                                                                                                                                                  EMBL; AE012276; AAM41041.1;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA
GO; GO:0005215; F:transporter activity;
GO; GO:0006810; P:transport; IEA.
              TonB-dependent receptor CIRA OR XAC1769.
                                                                                                                                                                                                                                                                                                      PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeid Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 33913 / NCPPB 528;
MEDLINE=22022145; PubMed=12024217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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8; Conserv
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                                         (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
axonopodis (pv.
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72.7%;
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                                         Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                         Score 46; DB Pred. No. 30; 1; Mismatches
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Almeida N.F.,
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SORRED DRAFT

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RP SEQUENCE FROM N.A.

RC STRAIN=306 / ATCC 13902 / XV 101;

RC STRAIN=306 / ATCC 13902 / XV 101;

RX MEDLINE=22022145; PubMed=1202417;

RX MEDLINE=22022145; PubMed=1202417;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Camargo L.E.A.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Martins E.C., Medhadis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Martins E.C., Medhadis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Martins E.C., Medhadis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Martins E.C., Katajima J.P.;

RA Martina E.C., Textita M.A., Sana J.A.D., Silva C., de Souza R.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Camarotticities "."

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:006810; P:transporte activity; IEA.

DR GO; GO:006810; P:transporte processor de la cativity; IEA.

DR GO; GO:006810; P:transporte processor de la cativity; IEA.

DR GO; GO:006810; P:transporte processor de la cativity IEA.

DR GO; GO:006810; P:transporte proces
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Best Local S
Matches
SEQUENCE FROM N.A.

STRAIN=ACCC 824 / DSM 792 / VRM B-1787;

MEDLINE-21359325; PubMed=11466286;

Noelling J., Breton G., Omelchenko M.V., Make Gilson R., Lee H.M., Dubois J., Qiu D., Hitti Tatusov R.L., Sabathe F., Doucette-Stamm L., Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of bacterium Clostridium acetobutylicum.";

Dacteriol. 183:4823-4838(2001).

EMBL, AB001436; AAK76807.1; -.

EMGL, AB001436; AAK76807.1; -.

EOG. GO:00046821; C:extrachromosomal DNA; IEA.

GO; GO:0003700; F:transcription factor activi
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Q97TN7;
Q1-OCT-2001
01-OCT-2001
01-JUN-2003
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Xanthomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pSOL1.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                              Clostridium
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Similarity 72.7%;
8; Conservative
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906 AA; 99417 MV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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        ; IEA.
activity;
                                                                                                                                                                                     , Makarova K.S.,
Hitti J., Wolf
m L., Soucaille
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          IEA
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P., Daly M.J.,
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RESULT CREATED TO THE PROPERTY OF THE PROPERTY
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003723; F:RIA binding; IEA.
GO; GO:0003735; F:structural constituent c
GO; GO:0006412; P:protein biosynthesis; IE
InterPro, IPROUT97; Ribosomal L21p.
Pfam; PF00829; Ribosomal L21p; 1.
ProDom; PD003604; Ribosomal L21p; 1.
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Q8F7U3;
                                                                                                                                                                                                                                                                                          Q63409;
01-NOV-1996
01-NOV-1996
01-OCT-2002
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STRAIN-Sprague-Dawley; Kerr S.M., Taggart M.H., Cooke H.J.; Kerr S.M., Taggart M.H., Cooke H.J.; "Unusally high sequence variation in rodent Ott genes."; Submitted (AUG-1956) to the EMBL/GenBank/DDBJ databases. EMBL; X99901; CAA68173.1; -. NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                      Rattus norvegicus (F
Eukaryota, Metazoa,
Mammalia, Eutheria,
                                                                                                                                                                                                                                                                                                                                                                          Q63409
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Bacteria; Spirochaetes;
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                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    protein
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(TrEMBLrel.
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(Fragment).
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oa; Chordata;
ia; Rodentia;
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22,
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Last
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Last
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Pred. No. 11;
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Sciurognathi; Muridae;
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annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of ribosome;
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; Murinae; Rat
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Best Local S
Matches
MEDLINE=22255708; PubMed=12368867;
Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.
                                                                                                                                                                                                                                                                01-MAR 2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DNAJ-like molecular chaperone protein, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete
SEQUENCE
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STRAIN-VPI-9482 / ATCC 29148;

MEDLIXE=22500858; PubMed=12663928;

Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

Chiang H.C., Hooper L.V., Gordon J.I.;

"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";

Science 299:2074-2076(2003).
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                                                                                                                                                                                               Plasmodium falciparum
Eukaryota; Alveolata;
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InterPro; IPR008969; CarboxypepD_reg.
InterPro; IPR008531; TonB_boxC.
Pfam; PF00593; TonB_dep_Rec; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE016937; AA077924.1;
GO; GO:00048020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA
GO; GO:0005215; F:transporter activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteroides thetaiotaomicron.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
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01-JUN-2003
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Ol-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Ol-JUN-2003 (TrEMBLrel. 25, Last sequence update)
Putative outer membrane protein, probably involved in nutrient
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=36329;
                                                                                                                                                                                                                                                   PFI0935W
                                                                                                                                                                                                                                                                                                                                                                          Q8I2W2;
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224 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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26983 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.7%;
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                                                                                                                                                                                                                         (isolate 3D7)
                                                                                                                                                                                               Apicomplexa;
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Pred. No. 26;
0; Mismatches
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Pred. No. 1.4e+02;
3; Mismatches 1;
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                                                                                                                                                                                  Haemosporida; Plasmodium
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· IEA.
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RESULT 12
Q8IQZ3
ID Q8IQ2
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Q87UR0
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                                                                                                                                                                                                                                        Buell R., Joardar V., Khouri H., Fedorova N., Tran B., R
Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn
Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., D
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W.,
White O., Fraser C., Collmer A.;
"Complete sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q87UR0 PRELIMINARY;
Q87UR0;
Q1-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                             EMBL; AE016875; AA058662.1;
TIGR; PSPT05236; -.
                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical PSPT05236.
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PROSITE; PS50076; DNAJ_2; 1.
SEQUENCE 370 AA; 43260 MW;
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GO; GO:0003754; F:chaperone
InterPro; IPR001623; DnaJ_N
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                                                                                                                                                                                                  Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=323;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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37 AA; 40
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4088 MW; F676ECF84E728069 CRC64;
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75.0%;
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72.7%;
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Pred. No. 5.
1; Mismatche
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Last sequence update)
Last annotation updat
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Pred. No. 55;
2; Mismatches
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                                                                                                                        ed. No. 5.4;
Mismatches
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n W., Davidsen
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Q8IQZ3

PRELIMINARY;

PRT;

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RX MEDILINE 20196016; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gorayne J.D.,
RA Ammanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Ammanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Plazed R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Basu A., Baxer B.G., Helt G., Welson C.R., Gabor G.L.,
RA Ballew R.M., Basu A., Baxer B.G., Helt G., Welson C.R., Gabor G.L.,
RA Ballew R.M., Basu A., Baxerdale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bandari D.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bendari I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Deller A., Deng Z., Mays A.D., Dew I. Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Barraz C., Ferriera S., Fleischmann W.,
RA de Pablos B., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Mattei B., McIntosh T.C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Shen H.,
RA Shie B.C., Siden Kianson S., Sanders R.D., Scheeler F., Shen H.,
RA Shie B.C., Siden Kianson S., Sanders R.D., Scheeler F., Shen H.,
RA Shie B.C., Schen Kianson S., Sanders R.D., Scheeler F., Shen H.,
RA Shie B.C., Shen S., Sander
                                                                    RA Gonzalez M., Houck J., Hoskins R.A., Matreira B., Walter B., Walter B., Wank K.H., Holt R.A., Rogers Y., Alams C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Ra Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., RA Bonzon J.W., Center A., Champe M., Davenport L.B., Dietz S.M., RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F., RA Pacleb J., Faragas V., Park S., Patel S., Fielfer B., Scheeler F., RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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CG32496-PA.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster
Misra S., Crosby M.A.,
Hradecky P., Huang Y.,
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  Bayraktaroglu L., Campbell Prochnik S.E., Smith C.D.,
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RESULT Q9VX04 ID Q9

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Q7XQVI
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Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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InterPro; IFR002181; Fibrinogen_C.
Pfam; Pr00147; fibrinogen_C; 1.
SMART; SM00186; FBG; 1.
PROSITE; PS00514; FIBRIN AG C DOMAIN;
SEQUENCE 251 AA; 29077 MW; FE87890
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SEQUENCE 356 AA;
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RX MEDLINGE-2019606; PubMed=10731132;
RX Adams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Andams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Andams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ananatides P.O., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Baridon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pteiffer B.D., RA Man K.H., Doyle C., Baxter E.G., Helt G., Walson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ra Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Belshakov S., Ra Ballow R.M., Basu A., Danter H., Cadieu E., Center A., Chandra I., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra de Pablos B., Delcher A., Dong Z., Mays A.D., Dew I., Davies P., Ra de Pablos B., Delcher A., Dong Z., Mays A.D., Dew I., Davies P., Ra de Pablos B., Collega F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., A Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Feltman G.S., Penn S., Pollard J., Puri V., Reese M.G., Ra Mount S.M., Welsen D.A., Weinsten D.R., Weinsten D.R., Weinsten D.R., Weinsten D.R., Weinsten D.R., Weinsten D.R., Weinstenbach J., Ra Alai M., Weinstenbach J., Ra Alai M., Kalush F., Zanders R.D.C., Scheeler F., Shen H., Ra Spier E., Zhan M., Zhang G., Zhao Q., Zheng L., Paradina M., Zhang G., Zh
                                                               Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

A Carlson J. W., Center A., Champe M., Davenport I.B., Dietz S.M.,

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A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Moshrefi A.,

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A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Moshrefi A.,

A Gonzalez M., Houck J., Wilson C., Nattei B., Moshrefi A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Hostin B., Moshrefi A.,

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A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A Pacleb J., Paragas V., Park S., Patel S., Pfeifer B.,

A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

A Stapleton M., Strong R., Svirskas R., Teotor C., Tyler D.,

Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

"Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Neoptera; Endopterygota; Diptera, Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Q8LNE3;
01-OCT-2002 (TrEMBLrel. 2
01-OCT-2002 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
                                                                                           STRAIN=cv. Nipponbare;
McCombie W.R., de la Bastide M., Spiegel L., Preston R.,
Kuit K., Nascimento L., Zutavern T., Balija V., Bell M.,
Miller B., Katzenberger F., Muller S., King L., Sullivan
Dike S., C'Shaughnessy A., Palmer L., Dedhia N.;
"Genomic sequence for Orzas sativa, Nipponbare strain, cl
OSJNBA0044A10, from chromosome 10, complete sequence.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
SEQUENCE
SEQUENCE FROM N.A. STRAIN=cv. Nipponbare; The Rice Chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical proof. OSJNBA0044A10.6
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                                                                                                                                                                                                                                                                  STRAIN-cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00147; fibrinogen_C; 1.
SMART; SM00186; FBG; 1.
PROSTITE; PS00514; FIBRIN_AG_C_DOMAIN;
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FlyBase; FBgn0030880; CG6788.
InterPro; IPR002181; Fibrinogen_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2002) to the EMBL; AE003507; AAF48780.2; EMBL; AY119053; AAM50913.1; HSSP; P02671; 1FZD.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=39947
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e EMBL/GenBank/DDBJ
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Baker J.,
1 P., Yang (
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1997年 日本海上

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"In-depth view of structure, activity, and evolution of rice RT chromosome 10.";
RL Science 300:1566-1569(2003).

RN [3]
RP SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RP SUBMITTER (MAY-2003) to the EMBL/GenBank/DDBJ databases.

Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.

BR EMBL; AC003943; AAM72666.1; -.

DR EMBL; AC003943; AAM72666.1; -.

DR EMBL; AC003943; AAM7266.1; -.

DR EMBL; AC003943; AAM7266.1; -.

R EMBL; AC003943; AAM7266.1; -.

SQ SEQUENCE 395 AA; 43122 MW; 3C9BD1816E36E9F2 CRC64;

Query Match
SEQUENCE 395 AA; 43122 MW; 3C9BD1816E36E9F2 CRC64;

Query Match
Best Local Similarity 50.0%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

SQ 1 RRSNYDRSWGDY 12

Db 1 RRSNYDRSWGDY 12

Db 56 RSKNFDRWGEW 67

Search completed: October 5, 2004, 08:13:31

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Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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# SUMMARIES

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### ALIGNMENTS

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RESULT 1
AAE10547
                                                                                                  AAE10547 standard; peptide; 12 AA.
Llama species antibody VHH CDR3 #16.
                                   10-DEC-2001
                                                                AAE10547;
                                   (first entry)
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Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.

EP1134231-A1. 19-SEP-2001. Lama ds.

(UNIL ) UNILEVER PLC.

20-FEB-2001; 2001EP-00200703.

14-MAR-2000; 2000EP-00200930.

Bezemer S, Van De Burg M, De Haard JJW, Tareilus Ħ

WPI; 2001-572718/65.

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Claim 4; Page 29; 37pp; English.

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region

Length 129;

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Best Local Similarity

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                                             The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings.
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resent peptide sequence is HPL inhibiting VHH fragment, (camelid) species

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Sequence 129 AA

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The present invention describes a polynucleotide (I) comprising a CC sequence of a Biidobacterium genome selected from the nucleotide CC sequences given in ABQ81842 and ABQ81843, or a sequence exhibiting at CC least 90% identity or which hybridises with the sequences given in CC ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding a CC in ABBC6258 to ABBC6354 ligated in frame to a polynucleotide encoding a CC heterologous polypeptide. (I) has antidiarrheic and antibacterial CC aprobe) is useful for the detection and/or identification of Bifidobacterium longum in a biological sample. A carrier containing the CC lactic acid bacterium gently creating diarrhoea brought about by pathogenic CC bacteria and/or rotavirus. The carrier is a food composition selected from milk, yogurt, curd, cheese, fermented milks, milk based fermented creams, infant formula, pet food or a pharmaceutical composition selected from tablets, liquid bacterial suspensions, dried oral supplement, wet oral supplement, dry tube feeding or wet tube feeding. CC expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent Bifidobacterium related nucleotide sequences given in the Sequence CC in the princed specification but is based on sequence information. N B. The sequence data for this patent is not represented in the princed specification but is based on sequence information.
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ABP65839
ID ABP6
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotide comprising a probe or primer for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in a biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rotavirus; food composition; pharmaceutical composition.
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12; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 583; 80pp; English.
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100.0%; Pred. No. 0.00026;
live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bifidobacterium genome sequence useful as and/or identifying Bifidobacterium longum
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RESULT 5
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Best Local S
Matches 6
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Best Local S
Matches 7
                                                                                                                                        The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human baings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Llama antibody; camelid; anorectic; heavy chain variable domain human dietary enzyme inhibitor; medicament; human pancreatic life food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.
                                                                                                                                                                                                                                                         New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
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                                                                                                                         Sequence
                                                                                                                                                                                                                                 Claim 4; Page 29;
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         AAE10558
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UNILEVER PLC.
                                                                                       Similarity 7; Conserv
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         standard;
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        peptide; 129
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54.5%;
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Pred.
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27;
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lipase; HPL;
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ABG01095
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DT 13-F
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                               Bezemer
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                                      protein;
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70.0%;
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13-FEB-2002

(first

entry)

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The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #22 from llama (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 10; 37pp; English.
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/note= "Complementarity
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110
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Pred. No. 14;
1; Mismatches
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) C sequences, (I) is useful as hybridisation probes, polymerase chain CC reaction (PCR) primers, oligomers, and for cromosome and gene mapping, CC and in recombinant production of (II). The polynucleotides are also used Ci in diagnostics as expressed sequence tags for identifying expressed conditions, (I) is useful in gene therapy techniques to restore normal C constituty of (II) or to treat disease states involving (II). (II) is C useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging CC of sites expressing (II). (I) and (II) are useful for treating disorders involving abserrant protein expression or biological activity. The CC polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in CC electronic format directly from Wipo at the control of the 
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Best Local
         Human polypeptide SEQ ID NO 19277
                                                                                                    AA005385;
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                                                      06-NOV-2001
                                                                                                                                          AAO05385 standard; protein; 137 AA
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          Length 110;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system discorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                  Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                     ABB62687 standard; protein; 274
            27-SEP-2001.
                                                                    Drosophila melanogaster
                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 14853
                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                          ABB62687;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 137 AA;
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N-PSDB; AAI85316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 19277; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acids and polypeptides, useful for and treating e.g. leukemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; hammonmodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                         Similarity 54.
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                                                                                                                                                                                                                                                                                                                                                                                      Score 42;
Pred. No.
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                                                   03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
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11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                              Human, cytokine, cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
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                                                                                                                                                                                                  05-FEB-2001; 2001WO-US004098
                                                                                                                                                                                                                                     09-AUG-2001.
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   (HYSE-) HYSEQ INC
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                                                   2000US-00496914
2000US-00560875
2000US-00598075
2000US-00698075
2000US-00620325
2000US-0064936
2000US-00663561
2000US-00663561
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2000US-00614150.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers
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Tang YT, Liu C,
Ma Y, Zhao QA,
Xue AJ, Yang Y,
WPI; 2001-476283/51.
             Wang D, W
, Wejhrman
                           Drmanac
              RT,
Wang
n T,
              Asundi V,
J, Zhang
Goodrich R
                     Ç
                       Xu C,
Chen
                     Cao
                       Y;
Wang
                        ZW;
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Nucleic acids encoding polypeptides with cytokine-like in diagnosis and gene therapy. activities, useful

Claim 20; Page 416; 6221pp; English.

The invention relates to polynucleotides (AAKS1456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, interest to cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NC 2110 (AAKS2581), 2111 (AAKS2582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication

Sequence 318 AA;

Similarity 6; Conserv Conservative 58.3%; 60.0%; 2; Score 42; DB Pred. No. 80; Mismatches 4 ν, Length 318 0

0

ABB82900 standard; protein; 3657

Human SMG-1 protein

SMG-1; phosphatidyl-inositol kinase-associated kinase; cytostatic; antibiotic; cancer; human; enzyme.

sapiens.

WO200295025-A1

28-NOV-2002

22-NOV-2001; 2001WO-JP010234

24-MAY-2001; 2001JP-00156088

(NISC-) JAPAN SCI & TECHNOLOGY CORP

WPI; 2003-120802/11. N-PSDB; ABZ24084.

New SMG-1 (phosphatidyl-inositol kinase-associated kinase), diagnosing and screening drugs for pathological conditions formation of an early transcription termination codon e.g. lung cancer. caused by

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RESULT 11
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CCC (HCGCII
CCC (HCCC)
CCC 
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Matches 6
                                                                                                               Sequence 314 AA;
                                                                                                                                                                                                                                                                                                                                                Hepatic parenchymal cell growth promoter peptide - is isolated from human or animal liver cell or produced by recombinant techniques and used for therapy of liver diseases.
                                                                                                                                                           AAQ77818 encodes AAR65759 rat hepatic parenchymal cell growth factor (HPGF). The protein or the N-terminal peptide (AAR65758) may be used in the diagnosis and treatment of liver diseases, such as liver cancer and cirrhosis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                           Claim 3; Page 34; 47pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-316940/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatic parenchymal cell growth factor; HPGF; liver diseases; liver cancer; cirrhosis.
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17-MAY-1995
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     Similarity
8; Conserv
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        Conservative
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                           56.98;
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     2;
     Score 41; DB 2;
Pred. No. 1.2e+02;
2; Mismatches 2
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1.1e+03;
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RESULT 13
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                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                    Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                    The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
Human; chromosome mapping; gene mapping; gene therapy; forensic;
                            Novel human diagnostic protein #23656.
                                                        18-FEB-2002
                                                                                    ABG23665;
                                                                                                             ABG23665 standard; protein; 236
                                                                                                                                                                                                                                                                                              Sequence 415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1280; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-120786/11
N-PSDB; ACF72960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Masignani V, Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-2001; 2001GB-00007661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibacterial; vaccine; gene therapy; enzymatic assay; antibiotic target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2002; 2002WO-IB002637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
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7; Conserv
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Pred. No. 1.6e+02;
                                                                                                             ΑA
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ABG15428
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XXX Human
KW Hood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 54024; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 236
                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                Novel human
                                                                                               18-FEB-2002
                                                                                                                                                              ABG15428 standard; protein; 293
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                                                              diagnostic protein #15419.
                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 1.3e+02;
0; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
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23-AUG-2000; 2000US-00649167
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                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                   Novel human diagnostic protein #2090.
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DB; AAS79615.
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) C sequences. (I) is useful as hybridisation probes, polymerase chain C reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polynucleotides are also used C genes. (I) is useful in gene therapy techniques to rescore mormal CC useful for generating antibodies against it, detecting or quantitating a CC useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging CI involving aberrant protein expression or biological activity. The CC involving aberrant protein expression or biological activity. The CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in CC electronic format directly from WIPO at CC fip.wipo.int/pub/published_pct_sequences
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N-PSDB; AAS66286.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                  probable thiosulfate sulfurtransferase - Mycobacterium tuberculosis (strain H37RV C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: G70809; D70921 C;Accession: G70809; D70921 G;Accession: G70809; D70921 G; Garnier, T.; Churcher, C.; Harris, D.; Go: R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go: Connor, R.; Davies, R.; Devlin, K.; Feltwell; T.; Gentles, S.; Hamlin, N.; Holro, Connor, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: G70809
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G70809
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B70455
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A; Residues: 1-293 < AGDF>
A; Cross-references: GB:AE000757; NID:g2984092; PIDN:AAC07633.1; PID:g2984095; GB:AE00065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: B70455
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C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
C;Accession: B70455
                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-277 <COL>
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C;Superfamily: thiosulfate sulfurtransferase
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R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                 A;Cross-references: GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAA17621.1; PID:g291687:
A;Experimental source: strain H37Rv
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A; Molecule type: DNA
                                                      A; Accession: D70921
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                             preliminary; nucleic acid sequence not shown;
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7; Conservative
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87.5%;
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A; Map p
A; Note:
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Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: A87184
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                            hypothetical protein T16L1.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr.1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C;Accession: A87184
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C;Superfamily: thiosulfate sulfurtransferase
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A;Cross-references: GB:Z95150; GB:AL123456; NID:g3250708; PIDN:CAB08374.1; PID:g2076692
A;Cxoss-references: GB:Z95150; GB:AL123456; NID:g3250708; PIDN:CAB08374.1; PID:g2076692
A;Experimental source: strain H37Rv
C;Comment: There are two identical copies of this protein in the Mycobacterium tubercul
                                                                                                                                                                                                              A;Reference number: Z15393
A;Accession: T04976
A;Molecule type: DNA
A;Residues: 1-466 <BEV>
                                                                                                                                                                                                                                                                              R;Bevan, M.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, November 1998
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A; Residues: 1-277 < STO>
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                                                                                                                               ;Map position: 4
;Note: T16L1.80
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Best Local
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134 VDEHDGSWNSY 144
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                                                             Similarity 6; Conserv
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6; Conservative
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                               ISSYDGSWNDY 12
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Pred. No. 2.
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Feltwell, T.;
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Fraser, A
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RESULT
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A;Description: Sulfolobus solfataricus complete genome.
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flagellar hook-basal body complex protein (flho) homolog -
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                                                                                                                                                A;Gene: cysA-1
C;Superfamily: thiosulfate sulfurtransferase
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A;Residues: 1-278 <KUR>
A;Cross-references: GB:AE006641; NID:g13814200; PIDN:AAK41282.1; GSPDB:GN00155
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A; Accession: C90253
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Best Local Similarity
When 8; Conserve
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A; Introns: 64/3; 350/3; 543/3; 572/3; 623/3; 775/1; 890/3; 1061/3; 1371/2
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A;Molecule type: mRNA
A;Residues: 1-1415 <MAT>
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
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A;Accession: T42392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, July 1995
A;Reference number: Z19395
A;Accession: T21244
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A;Cross-references: EMBL:Z50044; PIDN:CAA90359.1; GSPDB:GN00020; CESP:F22B5.7
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58.3%;
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Pred. No. 36;
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Pred. No. 8.
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: A70340
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-319 <AQF>
                                                                                                                                                               R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: F70196
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C;Accession: F70196
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C; Superfamily:
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A;Accession: G82436
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A; Residues: 1-276 < HEI>
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A; Residues: 1-300 < K
                                                                                                                            Nature 392, 353-358, 1998
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;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.;
;on, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
fature 390, 580-586, 1997
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;Cross-references: GB:AE001177; GB:AE000783; NID:g2688711; PIDN:AAC67131.1; PID:g26887:
;Experimental source: strain B31
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H.; Dragoi, I.; Sellers,
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R;Su, Z.H.; Tominaga, O.; Okamoto, M.; Osawa, S. Mol. Biol. Evol. 15, 1026-1039, 1998
A;Title: Origin and diversification of hindwingless Damaster A;Reference number: 217319; MUID:98384842; PMID:9718730
A;Accession: T14014
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Mol. Biol. Evol. 15, 1026-1039, 1998
A;Title: Origin and diversification of hindwingless Damaster
A;Reference number: Z17319; MUID:98384842; PMID:9718730
A;Accession: T14012
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Superfamily: CBS homology
F;203-250/Domain: CBS homology <CBS>
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C;Genetics:
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A;Variety: isolate Gifu
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
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                                                                    A;Genome: mitochondrion C;Superfamily: NADH deh: C;Keywords: membrane-as
                                                                                                                                      A;Cross-references: EMBL:D50427; PIDN:BAA08923.1
A;Experimental source: isolate Gifu; adult; thorax muscle
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A; Residues: 1-355 < SUZ>
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C;Keywords: men
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A; Residues: 1-355 < SUZ>
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submitted to the EMBL Data Library, January 1999
A;Reference number: Z20512
A;Accession: T28698
A;Molecuity preliminary.
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T28698
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C;Superfamily: NADH dehydrogenas
C;Keywords: membrane-associated
                                                            R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA-Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyz A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: D72494
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                                                                                                                                                                                            C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision
C;Accession: D72494
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A;Cross-references: EMBL:AL023496; NID:e1292348; PID:e1292365; PIDN:CAA18915.1
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A; Residues: 1-2314 <
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A;Molecule type: DNA
A;Residues: 1-355 <SUZ>
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <KAV
                                                                                                                                                                                                                                                               probable thiosulfate sulfurtransferase APE2595 - Aeropyrum pernix (strain K1
                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jetherance: mitochondrion
;Genome: mitochondrion
;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
;Superfamily: Mambrane-associated complex; mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Accession: T14016
;Su, Z.H.; Tominaga, O.; Okamoto, M.; Osawa, S.
ol. Biol. Evol. 15, 1026-1039, 1998
ol. Fitle: Origin and diversification of hindwingless Damaster;Reference number: Z17319; MUID:98384842; PMID:9718730;Accession: T14016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Species: Streptomyces coelicolor
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
;Accession: T28698
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6; Conserve
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Pred. No. 1.9e+0;
2; Mismatches
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Pred. No. 25;
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K;rarKnill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead. S. Barralli Nature 413, 523-527, 2001
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Search completed: October Job time : 2.94444 secs
                                                                                                                                                                                                                                                                                                                                    A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AH0146
                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable sulfurtransferase YPO1194 [imported] - Yersinia pestis (strain CO9 C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001 C;Accession:_AH0146
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C;Superfamily: thiosulfate sulfurtransferase
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A;Residues: 1-284 <KUR>
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ASTL COTUMAN
121R HUMAN
121R HUMAN
121R HUMAN
1206 BPT4
1065 BPT4
1HTM ECOLT
THIM ECOLT
THIR BOVIN
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IL3_SAGOE
NODH_RHITF
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CYRB_MOUSE
IL3_CALJA
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 P25324
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3 mycobacteri
5 saccharopol
4 gallus gall
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6 vibrio furn
0 schizosacch
2 chlamydia p
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8 mycobacteri
7 rhizobium s
escherichia
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bos taurus
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ALIGNMENTS

#### RESULT 1 THT1 MY D THT1 MY D THT1 MY AC P59989 DT 15-MAR MEDITURE 22709107; PubMed=12788972; Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H., Garnier T., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Prov M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003). Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003). -i- FUNCTION: May be a sulfotransferase involved in the formation of thiosulfate (By similarity). -i- CAPALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate. -i- SIMILARITY: Contains 2 rhodanese domains. EMBL; EX248336; CAD93700.1; PROSITE; PS00380; RHODANESE 1; FALSE\_NEG. PROSITE; PS00683; RHODANESE 2; 1. PROSITE; PS50206; RHODANESE 3; 2. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 15-MAR-2004 (Rel. 43, Created) 15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Putative thiosulfate sulfurtransferase 1 (EC protein 1). THT1\_MY Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. SEQUENCE FROM N.A. STRAIN=AF2122/97; NCBI\_TaxID=1765; Mycobacterium bovis. MYCBO STANDARD; 277 2.8.1.1) (Rhodanese-like

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255

VKNYDGSWTEY 265 ISSYDGSWNDY 12 Query Match Best Local S Matches 6

Similarity 6; Conserv

Conservative

68.1%; 54.5%;

Score 47; DB 1; Pred. No. 1.1; 3; Mismatches 2

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DOMAIN
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154 233 277 *1* 

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AC37B715D99565A9 CRC64;

Transferase; Repeat; Complete proteome.

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18 125 RHODANESE 1.

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154 274 RHODANESE 2.

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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R.M., Devlin K., Duthoy S., Fellwell T., Fraser A., Hamlin N.,

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

Rutter S., Seeger K., Simnon S., Simmonds M., Skelton J., Squares R.,

Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

Barrell B.G.;

"Maccino."
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15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
15-MAR-2004 (Rel. 4
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                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYCLE
                                                                                                                                                                                                                                                                    Pfam; PF00581; Rhodanese; 2. SMART; SM00450; RHOD; 2.
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EMBL; AL583924; CAC31153.1;
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Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                      PIR; A87184; A87184.
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-!- SIMILARITY: Contains 2 rhodanese domains.
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CYSA OR CYSA3
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InterPro; IPR001307; Rhodanese.
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CATALYTIC A
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233
277 A
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18 125 RHOI
154 274 RHOI
233 233 BY (
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                                                                                                   Conservative
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                                                                                                                                                                                                                          RHODANESE_1; FALSE_NEG.
RHODANESE_2; 1.
RHODANESE_3; 2.
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....ranaferase (EC 2.8.1.1)
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RHODANESE
RHODANESE
BY SIMILAR
                                                                                                                Score 47; DB 1;
Pred. No. 1.1;
                                                                                                                                                                   HODANESE 1.
HODANESE 2.
Y SIMILARITY.
                                                                                                                                                        527E05C9FE93969D CRC64;
                                                                                                   Mismatches
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    thiocyanate

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                                                                                   PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S
Hornsby T., Jagels K., Krogh A., Mclean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z95150; CAB08374.1; -- EMBL; AL022004; CAAL7621.1; -- EMBL; AE006973; AAK45079.1; -- EMBL; AE007136; AAK47539.1; -- EMBL; G70809; G70809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22206494; PubMed=12218036; MEDLINE=22206494; PubMed=12218036; Elsen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Bisen J.A., Gwinn M., Haft D., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M., Ermolaeva M., Salzberg S Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S Kolonay J.F., Nelson W.C., Umayam J., Khouri H., Gill J., Mikula Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M., "Whole-genome comparison of Mycobacterium tuberculosis clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature
[2]
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(CYSA1 OR CYSA OR RV3117 OR MT3199 OR MTCY164.27) AND (CYSA2 OR RV0815C OR MT0837 OR MTV043.07C).
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15-JUL-1998 (Rel. 36, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Putative thiosulfate sulfurtransferase (EC 2.8.1.1)
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SMART; SM00450; RHOD; 2.
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InterPro; IPR001763; Rhodanese-like
InterPro; IPR001307; Rhodanese.
                                                                                                                                                                                                                                                                                                                                 HSSP; P00586; 1RHS.
TIGR; MT0837; -.
TIGR; MT3199; -.
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PS00683;
PS50206;
                                                             Repeat;
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                                                                                   RHODANESE 1; FALSE_NEG RHODANESE 2; 1. RHODANESE 3; 2.
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RHODANESE
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Gill J., Mikula A.,
C.M.;
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P16385;
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SEQUENCE
                                                                                                                                                                                         DOMAIN
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharopolyspora erythraea (Streptomyces erythraeus).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacterio.
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J. Bacteriol. 172:350-360(1990).
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                                                                                                                                                                                                                                                                                                             PROSITE; PS00380; RHODANESE_1;
PROSITE; PS00683; RHODANESE_2;
PROSITE; PS50206; RHODANESE_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M29612; AAA88535.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00581; Rhodanese;
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InterPro; IPR001307; Rhodanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thiosulfate.
CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate CATALYTIC ACTIVITY = CONSISTS OF 2 DOMAINS OF VERY SIMILAR COMPAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR COMPONENTION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER, THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
SIMILARITY: Contains 2 rhodanese domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFORMATION, SUGGESTING A COMMON E
THE SEQUENCES OF THE 2 DOMAINS ARE
-!- SIMILARITY: Contains 2 rhodanese dc
PIR; A37209; A37209
HSSP; P00586; IRHS.
InterPro; IPR001763; Rhodanese-like.
InterPro; IPR001307; Rhodanese.
Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992
01-MAY-1992
10-OCT-2003
                                                                                                                         THTR RAT P24329; 01-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THTR CH
P25324;
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                                                                               01-MAR-1992
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00380; RHODANESE_1; 1.
PROSITE; PS00683; RHODANESE_2; 1.
PROSITE; PS50206; RHODANESE_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kohanski R.A., Heinrikson R.L.;
"Primary structure of avian hepatic rhodanese.";
J. Protein Chem. 9:369-377(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thiosulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91113289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                           Thiosulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Mitochondrial matrix.
TISSUE SPECIFICITY: Expressed in numerous tissues.
DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: Thiosulfate + cyanide =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHICK
                                                                                                                                                                                                                                                                        265
                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                  Similarity
5; Conserv
                                                                                                                                                                                                                                                                        VAVYDGSWSEW 275
                                                                                                                                                                                                                                                                                                               ISSYDGSWNDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                        289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 22, Last sequence update)
(Rel. 42, Last annotation update)
sulfurtransferase (EC 2.8.1.1) (Rhodanese)
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(Rel.
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(Rel.
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                                                               sulfurtransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22,
42,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244
245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158
284
186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
Veognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                        32286 MW;
                                                                                                                                                                                                                                                                                                                                                                           59.48;
45.58;
                                                                                 Last
                                                                                                                             Created)
                                                           annotation update)
ase (EC 2.8.1.1) (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAINS ARE VERY DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHODANESE 2.

MAY PLAY A ROLE IN SUBSTI-
SIMILARITY).

BY SIMILARITY.
SUBSTRATE (THIOSULFATE) I
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat.
RHODANESE
                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBSTRATE (THIOSULFATE) (BY SIMILARITY).
    Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                        8BFCF671DE0B2BA4
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domains.
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                                                                                                                                                                     295 AA.
    Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
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                                                               (Rhodanese)
                                                                                                                                                                                                                                                                                                                                                                                            Length 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sulfite + thiocyanate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND CYANIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                               (Fragment).
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                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95332330; PubMed=7608189; Magahara N., Okazaki T., Nishino T.; Nethino T.; Nishino T.; "Cytosolic mercaptopyruvate sulfurtransferase is evolutionarily related to mitochondrial rhodanese. Striking similarity in activation acid sequence and the increase in the mercaptopyruvate sulfurtransferase activity of rhodanese by site-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                            HSSP; P00586; 1RHS.
InterPro; IPR001763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                            SEQUENCE
                                                                                         MUTAGEN
                                                                                                                                                                                          ACT_SITE
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X56228; CAA39677.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;
                                                                                                                       MUTAGEN
                                                                                                                                                               ACT_SITE
                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                             PROSITE
                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001307; Rhodanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning, sequencing and characterization of cDNA to liver rhodanese, a thiosulphate sulphurtransferase."; Biochem. J. 275:227-231(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Sprague-Dawley; TISSUE-Liver; MEDLINE=91207296; PubMed=2018478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weiland K.L.,
                                                                                                                                                                                                                                                                                                                                                                          nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Mitochondrial matrix.
TISSUE SPECIFICITY: Expressed in numerous tissues.
DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIN
COMFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN.
THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
SIMILARITY: Contains 2 rhodanese domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOL. Chem. 270:16230-16235 (1995).
FUNCTION: INVOLVED IN THE FORMATION OF IRON-SULFUR COMPLEXES, FUNCTION: INVOLVED IN THE FORMATION OF SULFUR-CONTAINING CYANIDE DETOXIFICATION OR MODIFICATION OF SULFUR-CONTAINING ENZYMES. OTHER THIOL COMPOUNDS, BESIDES CYANIDE, CAN ACT AS SULFUR-CEPTORS. ALSO HAS WEAK MERCAPTOPYRUVATE SULFURTRANSFERASE ION ACCEPTORS. ALSO HAS WEAK MERCAPTOPYRUVATE SULFURTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                          S15081; S15081.
 Similarity
5; Conser
                                                                                                                                                                                                                                                                                                   PS00683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVITY
                                                            295
                                                                                         248
                                                                                                                                                                                               142
142
171
185
                                                                                                                                                                                                                                                                        Mitochondrion;
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                                                          AA;
                                                                                                                                                                                                                                                                     ; RHODANESE 1; 1.
; RHODANESE 2; 1.
; RHODANESE 3; 2.
; Chondrion; Repeat.
                                                                                                                  246
247
248
247
                                                                                                                                                                                             141
157
286
185
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                                                          33176 MW;
            59.48;
                                                                                                                                                                                                                                                                                                                                                                              Rhodanese-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is not removed.
Score 41; DB
Pred. No. 12;
5; Mismatches
                                                                                                                                                               RHODANESE 2.
MAY PLAY A ROLE :
SIMILARITY).
BY SIMILARITY.
                                                                                    SUBSTRATE (THIOSULFATE) BINDING.
SUBSTRATE (THIOSULFATE) BINDING.
R->G: UNATTERED RHODANESE ACTIVITY;
INCREASED MST ACTIVITY.
INCREASED MST ACTIVITY.
                                                                                                                                                                                               RHODANESE
MAY PLAY A
                                                                         UNALTERED MST ACTIVITY
                                                                                                                                                                                                                                         RHODANESE
                                                            24C55B35690934E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.
                            Usage
                                                                                                                                                                                             IN SUBSTRATE BINDING
۲.
                            Length 295;
                                                            CRC64;
   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
MBL outstation -
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ID THT2_MYCLE

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Query Match
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wheeler P.R., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96084954; PubMed=7489918;
Doukhan L., Predich M., Nair G., Dussurget O., Macole S.T., Smith D.R., Smith I.;
"Genomic organization of the mycobacterial sigma Gene 165:67-70(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U00012; AAA85919.1; -. EMBL; AL583919; CAC30237.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last amoutation update)
28-FBB-2003 (Rel. -41, Last amoutation update)
Putative thiosulfate sulfurtransferase sseA (
SSEA OR MI0728 OR B1308_C1_127.
                                                                                                                                                                                                                                                                                                          Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=96084954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium leprae.
Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Contains 2 rhodanese domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001763; Rhodanese-like InterPro; IPR001307; Rhodanese.
                                                                                                                                                                                                                                                                                                                                                                                                               eproma; ML0728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A87000; A87000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             P52197; 1E0C
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Similarity 5; Conserv
                                                                                                                                                                                                                                   PS00683;
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                                                                                                                                                                                                                                                                                       PS00380;
                                                                                                     296
                                                                                                                                                         168
                                                                                                                                                                            )00380; RHODANESE 1; 1.
)0683; RHODANESE 2; 1.
;0206; RHODANESE 3; 2.
protein; Transferase; Complete
31 138 RHODANDON
                                                                                                     AA;
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                                                                                                        33235 MW;
                     59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thiosulfate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinobacteridae; Actinomycetales;
Score 41; DB
Pred. No. 12;
4; Mismatches
                                                                                                                           RHODANESE 1.
RHODANESE 2.
BY SIMILARITY.
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THTR CRIGR P46635; 01-NOV-1995 01-NOV-1995 28-FEB-2003

(Rel. 32, Created)
(Rel. 32, Last sequence up
(Rel. 41, Last annotation
sulfurtransferase (EC 2.8)

tion update)
2.8.1.1) (Rhodanese)

update)

296

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Query Match
Best Local
            Matches
                                                                                                                                             EMBL; U23943; AAB84305.1; -.
HSSP; P00588; IRHS.
InterPro; IPR001763; Rhodanese-like.
InterPro; IPR001307; Rhodanese.
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                                                                                                                PROSITE; PS00380; RHODANESE 1; PROSITE; PS00683; RHODANESE 2; PROSITE; PS50206; RHODANESE 3;
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INIT_MET
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           Similarity
5; Conserv
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24 142
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SEQUENCE FROM N.A. TISSUE=Uterus;

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(See http://www.isb-sib.

.ch/announce/

There are no

restrictions on EMBL

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collaboration

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Trevino R.J., Hunt J., Horowitz P.M., Chirgwin J.M.; Chinese hamster rhodanese cDNA: activity of the expressed protein blocked by a C-terminal extension."

Protein Expr. Purif. 6:693-699(1995).

-I-- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE

K.

DETOXIFICATION. BINDS MOLECULAR OXYGEN AND SULFUR.
CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Mitochondrial matrix.
DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
SIMILARITY: Contains 2 rhodanese domains.

MEDLINE=96106946; PubMed=8535164; Trevino R.J., Hunt J., Horowitz P.M.,

Mammalia; Eutheria; Cricetulus.

NCBI\_TaxID=10029;

N.A.

Cricetulus

griseus (Chinese hamster). Metazoa; Chordata; Craniat

Rodentia;

Sciurognathi;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Cricetinae;

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THE TOTAL TO THE SECOND SECOND
                                                                                                        RX MEDILINE 1007165; PubMed=10591208;
RX MEDILINE 20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Barrill W.D., Barton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Cchey D., Corby N.R., Cole C.G., Collier R.E., Comnor R.,
RA Cchey D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Chibert J.G.R., Goward M.E., Grafham D.V., Grifiths M.N.D., Hall C.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Grifiths M.N.D., Hall C.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Grifiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tmaling G., Heathcott R.W., Ho S., Holmes S.,
RA Hall R.E., Hall-Tmaling G., Heathcott R.W., Ho S., Holmes S.,
RA Hall R.E., Hall-Tmaling G., Heathcott R.W., McLindy C.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Milliams L., Williams S.A., Williamson H., Walmer T.E., Wilming L.,
RA Milliams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Williams L., Chabra M., Schuer D., Smalley S., Smith M.L.,
RA Milliams S., Link S., Link S., Williamson H., Wilmer T.E., Wilming L.,
RA Milliams S., Link S., Link S., P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Lewis J., Lewis S., Link S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Martyn M., Walliams S., Shakh T., Sakawa S., Kodoh 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
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Biochem.
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TISSUE=Fetal liver;
MEDLINE=97223398; PubMed=9070219;
MEDLINE=97223398; PubMed=9070219;
Alta N., Ishii K., Akamatsu Y., Ogasawara Y., Tanabe
Alta N., Ishii K., Akamatsu Y., Ogasawara Y., Tanabe
"Cloning and expression of human liver rhodanese cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                        A.S., Lane L., Tila
DNA sequence of hum
re 402:489-495(1999)
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an liver rhodanese cDNA.";
231:56-60(1997).
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Strausberg R.D., Collins F.S., Wagner L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Schenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

Al Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

Al Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Al Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Al Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Al Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Al Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences";

Proc. Matl Acad Sci U. H. Sanchez L. Sanc
                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0004792; F:thiosulfate sulfurtransferase GO; GO:0009440; P:cyanate catabolism; TAS. InterPro; IPR001763; Rhodanese-like. InterPro; IPR001307; Rhodanese. Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D87292; BAA13327.1; -.
EMBL; Z73420; CAA97762:1; -.
EMBL; BC010148; AAH10148.1; -.
PIR; JC5286; JC5286.
HSSP; P00586; IRHS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for conmodified and this statement is not removed.
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PROSITE; PS00683; RHODANESE 2; 1.
PROSITE; PS50206; RHODANESE 3; 2.
                                                                                                       DOMAIN
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TISSUE=Platelet;
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CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.

SUBUNIT: Monomer:

SUBCELLULAR LOCATION: Mitochondrial matrix.

SUBCALIVITY: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR

CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,

THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.

SIMILARITY: Contains 2 rhodanese domains.
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FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES, CYANIDE PUNCTION: FORMATION OF IRON-SULFUR CONTAINING ENZYMES.

DETOXIFICATION OR MODIFICATION OF SULFUR-CONTAINING ENZYMES.

OTHER THIOL COMPOUNDS, BESIDES CYANIDE, CAN ACT AS SULFUR ION ACCEPTORS. ALSO HAS WEAK MERCAPTOPYRUVATE SULFURTRANSFERASE (MST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGNC:12388; TST.
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                                                                                                                                                                                                                                        Mitochondrion; Repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A. 99:16899-16903(2002).
RHODANESE 2.
MAY PLAY A ROLE IN SUBSTRATE BINDING
                                                                                                                                               RHODANESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Damme J., Staes A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                          ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity; TAS
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Best Local (
InterPro; IPR001763; Rhodanese-like.
InterPro; IPR001307; Rhodanese.
Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHODANESE 1; 1.
PROSITE; PS00380; RHODANESE 2; 1.
PROSITE; PS00380; RHODANESE 2; 1.
PROSITE; PS00683; RHODANESE 2; 1.
PROSITE; PS00266; RHODANESE 3; 2.
INIT MET 0 0 BY SIMILARIT DOMAIN 143 158 HINGE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P52196;
01-OCT-1996
30-MAY-2000
10-OCT-2003
Thiosulfate
                                                                                                                                                                                                                                                                                                            EMBL; U35741; AAC52342.1; --
PIR; JC4398; JC4398.
HSSP; P00586; 1RHS.
SWISS-2DPAGE; P52196; MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (Some or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96074596; PubMed=7488186;
Dooley T.P., Nair S.K., Garcia R.E., Courtney B.C.
"Mouse rhodanese gene (Tst): cDNA cloning, sequenc recombinant protein expression.";
Biochem. Biophys. Res. Commun. 216:1101-1109(1995)
                                                                                                                                                                                                                                                                                   MGD; MGI:98852; Tst.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Expressed in numerous tissues.
DOWAIN: THE STRUCTURE CONSISTS OF ZOMAINS OF VERY SIM
COMFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN.
THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
SIMILARITY: Contains 2 rhodanese domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Mitochondrial matrix.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DETOXIFICATION.
CATALYTIC ACTIVITY: Thiosulfate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 VAVYDGSWSEW 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ISSYDGSWNDY 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296
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(Rel. 39, Last sequence update)
(Rel. 42, Last annotation update)
sulfurtransferase (EC 2.8.1.1) (Rhodanese)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORMATION OF IRON-SULFUR COMPLEXES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AΑ;
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45.5%;
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Pred. No.
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BY SIMILARITY.
SUBSTRATE (THIOSULFATE) BINDING
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                        SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cyanide = sulfite + thiocyanate.
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12;
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Best Local S
Matches 5
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Bodcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                      Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                        STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THT2 MYCTU STANDARD; PRT; 297 AA.
196888;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT 2003 (Rel. 42, Last annotation update)
Putative thiosulfate sulfurtransferase SSEA (EC SSEA OR RV3283 OR MT3382 OR MTCY71.23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis
EMBL; Z92771; CAB07066.1; -. EMBL; AE007147; AAK47725.1; PIR; D70980; D70980.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                           J. Bacteriol. 184:5479-5490(2002).
-!- CATALYTIC ACTIVITY: Thiosulfate + cyanide
-!- SIMILARITY: Contains 2 rhodanese domains.
                                                                                                                                                                                                                                               laboratory strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268
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5; Conser
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186
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248
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186
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MAY PLAY A ROLE :
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB
Pred. No. 12;
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SUBSTRATE (THIOSULFATE)
(BY SIMILARITY).
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                                                                                                                                                                                                                sulfite + thiocyanate
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Y4MH_RHISN
JD Y4MH_RHISN
AC P55567,
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PROSITE; PS00683; RHODANESE 2; 1.

PROSITE; PS50206; RHODANESE 3; 2.

PROSITE; PS50206; RHODANESE 3; 2.

Hypothetical protein; Transferase; Companing 138 RHODANES 200MAIN 168 286 RHODANES 245 245 RY SIMII SEQUENCE 297 AA; 33320 MW; 5930AH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=97305956; PubM
                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical Y4MH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001763; Rhodanese:
InterPro; IPR001307; Rhodanese:
Pfam; PF00581; Rhodanese; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P52197; 1EOC.
TIGR; MT3382; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid sym pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P55567;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
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                                                                                                                                                                                  Pfam; PF04909; Amidohydro_2; 1
Hypothetical protein; Plasmid.
SEQUENCE 297 AA; 33885 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=394;
                                                                                                                                                                                                                                              EMBL; AE000085; AAB91771.1; -. InterPro; IPR006992; Amidohydro_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular basis of symb
Nature 387:394-401(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: None obvious.
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  260
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                                                                                     Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRNYDGSWTEW
  LESSYDAIWNAF 271
                                         LISSYDGSWNDY 12
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(Rel.
(Rel.
133.9
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                                                                                          Conservative
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35,
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58.3%;
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RHODANESE 2.
BY SIMILARITY.
                                                                                            Score 41; DB Pred. No. 12; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB
Pred. No. 12;
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                                                                                                                                                                                      4DE2324557B63131 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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                                                                                                                                      Length 297
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RESULT 13

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InterPro; IPR000282; Cyrok receptor_2.
InterPro; IPR008957; FN III-like.
InterPro; IPR003561; FN III.
InterPro; IPR003531; Hemtopoptn_S_F1.
Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the Buropean Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for the statement is not removed. Usage by and for the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IL3B MOUSE
P26954;
01-OCT-1993
01-OCT-1993
15-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Itoh N., Yonehara S., Schreurs J., Gor
Yahara I., Arai K., Miyajima A.,
"Cloning of an interleukin-3 receptor
receptor gene family.";
Science 247:324-327(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Interleukin-3 receptor class II beta chain pr
stimulating factor 2 receptor, beta 2 chain).
CSF2RB2 OR AI2CA OR IL3RB2 OR IL3R.
                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
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MGD; MGI:1339760; C:
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MEDLINE=90117145; PubMed=2404337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             eceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: In mouse, there are two classes of high-affinity IL3 receptors. One contains this IL3-specific beta chain and the ot contains the beta chain also shared by high-affinity IL5 and GN CSF receptors.
SUBCUNIT: Heterodimer of an alpha and a beta chain.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY A Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Subfamily 4.
420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00060; FN3;
                                                                                   Similarity 6; Conserv
                                       ISSYDGSWNDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS01355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             email to license@isb-sib.ch).
                                                                                                                                         440
441
462
463
878
8 95
8 264
310
62
350
97195 MW;
                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Csf2rb2.
                                                                                                                                                                                                                                                                                                                                                                                                                 22
878
                                                                                                   59,4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PO_REC_S_F1; 1.
Glycoprotein; Signal.
                                                                                                                                                                                     POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.

OF SIMIL
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                                                                                                      Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                    8EBC9092ADC24D56
                                                                                   Mismatches
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                                                                                                        DВ
37;
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                                                                                 2;
                                                                                                                        Length 878;
                                                                                                                                                                         CRC64;
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                                                                                                                                                                                                                   (POTENTIAL)
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RESULT 14

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RESULT 15
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P96156;
15-JUL-1999
15-JUL-1999
10-OCT-2003
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                 SMART; SM00495; ChtBD3; 2.
SMART; SM00636; Glyco_18; 1.
PROSITE; PS01095; CHITINASE_18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlcNAc)2 and (GlcNAc)3. Inactive (GlcNAc)2 and (GlcNAc)3. Inactive (CMCNAc)2 and (GlcNAc)5. To (GlcNAc)2 and (GlcNAc)3. Inactive towards chitin, glucosamine oligosaccharides, glycoproteins are glycopeptides containing (GlcNAc)2. Has optimum activity at plants of S-7.0 and at a temperature of 35-37 degrees Celsius.

-i- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-acetyl-D-glucosamine polymers of chitin.
                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                         Pfam; PF02839; CBM 5 12; 7
Pfam; PF00704; Glyco_hydro
ProDom; PD000471; Glyco_hyd
                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and PNP-(GlcNAc)3.
-!- PATHWAY: Chitin catabolism.
-!- SUBCELLULAR LOCATION: Periplasmic (Probable).
                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                    Chitin degradation; Hydrolase; Glycosidase; Periplasmic; Signal
                                                                                                                                                                                                                                                                                                                              InterPro; IPR003610; CBM 5 12.
InterPro; IPR001223; Glyco-hydro 18.
InterPro; IPR001579; Glyco-hydro-18A8.
InterPro; IPR000437; Prok Tipoprot 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       furnissii. Molecular cloning, periplasmic chitodextrinase."
                                                                                                                                                                                                                                                                                                                                                                                            PIR; T30199; T30199.
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U41418; AAC44673.1; -.
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MEDLINE=97125982; PubMed=8969204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 271:33414-33424(1996).
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SIMILARITY: Belongs to chitinase class II (family 18
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8; Conserv
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ChtBD3; 2.
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38, Last sequence update)
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recursor (EC 3.2.1.14).
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61.5%;
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Pred. No.
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RA Wood V. Gwilliam R., Rajandraam M.A., Lyne M., Lyne R., Stewart A., RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Jones M., Cronin A., Davis P., Feltwell T., Fraser A., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Gentles S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Jones M., Jones M., Leather S., McDonald S., McLean J., RA James K., Jones M., Leather S., McDonald S., McLean J., RA James K., Jones M., Leather S., Saunders D., Geger K., Sharp S., RA McHerford K., Rutter S., Saunders D., Seeger K., Sharp S., RA Skelton J., Simmonds M., Squares R., Squares X., Stevens K., RA Woodward J., Volckasert G., Aert R., Robben J., Grymonprez B., RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S., RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S., RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., RA Galibert F., Nues S., Kiang Z., Hunt C., Moore K., Hurst S.M., RA Galibert F., Nues S., Kiang Z., Hunt C., Moore K., Hurst S.M., Daga R.R., Cruzado L., Jimenez J., Sancher M., Gel Rey F., Benito J., RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., RA Gerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., Forsburg S.L., Forsburg S.L., Shanker P., Forsburg S.L., Shanker P.
Search completed: October 5, 2004, 08:01:49
Job time: 2.07407 secs
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Best Local Similarity
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C3H1.04c in chromosome I.
SPAC3H1.04C.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright: It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE 6
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54.5%;
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Matches

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Query Match
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SEQUENCE FROM N.A.

STRAINMA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

MEDLINE-21477403; PubMed=11572948;

Cmura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,

Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.

Kikuchi H., Shiba T., Sakaki Y., Hattori M.;

"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
metabolites.";
                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequen
01-OCT-2003 (TrEMBLrel. 25, Last annota
Putative thiosulfate sulfurtransferase.
CYSA2 OR SAV4037.
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InterPro; IPR003439; ABC transporter.
Pfam; PF00005; ABC tran; 2.
ProDom; PD00006; ABC transporter; 2.
SMART; SM00382; AAA; 2.
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NCBI_TaxID=33903;
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ABC transporters of Dictyostelium.";
DO2) to the EMBL/GenBank/DDBJ databases
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54.5%;
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Pred. No. 15;
3; Mismatches
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Q8CJU5
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Best Local S
Matches 6
Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
PROSITE; PS00683; RHODANESE_2; 1
PROSITE; PS00683; RHODANESE_3; 2
Transferase; Complete protecme.
SEQUENCE 281 AA; 31771 MW; B'
                                                                                                                                                                                                                                                                                                                                                           MEDIJINE-A3(2) / MAX-3, MEDIJINE-A3(2) / MEDIJINE-21996410; PubMed=12000953;

MEDIJINE-21996410; PubMed=12000953;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rubbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8CJU5 PRELIMINARY; PRT; 281 AA.
Q8CJU5;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative thiosulfate sulfurtransferase.
SCO4164 OR SCD84.31.
                                                                                                                                      EMBL; AL939119; CAD55474.1; -.
GO; GO:0004792; F:thiosulfate sulfurtransferase
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008272; P:sulfate transport; IEA.
InterPro; IPR001307; Rhodanese.
InterPro; IPR001763; Rhodanese-like.
                                                                                                                                                                                                                                                                                                       "Complete genome sequence coelicolor A3(2).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165; MEDLINE=22608306; PubMed=12692562; Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuch Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                   Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                       Hopwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.
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SEQUENCE 2
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SMART; SM00450; RHOD; 2.
PROSITE; PS00683; RHODANESE 2; 1.
PROSITE; PS50206; RHODANESE_3; 2.
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EMBL; AP005037; BAC71749:1; --
GO:0004792; F:thiosulfate sulfurtransferase activity;
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008272; P:sulfate transport; IEA.
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InterPro; IPR001763; Rhodanese-like
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79 AA; 31592 MW;
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    B72E4DA7735C790B CRC64;
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Best Local S
Matches 6
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Best Local S
Matches 6
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Q8JZN1;
01-OCT-2002
01-OCT-2002
01-OCT-2003
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STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
KAWATABAYSASI Y. Yamazaki J., Hino Y. Kikuchi H., Naki
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A.,
Iseo K., Suzuki M., Mashima J., Itoh T., Yamagishi A.,
Iseo K., Sugimoto S.;
"The entire genomic sequence of Corynebacterium efficis
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ database;
EMBL; APOOS217; BAC17866.1; -
Hypothetical proteoin; Complete proteome.
Hypothetical proteoin; Complete BAD266FBA7FD989 CRC64;
SEQUENCE 248 AA; 26598 MW; B2AD266FBA7FD989 CRC64;
                                                                                                                                                                                                                                                                                                       Hedrick S.M., Irimura T., Masni Y., Higas "Molecular Cloning and Characterization (type Lectin, mMGL2, Which Has a Distinct mMGL1.";
                                     J. Biol. Chem. 277:28892-28901(2002)
EMBL; AY103461; AAM52097.1; -.
EMBL; AY103462; AAM52098.1; -.
MGD; MGI:2385729; Mgl2.
GO; GO:0005529; E:sugar binding; IEA
GO; GO:0007157; P:heterophilic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BAB-14, and 129/SvJ;
MEDLINE=22151052; PubMed=12016228;
Tsuiji M., Fujimori M., Obashi Y.,
Hedrick S.M., Irimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Macrophage galactose-type C-type lectin 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium efficiens.
Bacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                              cell adhesion; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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t Carbohydrate Specificity from
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Nishio Y.,
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Best Local
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Q850Y4;
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Yangken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.O., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 3 BAC OSJNBA0078D06 genomic sequence.";
Supmitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAINSCV. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.
Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
White O., Salzberg S.L., Fraser C.W.;
"Oryza sativa chromosome 3 BAC OSJMB0027B08 genomic sequence.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN 2003 (TrEMBLrel. 24, Created)
01-JUN 2003 (TrEMBLrel. 24, Last sequence update)
01-OUT-2003 (TrEMBLrel. 25, Last annotation update)
11-JUN 2003 (TrEMBLrel. 25, Last annotation update)
12-JUN 2003 (TrEMBLrel. 25, Last annotation update)
13-JUN 2003 (TremBLrel. 25, Last annotation update)
14-JUN 2003 (TremBLrel. 25, Last annotation update)
15-JUN 2003 (TremBLrel. 26, Last sequence update)
15-JUN 2003 (TremBLrel. 24, Last sequence update)
16-JUN 2003 (TremBLrel. 24, Last sequence update)
17-JUN 2003 (TremBLrel. 24, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00059; lectin_C; 1.
Pfam; PF03954; lectin_N; 1.
PRINTS; PR00356; ANTIFEEZEII.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                            Submitted (MAY-2003) to the EMBL/GenBank/DDBJ
EMBL; AC133778; AA039856.1; -.
EMBL; AC133339; AAP46248.1; -.
InterPro; IPR004332; MLDR.
Pfam; PF03108; MLDR; 1.
                                                                                                                                         Hypothetical
SEQUENCE 3
                                                                                                                                                                                                                                                                                                        STRAIN=cv. Nipponbare;
Buell R.;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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InterPro; IPR005640;
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                                            Similarity 6; Conserv
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342 AA; 3
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                                                                                                                                      39429 MW;
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Pred. No.
                                                                     Score 45;
Pred. No.
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Best Local S
Matches 7
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PRELIMINARY; PRT; 466 AA.

C 081876;

O1-NOV-1998 (TrEMBLrel. 08, Created)

T 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

T 01-CCT-2003 (TrEMBLrel. 25, Last annotation update)

E Hypothetical protein.

N T16L1.80 OR A74G33590.

S Arabidopsis thaliana (Mouse-ear cress).

S Arabidopsis thaliana (Mouse-ear cress).

C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra

C Spermatophyta; Magnoliophyta; eudicotyledons; core eudic

C eurosids II; Brassicales; Brassicaceae; Arabidopsis.

N NCBI TaxID=3702;
                                                                                                  SEQUENCE FROM I Obermaier B., I Mayer K.F.X.;
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GO; GO:0005529; F:sugar binding; IEA.

InterPro; IPR001304; Lectin_C.

InterPro; IPR005640; lectin_N.

Pfam; PF00059; lectin_C; 1.

Pfam; PF00059; lectin_N; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                             Obermaier
Mayer K.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to macrophage galactose N-acetyl-galactosamine
                                                                                                                                                                                               Obermaier B., Deutschenbaur
Heijnen L., Vos P., Mewes H.
Submitted (AUG-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Mammary gland;
MEDLINE=2254683; PubMed=12466851;
The FANTCM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                     Submitted
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                                                                                                                         H.W.,
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udicots; rosids;
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Best Local S
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Q7Y0C0;
Q7Y0C0;
01-CCT-2003 (TrEMBLrel. 25, Last sec
01-CCT-2003 (TrEMBLrel. 25, Last and
Putative mutator-like transposase.
OSUNBA0079B15.18.
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QBIN69;

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QBIN69;

QI-OCT-2002 (TrEMBIrel. 22, Created)

OI-OCT-2002 (TrEMBIrel. 23, Last sequence update)

OI-MAR-2003 (TrEMBIrel. 23, Last annotation update)

OI-MAR-1003 (TrEMBIRel. 23, Partial (Fragment))
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EMBL; AL03139
EMBL; AL16158
PIR; T04976; '
Hypothetical |
SEQUENCE 466
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SEQUENCE
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBB0091N21 genomic sequence.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AC091122; AAM94925.1; -.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poa
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
                                                                                              Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
     STRAIN=CV.
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; PF03108; MuDR; 1.
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466 AA; 53537 MW; AFA5334895A06858
Nipponbare;
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Matches 6
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Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo Currie J., Collura K.;

"Rice Genomic Sequence.";

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ da-EMBL; AC099399; AAN05499.1; -.

InterPro; IPR004332; MuDR.

Pfam; PF03108; MuDR; 1.

SEQUENCE 779 AA; 87872 MW; 6A9D0335FE26C955
                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
OSJNBb0026L04.5 protein.
OSJNBB0026L04.5
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Q7XTH1;
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Q8H8E2;
01-MAR-2003
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
   Oryza sativa (Rice).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buell R.;
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RA Fu G:, Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., RA Sheng H.H., Gu J.L., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., RA Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H., RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X., RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., RA Zhang R.Q., Guan J.P., Hong G.F.;

SO SEQUENCE 794 AA; 91076 MW; 90FD1473227A71DE CRC64;
DE Putative mutator-like transposase.

GN OSJNBB0016H12.24.

CN OSJNBB0016H12.24.

CN OSJNBB016H12.24.

CN OSJNBB016H12.24.

CN OSJNBB016H12.24.

CN OSJNBB016H12.24.

CN OSJNBB016H12.24.

CN OSJNBB016H12.24.

CS Oryza sativa (japonica cultivar-group).

CN OSJNBB016H12.24.

CN OSJNB
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Q84R42
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Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL731601; CAE05018.1;
SEQUENCE 804 AA; 91227 MW; 172D5556EC7B7327 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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Pred. No. 80;
2; Mismatches
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C STRAIN=CV. Nipponbare;

G STRAIN=CV. Nipponbare;

Buell R.;

Appo3412.1;

E Submitted (Apr-2003) to the EMBL/GenBank/DDBJ databases.

E Submitted (Apr-2003) to the EMBL/GenBank/DDBJ databases.

E COSTO 1003676; F:nucleic acid binding; IEA.

R GO; GO:0003676; F:nucleic acid binding; IEA.

R Interpro; IPR004332; MuDR; CCHC.

R Interpro; IPR001878; Znf_SWIM.

R Interpro; IPR001878; Znf_SWIM.

R Pfam; PF03108; MuDR; 1.

Pfam; PF04434; SWIM; 1.

R Pfam; PF04434; SWIM; 1.

R PFAM; PF03108; MuDR; 1.

R PFAM; PR00339; CCHCZMFINGER.

R SMART; SM00575; ZnF_PMZ; 1.

R SMART; SM00575; ZnF_PMZ; 1.
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Suell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Suell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Xim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.C., Haas B.J., Sh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 3 BAC OSJNBb0016H12 genomic sequence.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
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5.1.6 Compugen Ltd.	GenCore version (c) 1993 - 2004	Gen (c)	pyright (	Cop		

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Claim 4; Page 29; 37pp; English.

Bezemer S,

Van De Burg M,

De Haard JJW, Tareilus

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WPI; 2001-572718/65.

14-MAR-2000; 2000EP-00200930

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AAG13401	AAG51758	AAG51760	AAG13402	AAG06051	AAG51755	AAG21393	ADC97223	0	AAG51761		0605	UT	u	S)	AAG21394	AAY86115	ABR55875	ABR55874	AAY52304
134	9517	Aag51760	œ.	Aag06051	517	Aag21393	c97	134	Aag51761	51	Aag06052	51	0	17	Aag21394	Aay86115	Abr55875	Abr55874	Aay52304
Ara	Ara	Ara	Ara	Arabi	Ara	Arabi	E.	Arak	Þ	Arab	Arab	Ara	Ara	Ara	Ara	S	Human mAb	Human	Vibrio f

# ALIGNMENTS

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#### Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HFL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3. 20-FEB-2001; 2001EP-00200703. EP1134231-A1. Lama sp. Llama species antibody VHH CDR3 #17. 10-DEC-2001 AAE10548 standard; peptide; 12 AA. 19-SEP-2001. AAE10548; (first entry)

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RESULT 2
AAE10558
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                 The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human baings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #22 from lama (camelid) species
                                                                                                                                                                          New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                          Example 2;
                                                                                                                                                                 of light chains.
                                                                                                                                                                                                                           WPI; 2001-572718/65
                                                                                                                                                                                                                                                Bezemer S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Llama antibody; camelid; anorectic; heavy chain variable domain; VHH;
human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL;
food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPL inhibiting VHH fragment,
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                                                                                                                                         Page 10; 37pp; English.
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nilarity 100.
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      note= "Complementarity
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Pred. No.
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                                                                                                                                                                                                                                                  JJW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from llama species
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Sequence

129

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RESULT 3
ADB74513
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Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-1993;
22-OCT-1993;
                                                                                                                                                                      Sequence
                                                                                                                                                                                                               seqdata.uspto.gov/sequence.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-2003
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302 VKNYDGSWTEY
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                                                                                   Similarity 6; Conserv
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                                       ISSYDGSWNDY
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93US-00142558.
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                                                                                Score 47; DB
Pred. No. 47;
3; Mismatches
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                                                                                                                            Length 324
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ABM67419 standard;

protein;

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RESULT 4
ABM67419
ADM67419
ADM66XX
AX ADM6
AX WO20
AX WO20
AX WO20
AX ADM6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/dentification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter
                                                                                                                                                                                                                                       Sequence 1647
                                                                                                                                                                                                                                                                                           genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            response or sensitivity to toxins and antibiotics produced by P. luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-2002; 2002WO-IB003040
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CNRS CENT NAT RECH SCI.
                                                                                                                Similarity 7; Conserv
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                                                         SYDGSWNDY 12
SYDAFWNDY
                                                                                                                   Conservative
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                                                                                                                                                                                                                                           AA,
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d; gene expression; plant; animal; microorganism; toxin;
opesticide; virulence factor; disease model; plague;
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                                                                                                                                             Pred. No.
                                                                                                                   Mismatches
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                                                                                                   DB 6; 5.5e+02; 2;
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                                                                                                                                                                          Length 1647;
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                                                                                                          Gaps
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RESULT 5 AAE10547

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                                                                                                                                                                                                                                                                                Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                      Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                          HPL inhibiting
                                                                                                     10-DEC-2001
                                                                                                                                AAE10551;
                                                                                                                                                        AAE10551 standard; peptide; 129 AA.
                                                                                                                                                                                                                                                                                                                                  Sequence 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 29; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bezemer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNIL )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-2001; 2001EP-00200703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1134231-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complementarity determining region 3; CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Llama antibody; camelid; anorectic; heavy chain variable domain; human dietary enzyme inhibitor; medicament; human pancreatic lipa food; human gastric lipase; HGL; cosmetic control; body weight;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Llama species antibody VHH CDR3 #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE10547 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-572718/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNILEVER NV.
                                                                                                                                                                                                                                                                               Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chains.
                                                                                                                                                                                                                           SNYDRSWGDY 12
                                                                                                                                                                                                                                                   SSYDGSWNDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van De Burg
                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000EP-00200930
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                                                                                                     (first entry)
                                                                            ΣĦ
                                                                          fragment,
                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                          63.8%;
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                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                             Score 44; DB
Pred. No. 3.7;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   De Haard JJW,
                                                                            HPL
                                                                            #11
                                                                             from
                                                                                                                                                                                                                                                                                            DB
3.7;
                                                                             llama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tareilus
                                                                                                                                                                                                                                                                                                      Length 12
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lipase;
                                      lipase; HPL;
                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                           The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #11 from
                                                             SAPHO syndrome; synovitis; acne; pustulosis; uveitis; endophthalmitis; bone; joint; centra inflammatory lesion; acne vulgaris; enzyme li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAR-2000; 2000EP-00200930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                          27-FEB-2002
                                                                                                                                                                                           AAU63004 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bezemer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MIL )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                    dermatological;
                                                                                                               Propionibacterium acnes immunogenic protein #23900.
                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 9; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-572718/65
                          Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                  present peptide sequence
na (camelid) species
                                                                                                                                                                                                                                                          100
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                                                                                                                                                                                                                                                                                                        Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                           129
                                                                                                                                                                                                                                                          SNYDRSWGDY 109
                                                                                                                                                                                                                                                                              SSYDGSWNDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van De Burg
                                                               me; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
ophthalmitis; bone; joint; central nervous system; ELISA;
lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                         (first entry)
                                                 osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= CDR2
/note= "Complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= CDR1
/note= "Complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label=
                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                     63.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : CDR3
"Complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĭ
                                                                                                                                                                                            88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Haard JJW,
                                                    neuroprotectant
                                                                                                                                                                                                                                                                                                                     Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                  DB
49;
                                                                                                                                                                                                                                                                                                                                 4;
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                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                 Length 129;
                                                                                                                                                                                                                                                                                                          Indels
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RESULT 8
ABM59523
ID ABM5
XX ABM5
AC ABM5
XX AC ABM5
XX AC ABM5
XX AC AC AC
XX AC Prop
DE Prop
XX Acne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, station in the control of the proteins and endophthalmitis. CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory Clasions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a CC sample with a binding agent that binds to the proteins of the invention can determining the amount of bound protein in the sample. The CC specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and CC downregulate expression and activity of P. acnes polypeptides and CC diagnostic agents for determining P. acnes presence, for example, by can appear to the printed specification, but was contained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium acnes vaccinating against and treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-2001;
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                                                             WO2003033515-A1
                                                                                                                Propionibacterium
                                                                                                                                                                       Acne vulgaris; antiseborrhoeic; dermatological; immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                          Propionibacterium acnes predicted ORF-encoded polypeptide #24199.
                                                                                                                                                                                                                                                                                                                       20-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM59523 standard; protein; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 24199; 1069pp;
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DB; AAS59630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 VISTEDGSWSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LISSYDGSWND 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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2000US-0208841P.
2000US-0216747P.
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e J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-US012865
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                       acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides and nucleic acids useful diagnosing infections, especially uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eful for
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RESULT 9
ABP66065
ID ABP6
XX ABP6
XX 19-N
XX Bifi
XX Bifi
XX Bifi
XX anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc encoding a Propionibacterium acnes protein. The invention also relates to golypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to climmunogenic fragments of P. acnes polypeptides. The invention also relates to compression vectors and host cells comprising a dimutospition proteins of proteins ratioodies against polypeptides of the invention; comprising a polypeptide of the invention; antibodies against polypeptides of the invention; a method for stimulating an immune response specific for a P. acnes complypeptide and an isolated T cell population comprising P. acnes polypeptides, polypucleotides, antibodies, fusion proteins, T cell populations, or comparison of electring or determining the presence or absence of P. acnes in a comparison of electring or determining the presence or absence of P. acnes in a comparison. The P. acnes polypeptides, polypucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides, antibodies, fusion proteins. The P. acnes polypeptides, polypucleotides, antibodies, fusion proteins. The polypucleotides can also be used as probes or primers for culgivis, or for stimulating an immune response specific for a P. acnes composition is useful for the primated specific action, but was obtained in electronic format directly from protein. The present of the print of the prin
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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Zhang Y,
Barth B,
Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria; rotavirus; food composition; pharmaceutical composition.
                                                                                                  Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID
                                                                                                                                                                                      ABP66065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                19-NOV-2002
                                                                                                                                                                                                                           ABP66065 standard; protein; 385 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 88 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-2001; 2001US-00978825
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                                                                                                                                                                                                                                                                                                                                14
                                                                                                                                                                                                                                                                                                                              1 LISSYDGSWND 11
:||: ||||:|
14 VISTEDGSWSD 24
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L, Skeiky YAW, Pe
Wang S, Jen S, I
Vallieve-Douglass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 24199; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                 60.9%;
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Lodes MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42;
Pred. No.
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Benson DR,
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                                                                                                       NO:809
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                                                                                                                                                                                                                                            RESULT 10
ABB58674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 385 AA;
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CC sequence of a Blidobacterium genome selected from the nucleotide comparison of a Blidobacterium genome selected from the nucleotide cC least 90% identity or which hybridises with the sequence given in CC least 90% identity or which hybridises with the sequence given in CC ABQ81842 and ABQ81843. Also described is a polypucleotide (II) encoding a CC in ABP65258 to ABP66354 ligated in frame to a polypucleotide encoding a CC activities, and can be used as an inhibitor of Salmonella. (I) (which is C aprobe) is useful for the detection and/or identification of Salmonella. (I) (which is C aprobe) is useful for the detection and/or identification of Salmonella. (I) (which is C aprobe) is useful for the detection and/or identification of Salmonella. (I) (which is C aprobe) is useful for the detection and/or identification of Salmonella. (I) (which is C aprobe) is useful for the detection and/or identification of Salmonella. (I) (which is C aprobe) is useful for the detection and/or identification of Salmonella. (I) (which is C aprobe) is useful for the detection and/or identification of Salmonella. (I) (which is C aprobe) is useful for the sex fermented milks, milk based fermented C products, ide-creams, fermented ceral based products, milk based fermented C products, infant formula, pet food or a pharmaceutical composition C selected from tablets, liquid bacterial suspensions, dried oral corposition of the Bitidobacterium gene. ABQ81850 represent C expression of the Bitidobacterium gene. ABQ81850 represent C I isting from the present invention but not mentioned further within the Sequence C in the printed specification but is based on sequence information C in the printed specification but is based on sequence information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 809; 80pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001EP-00102050.
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Query Match
Best Local
pharmaceutical.
           Drosophila; developmental biology; cell signalling; insecticide;
                                Drosophila melanogaster polypeptide SEQ ID NO 2814
                                                                                 ABB58674;
                                                                                                     ABB58674 standard; protein; 543
                                                         26-MAR-2002
                                                                                                                                                                 309
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                                                                                                                                                                                                              Similarity 7; Conserv
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                                                         (first entry
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Pred. No.
2; Mismatc
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Thes 7; Conserv
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                                                                                                                                                                                          Drosophila, developmental biology, cell signalling, insecticide, pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid genes from Drosophila and
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11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 1542
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                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                                                        26-MAR-2002
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           Venter JC,
                                                           23-MAR-2000;
11-JUL-2000;
                                                                                             23-MAR-2001; 2001WO-US009231
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                                    (PEKE ) PE
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                                    CORP NY
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            Adams M,
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                                                         2000US-0191637P.
2000US-00614150.
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            PWD,
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Pred. No. 4.7e+02;
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            EW.
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL130511), expressed DNA sequences (ABL16176-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical.
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                                                                                   Disclosure; SEQ ID NO 28644; 21pp + Sequence Listing;
                                                                                                                                                                          N-PSDB; ABL11387
                                                                                                                                                                                        WPI; 2001-656860/75
                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                            23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 28644.
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                                                                                                                 interactions.
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                                                                                                                                                                                                                    Myers EW;
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                                                                                     English.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventive seful in developmental biology and in elucidating cell signaling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention

The invention signalling and

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RESULT 13
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a cit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound that regulates the activity of one or more of the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  discloses genomic DNA sequences (ABL16176-ABL30511), expressed sequences (ABL01940-ABL16175) and the encoded proteins (ABB5773 ABB72072). The sequence data for this patent did not form part printed specification, but was obtained in electronic format diffrom WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                           New composition comprising preparing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
nic constriction injury; CCI; spared nerve injury; SNI; Chung.
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BAYER AG.
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Pred. No. 4.8e
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                                                                                                                                                                                                                                                                                                                                                                                                                           Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE63680 standard; protein; 295 AA.
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                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
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45.5%;
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, CCI; spared nerve injury; SNI; Chung.
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Pred. No. 3.4e+02;
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14-AUG-2001; 01-NOV-2001; 26-NOV-2001; GENBANK; P24329 WPI; 2003-268312/26 Woolf C, (GEHO ) (FARB ) 27-FEB-2003 14-AUG-2002; 2002WO-US025765 GEN HOSPITAL CORP BAYER AG. D'urso D, ; 2001US-0312147F. ; 2001US-0346382F. ; 2001US-0333347F. Befort × Costigan

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a The invention discloses a composition comprising two or more or human polynucleotides or a polynucleotide which represents derivative or allelic variation of the nucleic acid sequence. or more isolated rat Also fragment,

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RESULT 15
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                                                                                                                                               Claim 1; Page 91; 126pp; English.
                                                                                                                                                                                          Novel polypeptide of somatic protein extract useful as vaccine against virulent Mycobacterium infection, isolated from cell wall, cell membra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculosis; TB; antigen; vaccine; diagnosis; somatic; tuberculostatic; infection; interferon-gamma; IFN-gamma; protective immunity; therapy; delayed type hypersensitivity response; TB33.
                                                                                                                                                                                                                                     WPI; 2000-317931/27.
N-PSDB; AAA39565.
                                                                                                                                                                                                                                                                                  Andersen P, Weldingh K, I
Skjot RLV, Rosenkrands I;
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21-JAN-1999;
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This invention describes a novel polypeptide (PP) of somatic proteins extract (I) which have tuberculostatic activity. (I) or their subsequence has at least one of the following properties: (a) the PP induces an in vitro recall response, or an in vitro response, during primary infection with virulent Mycobacterium, determined by a release of interferon (IFN)-gamma, (b) PP induces a protective immunity, determined by vaccinating an animal with PP and an adjuvant, three times at two weeks intervals, (c) PP induces an in vitro response, or in vitro recall response, determined by release of IFN-gamma of at least 1000 pg/ml or 500 pg/ml,

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                                                                                                                                                          from TB patients, or PPD positive individuals, 6 months after diagnosis, (d) PP induces a specific antibody response in a TB patient, as determined by enzyme linked immunosorbent assay (ELISA) technique or a western blot, (e) PP induces a positive delayed type hypersensitivity (DTH) response, determined by intradermal injection. (I) and (II) are useful in preparing a prophylactic or therapeutic medicine as a vaccine for induction of a protective or generation of an immune response in a mammal against infection with a virulent Mycobacterium. (I) and (II) are also useful as diagnostic reagent for the diagnosts of a virulent Mycobacterium infection. The vaccine of the invention induces efficient immunological memory, providing long term protection against TB. This sequence represents a Microbacterium tuberculosis TB33 antigen described
                                                                                             Sequence 297
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Job time : 12.1296 secs Search completed: October 5, 2004, 07:59:59 밁 Ş

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029441 archaeoglob
044052 arthrobacte
Q12888 homo sapien
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P33331 saccharomyc
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RESULT

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CA2B MOUSE STANDARD,
CA2B MOUSE STANDARD,
Q64739; Q61432; Q921W0;
15-UTL-1998 (Rel. 36, Created)
10-OCT-2003 (Rel. 42, Last sequence up
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KHSE_DEIRA

Q9RRU5;

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InterPro; IPR006204; GHMPkinse ATP.
InterPro; IPR006203; GHMPkinse ATP.
InterPro; IPR000870; Homosser Kin.
Pfam; PF00288; GHMP kinases; 1.
PRINTS; PR00958; HOMSERKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genous ריי";
radiodurans Rl.";
Science 286:1571-1577(1999).
היישאויאחדור ACTIVITY: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White O., Risen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AEC02069; AAF11935.1; PIR; G75280; G75280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                        Complete proteome. NP_BIND 91
                                                                                                                                                                                                                                                                                                  Threonine biosynthesis; Transferase;
                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; DR2390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
MEDLINE=20036696; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Deinococcus-Thermus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THRB OR DR2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deinococcaceae; Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deinococcus radiodurans.
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                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Threonine biosynth
SUBCELLULAR LOCATION: Cytor
SIMILARITY: Belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subfamily.
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                                                                                                                                                                                                   Similarity
8; Conser
                                                                                                                                                                                                                                                                                                               PS00627; GHMP_KINASES_ATP; 1.
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                                                                                                                                                                                                                                                         307 AA;
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40, Last sequence update)
41, Last annotation update)
(EC 2.7.1.39) (HK).
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                                                                                                                                                                                                              Score 43;
Pred. No.
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                                                                                                                                                                                                   Mismatches
                                                                        1736
                                                                                                                                                                                                                                                                                                  Kinase; ATP-binding;
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7.2;
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                                                                                                                                                                                                  2;
                                                                                                                                                                                                                             Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homoserine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O-phospho-L-
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between the Swiss Institute of Bioinform the European Bioinformatics Institute of Bioinform use by non-profit institutions as long modified and this statement is not instituted.
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                                                              This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
                                                                                                                     ISOId=Q64739-1; Sequence=VSP 007345; VSP_007347;
-:- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
-:- SIMILARITY: BELONGS TO THE FIBRILLAR CLASS OF COLLAGENS.
-:- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Separable cis-regulatory elements that contribute site-specific alpha 2(XI) collagen gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96427460; PubMed=8830784;
Tsumaki N., Kimura T., Matsui Y., Ochi T
"Separable cis-regulatory elements that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-624 FROM N.A. (ISOFORMS STRAIN=129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vandenberg P., Vuoristo M.M., Ala-Kokko L., Prockop D.J.; "The mouse collla2 gene. Some transcripts from the adjacent rxr-beta gene extend into the collla2 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-1678 FROM N.A. (ISOFORM 7). STRAIN=FVB/N, and 129/Sv; TISSUE=Cartilage; MEDLINE=97135795; PubMed=8981332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., M: Hall J., Lasky S., Hood L.; "Sequence of the mouse major histocompatibility locus class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsumaki N., Kimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95138212; PubMed=7836472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matrix Biol. 15:359-367(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLLIA2.
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                                                                                                                                                                                                                              Name=7
                                                                                                                                                                                                                                             Name=6; Synonyms=E59; IsoId=Q64739-7; Seq
                                                                                                                                                                                                                                                                                                                                               Name=3; Synonyms=E5789;
IsoId=Q64739-4; Sequence=VSP_007345;
Name=4; Synonyms=E569;
                                                                                                                                                                                                                                                                                                                                                                                                                                Name=2;
                                                                                                                                                                                                                                                                                     IsoId=Q64739-5; Sequence=VSP_007346, VSP_007347;
ame=5; Synonyms=E589;
IsoId=Q64739-6; Sequence=VSP_007345, VSP_007346;
                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q64739-2; Sequence=Displayed; ame=2; Synonyms=E5689; IsoId=Q64739-3; Sequence=VSP_007346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chem. 270:2372-2378 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qin S., Madan
Lasky S., Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Metazoa;
Eutheria;
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Rodentia;
                                                                                                                                                                                                                                                                                 Sequence=VSP_007345, VSP_007346;
                                                                                                                                                                                                                                           Sequence=VSP_007345,
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                                                              Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ochi T.;
                                                     It is produced through informatics and the E
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the embryon
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EMBL; U16789; AAA67751.1; -
EMBL; U16790; AAA67752.1; -
EMBL; D38412; BAAL8910.1; -
EMBL; D38412; BAAL8910.1; -
EMBL; D84066; BAAL2208.1; -
MGD; MGI:88447; C0111a2.
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SIGNAL
CHAIN 2
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MGD; MGI:8
InterPro;
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pfam; pF01391; Collagen; 18.

pfam; pF0210; TSPN; 1.

proDom; pD000007; Clg_helix; 1.

proDom; pD000007; Fib collagen_C; 1.

SMART; SM00038; COLFI; 1.

SMART; SM00038; COLFI; 1.

SMART; SM00282; LamG; 1.

SMART; SM00210; TSPN; 1.

Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Alternative splicing; Signal.
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; IPRO08160; Collagen.
; IPRO08985; Cond_like_lec_gl.
; IPR000865; Fib_collagen_C.
; IPR001791; Laminin_G.
; IPR003129; TSPN.
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REGENER SG?????; Tig.

REGENER SG?????; TKBP_PPlase.

REGENER InterPro; IPRO01179; FXBP_PPlase.

REGENER InterPro; IPRO08880; Trigger_C.

DR InterPro; IPRO08881; Trigger_N.

Pfam; PF05698; Trigger_C; 1.

DR Pfam; PF05698; Trigger_C; 1.

DR Pfam; PF05697; Trigger_N; 1.

DR Pf05ITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.

DR PROSITE; PS00454; FKBP_PPIASE_3; 1.

PROSITE; PS00454; FKBP_PPIASE_3; 1.

PROSITE; PS00454; FKBP_PPIASE_3; 1.
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Salmonella typhimurium,
Salmonella typhi.
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Enterobacteriaceae; Salmor
NCBI_TaxID=602, 601;
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MEDLINE=21534947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 413:852-856(2001).
                                                                                                                                                                                                                                                              EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comparative genomics of and CT18.";
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AL627266; CAD08906.1;
AE016842; AAO70003.1;
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SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latre Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., L Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvan Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parkhill J. Dougan G., James K.D., Thomson N.R., Pickard D., Wain Parkhill J. Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebalhia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davise R.M., Dowd L., White N., Farrar J., Peltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica servorar Typhi CT18.";
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                                                                                                                                                                                                                                                                                                            J. Bacteriol. 185:2330-2337(2003).

-!- FUNCTION: Involved in protein export. Acts as a chaperone maintaining the newly synthesized protein in an open confi (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner
"Comparative genomics of Salmonella enterica serova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trigger factor
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OR STM0447 OR STY0489 OR
                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the FKBP-type PPIase family.
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attner F.R.;
serovar Typhi strains
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MRT. Outstation -
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Matches 8
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28-FEB-2003 (Rel. 41, Las
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Trigger factor (TF)
TIG OR YPO3158 OR Y1026.
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MEDINE22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Lis
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Petherston J.D., McDonoudh K.A., Nilles M.L., Matson J.S., Blattner
                                           HAMAP; MF_00303; -; 1.
InterPro; IPR001179; FKBP PPIASe.
InterPro; IPR005215; Triggfac.
InterPro; IPR008880; Trigger_C.
InterPro; IPR008881; Trigger_N.
                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 184:4601-4611(2002).
-!- FUNCTION: Involved in protein export.
maintaining the newly synthesized pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21470413; PubMed=1158636; Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Parkhill J., Wren B.W., Thomson N.R., Churcher C., Mungall K.L., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Genome sequence of Yersinia pestis, the causative agent of plague."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
SEQUENCE
                                                                                                                                           EMBL; AJ414155; CAC92393.1; -.
EMBL; AE013706; AAM84607.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CO-92 / Biovar Orientalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yersinia pestis.
Bacteria, Proteobacteria; Gam
Enterobacteriaceae, Yersinia.
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                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of Yersinia pestis KIM.";
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                                                                                                                              AF0383;
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PF00254; FKBP; 1.
PF05698; Trigger_C; 1.
PF05697; Trigger_N; 1.
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                                                                                                                                                                                                                                                                                                                                   similarity)
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Biovar Mediaevalis;
7863; PubMed=12142430;
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Pred. No.
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XRN2_M
                                                                                                                                                            RA Okazaki Y., Puruno M., Kasukawa T., Adachi J., Bono H., Kondo S., RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Mikaido I., Osato N., Saito R., Schorbach C., Gojobori T., RA Saldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Balake J.A., Bract D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Blake J.A., Bractohar C.F., Forrest A., Frazer K.S., RA Blake J.A., Schorlid M., Gissi C., Godzik A., Gough J., RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., RA Grimmond S., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Wastahia T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Pavan W.J., Pertea G., Pesole G., RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Ra Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., RA Nagashima T., Reed D.J., Reid J., Ring B.Z., Ringwald M., RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada M., Wastahia T., Reed D.J., Reid J., Ring B.Z., Ringwald M., RA Sandelin A., Schneider C., Wang Y., Watanabe Y., Wells C., RA Wilming L.G., Washaw-Boris A., Yangi S., Watanabe Y., Wells C., Wang Y., Jarvis D., Walls C., Wang Y., Watanabe Y., Wells C., Wang J., Jarvis D., Jarvis D., Jarvis D., Shimada R., Sakai K., Kawai J., Aizawa K., Arakawa T., Fukuda S., RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Yagawa I., RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., RA Hirozane-Kishikawa T., Sasaki D., Shibata K., Shinagawa A., RA Haria A., Yashiraki Y., Sasaki D., Shibata K., Shinagawa I., RA Hara A., Hashirume W., Sasaki D., Shibata K., Shinagawa A., RA Hara A., Sakai Y., Sasaki D., Shibata K., Shinagawa A., RA Hara A., Sakai Y., Sasaki D., Shibata K., Shinagawa A., Ra Hara A., Sakai Y., Sasaki D., Shibata K., Shinagawa I., Ra Mayashizaki Y., Takawa K., Lander E.S., Rogers J.,
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Q9DERI, Q61489; Q99KS7;

Q9DERI, Q61489; Q99KS7;

10-CCT-2003 (Rel. 42, Last sequence up:
15-MAR-2004 (Rel. 43, Last annotation
15-MAR-2004 (Rel. 43, Last annotation
                                                                                 Birney E., Hayashi:
"Analysis of the mo
60,770 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00453; FKBP PPIASE 1; FALSE NEG.
PROSITE; PS00454; FKBP PPIASE 2; FALSE_NEG.
PROSITE; PS50059; FKBP PPIASE 3; 1.
Cell division; Chaperone; Isomerase; Rotamase; Complete DOMAIN
161
246
PPIASE, FKBP-TYPE.
SEQUENCE 434 AA; 48240 MW; D44CB4FB9ABSCAEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dhp1+ gene:
Nucleic Acio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shobuike T., Sugano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95192042; PubMed=7885830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XRN2 OR DHM1.
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                                                                                                                                               Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              structural
                                                                              the mouse transcriptome length cDNAs.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S., Yamashita T., Ikeda H.;
cDNA encoding mouse homolog of f
al and functional conservation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.9%;
66.7%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eye,
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                                                                                                                     functional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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FROM N.A.

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Foshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Robert S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
A Villalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length human
"Generation and Schmerges"."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D38517; BAA07524.1; --
EMBL; AK004800; BAB33573.1; --
EMBL; AK031247; BAAC27318.1; --
EMBL; AK053643; BAC27318.1; --
EMBL; BC054028; AAH04028.1; ALT_INIT.
EMBL; BC054743; AAH54743.1; --
EMBL; BC054743; AAH54743.1; --
EMBL; BC054743; AAH54743.1; --
EMBL; BC054743; AAH54743.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-:- FUNCTION: Possesses 5'->3' exoribonuclease activity and may involved in homologous recombination and RNA metabolism, sur RNA synthesis and RNA trafficking.
                                                                                                                                                                                                                             RNA-binding; Zinc-finger; Alternative splicing.
ZN_FING 262 278 CCHC-TYPE.
VARSPLIC 931 951 GYPREGRKYPLPPPSGRYY
                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004859; Put 53exo.
InterPro; IPR001878; Znf CCHC.
Pfam; PF031159; XRN N; 1.
SMART; SM00343; ZnF C2HC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6, and Czech II; TISSUE=Brain, and Mammary gland; MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung, liver, skeletal muscle, and kidney. SIMILARITY: Belongs to the 5'-3' exonuclease family. SIMILARITY: Contains 1 CCHC-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear (Potential).
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                         I; SM00343; ZnF_C2HC; 1.
ITE; PS50158; ZF_CCHC; FALSE_NEG.
Processing; Hydrolase; Nuclease; Exonuclease; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9DBR1-2; Sequence=VSP_007235; Note=No experimental confirmation available. May result from the retention of an intron in the cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          soId=Q9DBR1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIFICITY: Expressed in the spleen, testis, heart,
       122
221
332
336
493
563
712
/FTId=VSP_007335.

SKE -> IKG (IN REF. 1).

H -> Q (IN REF. 1).

I -> N (IN REF. 1).

V -> E (IN REF. 1).

V -> R (IN REF. 1).

Y -> L (IN REF. 1).

Y -> L (IN REF. 2; BAC27318).

P -> H (IN REF. 2; BAC27318).
                                                                                                                                                                                                          GYPREGRKYPLPPPSGRYSWN -> VISTMWAVEGKQHTAI
C (in isoform 2).
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TId=VSP_007235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINIE-21016719; PubMed=11130712;

AT Theologis A., Ecker J.R., Palm C.J., Pederspiel N.A., Kaul S.,

AT Theologis A., Ecker J.R., Palm C.J., Pederspiel N.A., Kaul S.,

AN Mhite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

AN Dunn P., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

AN Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

AN Dunn P., Etgu P., Pedlblyum T.V., Feng J.-D., Fong B., Fuji C.Y.,

AN Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

AN Hinter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

AN Hinter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

AN Hinter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

AN Hinter J.L., Jenkins J., Johnson-Hopson C., Marti R.,

AN Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

AN Lin X., Liu S.X., Liu A., Luros J.S., Maiti R., Marziali A.,

AN Hiltscher J., Miranda M., Nguyen M., Nierman M.C., Osborne B.I.,

AN Miltscher J., Miranda M., Squyen M., Nierman M.C., Osborne B.I.,

AN AN Hollscher J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

AN AN AN AND M. Town C.D.,

BAN AND H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,

"Sequence and analysis of chromosome 1 of the plant Arabidopsis

T. Thaliana.",

The Company A.B., Charles T. Rowley D.,

Thaliana.",

The Company A.B., Charles T., C.,

The Company A.B., Charles T., C.,

Thaliana.",

The Company A.B., Charles T., C.,

The Company A.B., Charles T.,

Thaliana.",

The Company A.B., Charles T., C.,

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The Company A.B., Charles T.,

Thaliana.",

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) VP41 ARATH STANDARD; PRT; 976 AA.
) P93043; O9SGE1;
[ 01-NOV-1997 (Rel. 35, Created)
[ 16-OCT-2001 (Rel. 40, Last sequence update)
[ 10-OCT-2003 (Rel. 42, Last annotation update)
[ Vacuolar assembly protein VP541 homolog.
] Vacuolar ATIGO8190 OR T23G18.5.
| VP541 OR ATIGO8190 OR T23G18.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 644-976 FROM N.A.

MEDITUS=97303186; PubMed=9159129;
Radisky D.C., Snyder W.B., Emr S.D., Kaplan J.;

"Characterization of vPS41, a gene required for "and high-affinity iron transport in yeast.";

Proc. Natl. Acad. Sci. U.S.A. 94.5662-5666(1997)

-1- FUNCTION: Required for vacuolar assembly and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                         SIMILARITY: BELONGS TO THE VPS41 FAMILY.
SIMILARITY: Contains 2 WD repeats.
CAUTION: Ref.1 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                    similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       820
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7; Conservative
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1; Mismatches
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O -> K (IN REF. 1

P -> H (IN REF. 2

O -> QV (IN REF.
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for vacuolar trafficking
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F. 2; BAC27318).
D18B9 CRC64;
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InterPro; IPR001840; WD40.

InterPro; IPR001840; WD40.

InterPro; IPR001841; Znf ring.

Pfam; PF00637; Clathrin; 1.

Pfam; PF00637; Clathrin; 1.

Pfam; SM0029; CLH; 1.

SMART; SM0029; CLH; 1.

SMART; SM00184; RING; 1.

SMART; SM00320; WD40; 1.

SMART; SM00320; WD40; 1.

PROSITE; PS50082; WD_REPEATS_1; FALSE_NEG.

PROSITE; PS50082; WD_REPEATS_2; 1.

PROSITE; PS50082; WD_REPEATS_REGION; FALSE_NEG.
      Synthetase gene duplications.";

Proc. Natl. Acad. Sci. U.S.A. 92:2441-2445(1995)
-!- CATALYTIC ACTIVITY: ATP + L-isoleucine + tRN.
diphosphate + L-isoleucyl-tRNA(Ile).
-!- COFACTOR: Binds 1 zinc ion per subunit (By s-isoleucine) sysimilarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cyroplasmic.
-!- SUMILARITY: Belongs to class-I aminoacyl-tRN
                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-MSB8 / DSM 3109 / ATCC 43589;

MEDLINE=9287316; PubMed=10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

MCDonald L., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from

genome sequence of Thermotoga maritima.";
                                                                                                           MEDLINE=95223956; PubMed=7708661;
Brown J.R., Doolittle W.F.;
"Root of the universal tree of life based on ancient aminoacyl-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYI THEMA
P46213;
01-NOV-1995
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CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                    SEQUENCE OF 95-599
                                                                                                                                                                                                                                                                                                                                                                                            Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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30-MAY-2000 (Rel. 39, Last seq
15-MAR-2004 (Rel. 43, Last ann
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15-MAR-2004 (Rel. 43, Last annotation update)
7-3-1-1-1 (Isoleucine--tRNA ligase)
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8; Conserv
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211 PO
33 PO
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57.1%;
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POLY-GLU.
POLY-ALA.
R -> G (IN REF. 2).
E -> EE (IN REF. 2).
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Pred. No. 48;
0; Mismatches
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       aminoacyl-tRNA synthetase family.
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                                                 similarity).
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Matches 7
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21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
10-OCT-2003 (Rel.
           SEQUENCE OF 1-29 FROM N.A.
MEDLINE=82174546; PubMed=7041115;
Grundstroem T., Jaurin B.;
                                                                                                                                                                       Jaurin B., Grundstroem T.;

"ampC cephalosporinase of Escherichia coli K-12 has a different
evolutionary origin from that of beta-lactamases of the penicillinase
                                                                   Blattner F.R.;
"Analysis of the region from 92.8
                                                                                                  STRAIN=K12 / MG1655;
MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, So
                                                                                                                           SEQUENCE FROM
STRAIN=K12 / N
                                                                                                                                                                                                                                                                                                                  10-OCT-2003 (Rel. 42, Last annotation update)
Beta-lactamase precursor (BC 3.5.2.6) (Cephalosporinase)
                                                                                                                                                                                                                 MEDLINE=82060161; PubMed=6795623;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
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EMBL; 137104; AAC41448.1; -.
PIR; B7263; B7263.
HSSP; P41972; 1FFY.
TIGR; TM1361; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is posture of the Swiss Institute of Bioinformatic the Buropean Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                       Escherichia coli genome through 100 minutes."; s. 23:2105-2119(1995).
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46.7%;
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Last sequence update)
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frd operons on the Escherichia coli
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Pred. No. 55;
3; Mismatches
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                                                                                                  Sofia H.J., Daniels D.L.,
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chromosome."; Proc. Natl. A

Acad.

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amino acid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complexed structure and antimicrobial activity of a non-beta-lactam inhibitor of AmpC beta-lactamase.";

protein Sci. 8:2330-2337(1999).

-i- FUNCTION: THIS PROTEIN IS A SERINE BETA-LACTAMASE WITH A SUBSTRATE SPECIFICITY FOR CEPHALOSPORINS.

-i- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Three-dimensional structure of AmpC beta-lactamase from Escherichia coll bound to a transition-state analogue: possible implications for the oxyanion hypothesis and for inhibitor design."; Biochemistry 37:16082-16092(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLLINE=99036630; PubMed=9819201;
Usher K.C., Blaszczak L.C., Weston G.S
Remington S.J.;
   SWISS-2DPAGE; PO0811; COLI.

ECO2DBASE; 1035.7; 6TH EDITION.

ECO2DBASE; 1PR00146; Beta_lactamase.

InterPro; IPR00146; Beta_lactamase.

InterPro; IPR001437; Prok_lipoprot_S.

Pfam; PP00144; beta-lactamase; 1.

PROSITE; PS00336; BETA_LACTAMASE_C; 1.

PROSITE; PS00336; BETA_LACTAMASE_C; 1.
                                                                                                                                                                                                                                                                                                                                                    EMBL; J01611; AAA23441.1; -.
EMBL; U14003; AAA97049.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
MEDLINE=20060984; PubMed=10595535;
Powers R.A., Blazquez J., Weston G.S., Morosini M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Monomer.
SUBCELLULAR LOCATION: Periplasmic.
SIMILARITY: Belongs to the class-C beta-lactamase family.
                                                                                                      04-MAR-03.
04-MAR-03.
                                                                                                                                                                                                                                                                          04-DEC-00.
                                                                                                                                                                                                                                                                                                                                  CAA23537.1; -.
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Matches 6; Conserv
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         50.6%;
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; Pred. No. 28;
3; Mismatches
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          DB 1; Length 377; 28;
    Indels
    0
    Gaps
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EMBL; AE000487; EMBL; V00277; CA PIR; A01007; QKE

PDB PDB PDB PDB PDB

1GA9

PDB; 11EL; 15-2 PDB; 1XISM; 17-3 PDB; 1XXS; 17-3 PDB; 1XXS; 17-3 PDB; 1XCS; 27-X PDB; 27-X PDB;

. UNW;

proteome.

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HITPAGSSNYVYGY

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Pfam; Pf0314; L. Pfam; Pf0314; ELONGALL.

PRINTS; PR00315; EF-Tu; 1.

TIGRFAMS; TIGR00485; EF-Tu; 1.

TIGRFAMS; TIGR00231; small GTP; 1.

PROSITE; P800301; EFACTOR GTP; 1.

A PROSITE; P800301; Protein biosynthesis; GTP-binding; Transit peptide; Chloroplast; Multigene family.

Transit peptide; Chloroplast; Multigene family.

TRANSIT 1 70 CHLOROPLAST (POTENTIAL).

FT TRANSIT 1 479 ELONGATION PACTOR TU.

FT CHAIN 89 96 GTP (BY SIMILARITY).

TO GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

CD65F0E262BD77B CRC64;
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EFT2_SOYBN
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InterPro; IPR004545; EF GTPbind.
InterPro; IPR004160; EFTU_Cterm.
InterPro; IPR004161; EFTU_D2.
InterPro; IPR009001; Elong_init |
InterPro; IPR009205; Small_GTP.
InterPro; IPR009205; Translat_fa.
Pfam; PF00009; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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01-NOV-1995
15-DEC-1998
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HSSP; P02990; 1EFU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression.";
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SIMILARITY: Belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: This protein promotes the GTP-dependent binding aminoacyl-trna to the A-site of ribosomes during protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EF-Tu/EF-1A subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sci. 117:83-92(1996).
 1 HITPAGSSNYVY 12
                          Similarity 6; Conserv
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(Rel.
(Rel.
                          Conservative
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37,
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# BETU Cterm.

# BETU D2.

# Blong init C.

# Small GTP.

# Translat factor.
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                        4.
                                      Score 40;
Pred. No.
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                        Mismatches
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                                            EMBL; X95653; CAA64955.1; -.
EMBL; U61145; AAC51520.1; -.
EMBL; U52965; AAC50591.1; -.
PIR; G02838; G02838.
TRANSPAC; T04888; -.
Genew; HGNC:3527; EZH2.
MIM; 601573; -.
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                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0003677; F:DNA binding; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 134-746 FROM N.A.
MEDILINE=96220494; PubMed=8649418;
HOBERT O., Jallal B., PubMed=86849418;
"Interaction of Vav with ENX-1, a putative transcriptional regulator of homeobox gene expression.";
of homeobox gene expression.";
Mol. Cell. Biol. 16:3066-3073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mediate gene silencing in Drosophila heterochromatin and a cerevisiae telomeres.";
EMBO J. 16:3219-3232(1997).
                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98167853; )
Cardoso C., Timsit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hum. Mol. Genet. 7:679-684(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain of the human EZH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colleaux L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=97357309;
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Chen H., Rossier C., Antonarakis S.E.;
"Cloning of a human homolog of the Drosophila enhancer of zeste gene
(EZH2) that maps to chromosome 21q22.2.";
Senomics 38:30-37(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Specific
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20 HFSPSPSSNYLF 31
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s., Villard L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=9214638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Khrestchatisky M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulation of gene
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99160476; PubMed=10051331;
Laible G., Haynes A.R., Lebersorger A., O'Carroll D., Mattei M.-G.,
Denny P., Brown S.D., Jenuwein T.;
"The murine polycomb-group genes ezhl and ezh2 map close to hox gene
clusters on mouse chromosomes 11 and 6.";
Mamm. Genome 10:311-314(1999).
-!- FUNCTION: May be involved in the regulation of gene transcription
and chromatin structure.
-!- SUBUNIT: BINDS ATRX VIA THE SET DOMAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MEDLINE=97014262; PubMed=8861097;
MEDLINE=97014262; PubMed=8861097;
Hobert O., Sures I., Ciossek T., Fuchs M., Ullrich A.;
"Isolation and developmental expression analysis of Enx-1, a
mouse Polycomb group gene.";
Mech. Dev. 55:171-184(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q611Be; Q9R090;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence |
28-FEB-2003 (Rel. 41, Last annotation
Enhancer of zeste homolog 2 (ENX-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00856; SET; 1.
SMART; SM00717; SANT; 2.
SMART; SM00317; SET; 1.
PROSITE; PS50280; SET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EZH2
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DOMAIN 490 495 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)

DOMAIN 523 605 CYS-RICH.

DOMAIN 611 731 SET.

CONFLICT 224 224 F -> L (IN REF. 1).

CONFLICT 724 724 F -> V (IN REF. 1).
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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ISOId=Q61188-2; Sequence=VSP_001501;
TISSUS_SPECIFICITY: WIDELY EXPRESSED IN EARLY EMBRYOS. IN LATER EMBRYOGENESIS, EXPRESSION RESURTICIED TO CENTRAL AND PERIPHERAL NERVOUS SYSTEM, LIVER AND THYMUS. IN ADULT, HIGHEST EXPRESSION IN SPLEEN, TESTIS AND PLACESVA. LOWER LEVELS IN INTESTINE AND MUSCLE AND VERY LOW LEVELS IN BRAIN AND LIVER. NO EXPRESSION IN HEART, THYROID GLAND, LUNG AND KIDNEY.
DEVELOPMENTAL STAGE: EXPRESSED IN BOTH ADULT AND EMBRYO WITH HIGHEST LEVELS IN EARLY EMBRYOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear (Probable) ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                   Name=ENX-1A;
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                                                                                                                                                                                                                                                                                 IsoId=Q61188-1; Sequence=Displayed;
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77.8%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Best Local :
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Q45710;
16-OCT-2001
                                                                     Patent number WO9416079, 21-JUL-1994.

-i- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING
-i- DEVELOPMENTAL STAGE: The crystal protein is produce sporulation and is accumulated both as an inclusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                               STRAIN=NRRL B-18679 / PS80JJ1;
Payne J.M., Narva K.E.;
                                                                                                                                                                                                                           CRY14AA OR CRYXIVA(A).
Bacillus thuringiensis (subsp. sotto)
Bacteria; Firmicutes; Bacillales; Bac
                                                                                                                                                                                                                                                                                                                                                                          BACTS
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VARSPLIC
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                      -!- SIMILARITY: Belongs to the delta endotoxin family
                                               the spore coat.
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GO; GO:0005515; F:protein binding; IP
InterPro; IPR00105; Myb DNA_binding.
InterPro; IPR001214; SET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U52951; AAC52655.1; ~.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 SET domain.
-!- SIMILARITY: Belongs to the EZ family.
                                                                                                                                                     "Novel
                                                                                                                                                                                                                   NCBI_TaxID=29340;
                                                                                                                                                                                                                                                                                                         16-OCT-2001
16-OCT-2001
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                                                                                                                                      arvae.
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OMAIN 490 495 NUCLE
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SM00317; SET; 1.
E; PS50280; SET; 1.
                                                                                                                                                   Bacillus thuringiensis toxins active against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159
746 AA;
                                                                                                                                                                                                                                                                         (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
(Rel. 40, Last annotation update)
crystal protein cry14Aa (Insecticidal delta-endotoxin
(Crystaline entomocidal protoxin) (132 kDa crystal
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611
511
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85336 MW;
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731
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                                               segment of the
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Pred. No. 54;
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/FTId=VSP_001501.
MISSING (IN REF. 2).
0435C021963ED24E CRC64;
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                                                                                                                                                                                                                              Bacillaceae;
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                                               protein is located in the
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Best Local
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                                                                                                                                                       InterPro; IPR003391; Adeno_terminal.
Pfam; PF02459; Adeno_terminal; 1.
DNA replication; Covalent protein-DNA linkage.
BINDING 545 COVALENT LINKAGE OF VIRAL DNA
SIMILARITY).
                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ojkic D., Yagubi A., Bautista D., Haj-Ahmad Y.;
"Sequence analysis of the terminal protein precursor coding
from bovine adenovirus serotypes 2 and 3.";
Intervirology 40:253-262(1997).
-I- FUNCTION: This protein is covalently attached to the ter
replicating DNA in vivo and nascent DNA synthesized in v
may play some role in DNA replication.
                                                                                                                                                                                                                                                                                        EMBL; AF252854; AAB88488.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98275674; PubMed=9612727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=114429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine adenovirus type 2
Viruses; dsDNA viruses, n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA terminal
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055438;
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15-MAR-2004
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Pro; IPR005638; endotoxin.N.
Pro; IPR005639; endotoxin.N.
Pro; IPR008979; Gal bind_Tike
Pr0; Pro; Pr00855; endotoxin; 1.
Pr00555; endotoxin; 1.
     N
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                                              Similarity
9; Conser
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ITPAG---SSNYVYGY 14
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                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 43, Last annotation updat
protein (Bellett protein) (pTF
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                                                                                                                                          71440 MW;
                                                                  56.2%;
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10 RNA stage; Adenovir:
                                                                Score 39.5;
Pred. No. 55;
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Pred. No. 85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adenoviridae; Mastadenovirus.
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modified and this statement is not removed.
entitles requires a license agreement (See )
or send an email to license@isb-sib.ch).
                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR005421; Pfam; PF00822; PMP22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1206582; Cacng1
InterPro; IPR004031; PMP
InterPro; IPR008368; VDC
                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wissenbach U., Bosse-Doenecke E., Freise D., Hofmann F., Flockerzi V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 16-OCT-2001 (Rel. Voltage-dependent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129/SvJ; TISSUE=Skeletal muscle;
MEDLINE=98163244; PubMed=9504716;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. Chem. 379:45-50(1998).

FUNCTION: This protein is a subunit of the dihydropyridine (DHP) sensitive calcium channel. Plays a role in excitation-contraction coupling. The skeletal muscle DHP-sensitive Ca(2+) channel may function only as a multiple subunit complex.

SUBUNIT: The L-type calcium channel is composed of five subunits: SUBCNAL-1, alpha-2/delta, beta and gamma. SUBCELULIAR LOCATION: Integral membrane protein.

SIMILARITY: Belongs to the PMP-22 / EMP / MP20 family. CACNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subfamily.
                                                                                                                                                                                                                                                                                                                                                                              S; PR01792; VDCCGAMMA1.
S; PR01601; VDCCGAMMA1.
channel; Transmembrane; Ion transport; Voltage-gated channel;
72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJ006306; CAA06966.1; -.
                                           1 HITPAGSSNYVY
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2
                                                                                          Similarity 6; Conserv
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HVTPSGEKNCSY
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141
181
                                                                                          Conservative
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40, Last sequence update)
40, Last sequence update)
40, Last annotation update)
calcium channel gamma-1 subunit (Dihydropyridine-
skeletal muscle calcium channel gamma subunit).
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2_Claudin; 1.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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POTENTIAL.
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                                                                                             Mismatches
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                                                                                          4
                                                                                                                                      Length 223;
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                                                                                                                                                                                       CRC64;
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Job time : 3.25309 secs

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Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
 Query
Match
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*
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Gapop 10.0 , Gapext 0.5
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Copyright
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sp_mhc:*
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337
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                                 Q94257
Q85902
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Q94257 caenorhabdi
Q89ym5 bacteroides
Q886n2 oryza sativ
Q9qtc3 marek's dis
Q859q1 bacteriopha
Q33707 streptomyce
Q9zua7 arabidopsis
Q8fwt3 brucella su
Q82410 chlamydophi
Q7ub23 shigella fi
Q9mm70 campylobact
Q95076 drosophila
Q9v7u9 drosophila
Q9v7u9 drosophila
Q9v7u9 drosophila
Q9v7u9 streptococc
Q8zun9 pyrobaculum
Q8tmu9 methanosarc
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### ALIGNMENTS

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SEQUENCE 117 AA; 12672 MW; 4749892B70E08919 CRC64;	Hypothetical protein.	Wormpen: K04A8.3: CE11704.	PIR; D89075; D89075.	EMBL; U64849; AAC48049.1;	Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.	ssion.";	Waterston R.;	STRAIN=Bristol N2;	SEQUENCE FROM N.A.	[3]	itted (NOV-1996)	ence of C. elegans cosmid K04A8.";	₩ H.;	STRAIN=Bristol N2;	SEQUENCE FROM N.A.	[2]	Science 282:2012-2018(1998).	gating biology. The C. elegans Sequencin	ode C. elegans: a pl		MEDLINE=99069613; PubMed=9851916;	STRAIN=Bristol N2;	SEQUENCE FROM N.A.		NCBI_TaxID=6239;	Rhabditidae; Peloderinae; Caenorhabditis.	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			l protein.	(TrEMBLrel. 25, Last annotation	(TrEMBLrel. 02,	(TrEMBLrel. 02, Created)	7;	Q94257 PRELIMINARY; PRT; 117 AA.	57

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RESULT 3

Q8S6N2

ID Q8S6N2

AC Q8S6

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Matches 9
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Best Local Similarity
Matches 7; Conserv
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01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
05JNBA0073101.15.
05JNBA0073101.15.
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                   SEQUENCE F
STRAIN=cv.
                                                                                                                             STRAIN-cv. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.P.
"Oryza sativa chromosome 10 BAC OSJNBa0073L01 genomic sequence.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-VPI-5482 / ATCC 29148;

MEDLINE-2255658; PubMed-12663928;

MEDLINE-2255058; PubMed-12663928;

Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

Chiang H.C., Hooper L.V., Gordon J.I.;

"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";

Science 299:2074-2076(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q89YM5;
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GO; GO:0019013; C:viral nucleocapsid;
InterPro; IPR003486; Nairo_nucleocap, 1.
ProDom; PD006459; Nairo_nucleocap; 1.
Complete proteome.
SEQUENCE 307 AA; 35341 MW; 5DD1304
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NCBI_TaxID=818;
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Bacteroidaceae; Bacteroides.
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Bacteria; Bacteroidetes; Bacteroides
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01-OCT-2003
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                            FROM N.A.
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2 (TrEMBLrel. 21, I
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Last annotation update)
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0; Mismatches
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Strain HPRS24.";
Curr. Top. Microbiol. Immunol. 0:0-0(20 EMBL; AB024414; BAA82917.1; -.
EMBL; AB049735; EAB16531.1; -.
EMBL; AB049735; EAB16531.1; -.
InterPro; IPR003493; Herpes glycopH.
InterPro; IPR003493; Herpes glycopH.
Pfam; PF02489; Herpes glycopH; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
UJ22 product homolog (Glycoprotein H).
ORF 29 OR UL22.
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Q9QTC3;
01-MAY-2000
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[3]
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Marek's disease-like viruses.
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Izumiya Y., Jang H., Ono M., N
Submitted (OCT-2000) to the EN
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EMBL; AE017083; AAP53324.1;
Gramene; Q856N2; -
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Buell C.R., Wing R.A., McCombie W.R., Messing
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ
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34.6%;
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Ono M., Mikami T.;
to the EMBL/GenBank/DDBJ
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GO; GO:0003B24; F:cattalytic activity; IEA.
GO; GO:0009103; F:cipopolysaccharide biosynthesis;
InterPro; IPR000088; dTDP sugar isom.
Pfam; PF00908; dTDP sugar isom; 1.
ProDom; PD001462; dTDP sugar isom; 1.
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MEDLINE=97352712; PubMed=9209071;

Otten S.L., Gallo M.A., Madduri K., Liu X., Hutchinson C.R.;

"Cloning and characterization of the Streptomyces peucetius dr

"Cloning and characterization of the Streptomyces of the genes encoding three enzymes required for biosynthesis of the daunorubicin precursor thymidine diphospho-L-daunosamine.";

J. Bacteriol. 179:446-4450(1997).

EMBL; AF006633; AAB63046.1; -.
Q9ZUA7
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HSSP;
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Kazmierczak K.M., Rothman-Denes L.B.;

"Partial sequence and sequence analysis of the Bacteriophage N4 virion

RNA polymerase and five other phage late gene products.";

Submitted (FEB-2001) to the EMBL/GenBank/DDBU databases.

EMBL; AF350004; AA024829.1; -.
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Viruses; dsDNA viruses,
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NCBI_TaxID=1950;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces peucetius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative epimerase.
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                                                                                                                                                                    ITPAGSSNYVY
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                                                                                                                                 VTPPGSAKYVY
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                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                     AA
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16094 MW; 59F013A080B9A600 CRC64;
                                                                                                                                                                                                                                                                                                 sugar_isom; 1.
TDP_sugar_isom; 1.
22632 MW; 5E6C1866853A8529 CRC64;
                                                                                                                                                                                                                                 54.4%;
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Last annotation update)
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                                                                                                                                                                                                                                      Score 43;
Pred. No.
                      PRT;
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces
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RESULT 8

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DT 01-M
DT 01-M
DT 01-M
DT 01-G
BRAG
GN BRAG
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Best Local
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InterPro; IPR008974; Traf_dom.
Pfam; PP00917; MATH; 1.
SMART; SM00061; MATH; 1.
PROSITE; PS50144; MATH; 1.
SEQUENCE 269 AA; 30515 MW;
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01-MAY-1999 (TrEMBLrel. 1
01-OCT-2003 (TrEMBLrel. 2
At2901790 protein.
AT2G01790
Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam I., Brinkac L.M., Beanan M.J., Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.; "The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts.", proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Columbia;

MEDLINE=20083487; bubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carreara A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Copenhaver G.F., Fraser C.M., Venter J.C.;

"Sequence and analysis of chromosome 2 of the plant Arabidopsis

thaliana.";
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=1330 / Biovar 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
Site-specific recombinase, p
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brucella suis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BRA0362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8FWT3;
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                                                                                                                                                                                                                                                           MEDLINE=22247741; PubMed=12271122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=29461;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Last sequence update,
Last annotation updat
phage integrase family
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e family.
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AC Q7UBZ
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Best Local S
Matches 8
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               Q7UBZ3;
Q7UBZ3;
01-OCT-2003
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Q824I0;
Q824I0;
Q824I0;
Q824I0;
Q1-JUN-2003
Q1-JUN-2003
Q1-CCT-2003
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01-JUN-2003 (TrEMBLrel. 24, I
01-OCT-2003 (TrEMBLrel. 25, I
Peptide chain release factor
PRFB OR CCA00166.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR005139; PCRF.
InterPro; IPR000352; Pep rel_factor_I
InterPro; IPR004374; PrfB.
Pfam; PF03462; PCRF; 1.
Pfam; PF03462; RF-1; 1.
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EMBL; AE016994; AAP04917.1; -
TIGR; CCA00166; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Chlamydophila caviae (Chlamydia examining the role of niche-specific genes in the eventhamydiaceae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydophila caviae.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae;
NCBI_TaxID=83557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00589; Phage_integrase; 1.
                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H. Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                    PRÓSITE;
                                                                                                                                                                                                                                                                                                                                                                                        rigrfams;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GC:0005737; C:cytoplasm; IEA.
GO:0016149; F:translation release factor
GO:0006415; P:translational termination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0003677; F:DNA binding; IEA.
GO:0015074; P:DNA integration; IEA.
GO:0006310; P:DNA recombination; IE
erPro; IPR002104; Phage_integrase.
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8; Conserv
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8; Conserv
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PS00745; RF_PROK_I; 1.
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57.1%;
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Q960R6;
01-DEC-2001
01-DEC-2001
01-OCT-2003
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ datab:
EMBL; AUZ49744; CAB56502.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0015055; F:protein disulfide oxidoreductase
GO; GO:0006118; F:electron transport; IEA.
InterPro; IPR003752; DsbB.
Pfam; PF02600; DsbB: E6246 MW: 10A8E12EA925F826 CRC
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01-MAY-2000 (TrEMBLrel. 13, Las
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Putative membrane protein CjaE.
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MEDLINE=22590274; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Pournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling J.
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 24577.";
Infect. Immun. 71.2775-2786(2003).
EMBL; AB016986; AAP17879.1;
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$2723.
Shigella flexneri.
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NCBI_TaxID=623;
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NCBI_TaxID=197;
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Bacteria; Proteobacteria;
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RA Adams M.D. (Calniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Goller R.F., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Goller R.F., RA Adams M.D., Celniker S.E., Holt R.A., Zhang Q., Chen L.X., RA Bautcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., R.A. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., R.A. Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., R.A. Barladon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., R.A. Barladon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., R.A. Barladon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., R.A. Barladon R.C., Baxendale J., Bayraktroglu L., Beasley E.M., R.A. Barladon R.C., Baxendale J., Bayraktroglu L., Beasley E.M., R.A. Barlaw R.M., Basu A., Baxendale J., Bayraktroglu L., Belshakov S., Pleison R.M., Bouck J., Brokstein P., Brottier P., Rottier P., Candra I., R.A. Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Chandra I., R.A. Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., R.A. Dockson R., Dollaker R., Bouck J., Brokstein P., Brottier P., Rottier P., Rottier P., Bornkov B.C., Dunn P., R.A. Dockson R., Dollaker G., Davenport L.B., Davies P., R.A. Dockson K., Dough L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., R.A. Dodson K., Dowles R., Dugan-Rocha S., Dunkov B.C., Dunn P., Harris M., J., Wolf M., Glasser K., R.A. Harris M.J., Weisen T.J., Hernandez J.R., Houck J., R.A. Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., R.A. Hostin D., Holtson K.A., Howland T.J., Wei M.-H., Dowland C.J., R., Houck J., Liang Y., Lin X., R.A. Lisko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X., R.A. Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., R.A. Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., R.A. Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Li Z., L
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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PSI OR EG:EG0003.2 OR CG8912.
PSI OR EG:Honogaster (Fruit fly).
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C -! - SIMILARITY: CONTAINS 3 KH DOMAINS.

R EMBL; AY051900; AAX93324.1; -.

R EMBL; AE003805; AAX70893.1; -.

R FlyBase; FBgn0014870; Psi.

R GO; GO:0006371; P:mRNA processing; IDA.

R GO; GO:0006371; P:mRNA splicing; IDA.

R GO; GO:0006371; P:mRNA splicing; IDA.

R GO; GO:0006371; P:mRNA splicing; IMP.

R InterPro; IPR004089; KH_Cype-1.

R InterPro; IPR004089; KH_Cype-1.

I InterPro; IPR004088; KH_Type-1.

I InterPro; IPR002173; PFKB.
MEDINE-2019(06; PubMed=10731132;
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Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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01-CCT-2002 (TrEMBLrel. 22, L
01-CCT-2003 (TrEMBLrel. 25, L
CG8912 protein (PSI protein).
PSI OR EG:EG0003.2 OR CG8912.
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Q9V7U9;
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Eukaryota; Metazoa; Archropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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element pre-mRNA splicing.";
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Dahlke C., Davenport L.B., Davis
A., Deng Z., Mays A.D., Dew I., Di
Downes M., Dugan-Rocha S., Dunkov
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EMBL/GenBank/DDBJ
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L.B., Davies
, Dew I., Diet
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Reese M.G.,
Then H.,
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Rogers Y.,
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RESULTS REPORTED TO SERVICE TO SE
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Matches 7
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FlyBase; FBgn0014870; Psi.

GO; GO:0006397; P:mRNA processing; II

GO; GO:0006371; P:mRNA splicing; IDA

GO; GO:0007283; P:spermatogenesis; II

InterPro; IPR004088; KH_cvpe_1.

InterPro; IPR004088; KH_cvpe_1.

InterPro; IPR00413; PfkB.

Pfam; PF00013; KH; 4.

SMART; SM00322; KH; 4.
                                                             SPECIBS-S.pyogenes; STRAIN-MGAS315 / Serotype M3; MEDLINB-2213808; PubMed=1212206; Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hof Mammarella N.D., Liu M.-Y., Smoot J.C., Forcella Campbell D.S., Smith T.M., McCormick J.K., Leung Schlievert P.M., Musser J.M.; Schlievert P.M., Musser J.M.; Waster J.M.; Tarain of group phage-encoded toxins, the high-virulence phenotyp.
                                                                                                                                                                                                                                                                                                                                                 Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S. Parkkis L.D., Beres S.B., Campbell S. Smith T.M., Zh Kapur V., Daly J.A., Veasy L.G., Musser J.M., "Genome sequence and comparative microarray analysis of group A Streptococcus strains associated with acute rhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perretti J.J., McShan W.M., Ajdic D.J., Savic I
Primeaux C., Sezate S., Suvorov A.N., Kenton S.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H.S.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes (serotype M3). Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes (serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative repressor protein.
SPY1496 OR ARGR OR SPYM18_1514 OR SPYM3_1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50084; KH_TYPE_1; 4.
PROSITE; PS00583; PFKB_KINASES
SEQUENCE 796 AA; 81588 MW;
                      emergence.";
Proc. Natl.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=MGAS8232 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome sequence of an M1 strain of Stroll. Acad. Sci. U.S.A. 98:4658-4663(2001)
                                                                                                                                                                                                                                                                                                            Acad.
                           Acad.
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                           SC1.
                                                                                                                                                                                                                                                                                                            Sci. U.S.A. 99:4668-4673 (2002)
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Pred. No. 1.5e+02;
2; Mismatches
                             99:10078-10083 (2002)
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_4B9423E033677EF5 CRC64;
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                                                                                                                                Lei B., Hoff J.S.,
Porcella S.F., Pa
.K., Leung D.Y.M.,
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                                                                     of group A phenotype,
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H., Song L.,
                                                                                                group A
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F., Parkins
                                                                       Streptococcus and clone
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RI of S. pyogenes SSI-1, SF970 and MGAS8232.";

RI Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AE006583; AAK34295.1; -.

DR EMBL; AE014066; AAL98085.1; -.

DR EMBL; AP005143; BAC63805.1; -.

DR EMBL; AP005143; BAC63805.1; -.

DR HSSP; O31408; 1B4A.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR HTSP; O31408; AF9 repress.

DR Pfam; PF01316; Arg_repress.

DR Pfam; PF01316; Arg_repressor; 1.

DR Pfam; PF01316; Arg_repressor; 1.

DR ProDom; PF007402; Arg_repress; 1.

DR ProDom; PF007402; Arg_repressor; 1.
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                        Query Match 51.9%;
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                   "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

EMBL; AE009889; AAL64367.1; -..
EMBL; AE009889; FAL64367.1; -..
EQ; GQ:0016853; F:iscomerase activity; IEA.
GQ; GQ:0008152; F:metabolism; IEA.
InterPro; IPR002529; FAA hydrolase.
Pfam; PF01557; FAA hydrolase.
FEAM: PF01557; FAA hydrolase.
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OBZUN9; O1-MAR-2002 (TrEMBLrel. 20, Created)

O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)

O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                      Isomerase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
MEDLINE=21664397; PubMed=1, Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.pyogenes; STRAIN=SSI-1 / Serotype M3;
Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
Hayashi H., Hamada S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrobaculum aerophilum.
Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                  Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2-hydroxyhepta-2,4-diene-1,7-dioate isomerase, conjectural.
PAB2688.
153 YIDPARALDYVFGY 166
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                                   1 HITPAGSSNYVYGY 14
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                                                                                                                                                    Complete proteome. 306 AA; 34384 MW; 137048EEB3B97347 CRC64;
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                                                                        ; Score 41; DB; Pred. No. 77; 4; Mismatches
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                                                                            Mismatches
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Minimum
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Maximum Match 100%
Listing first 45 summaries
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79
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1: geneseqp1980s:*
2: geneseqp1990s:*
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geneseqp2003as:*
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geneseqp2004s:*
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geneseqp2001s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	79	00.	14	44	AAE10549	랔
2	79	0	131	4.	1055	5 HPL inhī
ω	44	5	110	o.	97	G
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12	41	ŗ	930	4	ABU53195	195 F
13	41	÷	3508	4	ABB64461	Abb64461 Drosophil
14	. 40	0	61	4	AA006759	6759
15	40	0	242	7	ADE09113	113 Novel
16	40	0	380	N	AAY32049	049 Bovine
17	40	0	707	7	ADB65008	Adb65008 Human pro
18	40	0	746	N	AAW05260	Aaw05260 Chromatin
19	40	0	746	თ	ABU56461	5
20	40	0	1186	N	AAR56449	
21	40	0	1186	N	AAW10652	Aaw10652 Bacillus
22	40	0	1186	N	AAW21694	Aaw21694 Bacillus
23	40	0	1186	N	AAW31503	
24	39	49.4	178	N	AAY29541	Aay29541 Human lun
25	39	9	178	ω	AAB44453	Aab44453 Human lun

<b>4</b> 5	44	43	42	41	40	39	38	37	36	S	34	ω ω	32	ω μ	30	29	28	27	26	
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#### ALIGNMENTS

AAE10549 standard; peptide; 14 AA.

AAE10549;

10-DEC-2001 (first entry)

Llama species antibody VHH CDR3 #18

Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.

Lama sp.

EP1134231-A1.

19-SEP-2001.

20-FEB-2001; 2001EP-00200703.

14-MAR-2000; 2000EP-00200930.

(UNIL ) UNILEVER NV. UNILEVER PLC.

Bezemer S, Van De Burg M, De Haard JJW, Tareilus Ħ

WPI; 2001-572718/65

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Claim 4; Page 29; 37pp; English.

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HFL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region

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RESULT 2
AAE10555
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Matches 14
                    The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #15 from llama (camelid) species
                                                                                                                                                                            New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                         Example 2; Page 9; 37pp; English.
                                                                                                                                                                   of light
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody; camelid; anorectic; heavy chain variable domain; VHH; dietary enzyme inhibitor; medicament; human pancreatic lipase; human gastric lipase; HGL; cosmetic control; body weight.
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Pred. No. 8.4e-07;
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Sequence

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Best Local Similarity
                                                                                                                       The invention describes a new recombinant antibody fragment (1) with specificity for an infectious bursal disease virus (IBDV) antigenic determinant, comprises at least a variable region having a heavy chain region (VH) with any of 35 amino acid sequences, and a light (VL) chain where (I) additionally comprises any of 42 sequences amino acid sequences. The process is useful for identifying recombinant IBDV antibodies as immunodiagnostic or immunotherapeutic agents. (I) is useful for the diagnosis of an infection caused by at least one IBDV strain. The prevention, diagnosis and treatment against IBDV related aliments in animals. This is the amino acid sequence of a recombinant anti-IBDV-antibody light chain variable region
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                  New recombinant antibody fragment having a binding specificity for an infectious bursal disease virus (IBDV) antigenic determinant, useful the prevention, diagnosis and treatment of IBDV related ailments in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant antibody; IBDV; infectious bursal disease virus; virucide; gene therapy; heavy chain variable region; light chain variable region immunodiagnostic; immunotherapeutic; infection.
                                                                                                                                                                                                                                                                                                              Claim 4; Fig 4I; 265pp; English
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8; Conserv
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RESULT 5
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AC AAW7
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KW 8612
KW 1epi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant antibody; IBDV; infectious bursal disease virus; virucide; gene therapy; heavy chain variable region; light chain variable region; immunodiagnostic; immunotherapeutic; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant antibody fragment having a binding specificity for an infectious bursal disease virus (IBDV) antigenic determinant, useful the prevention, diagnosis and treatment of IBDV related ailments in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       animals.
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                                                                                                                                                                                                                                                                                                                         Sequence 250 AA;
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                                           Amino acid
                                                                        02-DEC-1998
                                                                                                    AAW75775;
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                  fragment
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                                                                                                                                                                                                      ITCSGGSNYYYGW 171
                                         sequence of lepidoteran-active 8612 toxin.
                                                                                                                                                                                                                                                               Conservative
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Pred. No. 29;
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strain. The
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8612 toxin; PCR; primer; amplification; Bacillus thuringiensis; probe; lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens;

Schnepf HE,

Narva KE,

Muller-Cohn

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RRESULT 6
AAW75774
ID AAW75
AC AAW7
AC AAW7
AC AAW7
DT 02-D
DT 02-D
XX HD52
XW HD51
XW Heli
XW Heli
XX Hoose
Baci
XX WOS8
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Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of a novel Bacillus thuringiensis toxin used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pesticides, especially for the control of obtrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New insecticidal Bacillus thuringiensis toxins - useful for controlling lepidopteran pests, especially Ostrinia nubilalis, Heliothis virescens and Helicoverpa zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 633 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 36-38; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schnepf HE, Narva KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9840490-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicoverpa zea; hybridisation
                                                                                                                                                                                                                                                                                                                                       AAW75774;
                                                                                                                                                                                                                                                                                                                                                                   AAW75774 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-1998
                                                                                                                                                                                                                  HD525 toxin; PCR; primer; amplification; Bacillus thuringiensis; probe; lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens; Helicoverpa zea; hybridisation.
                                                                                                                                                                                                                                                                            Amino acid sequence of lepidoteran-active HD525 toxin.
                                                                                                                                                                                                                                                                                                            02-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MYCO)
                                                                       13-MAR-1997;
                                                                                                   13-MAR-1998;
                                                                                                                                                             WO9840490-A1
                                                                                                                                                                                         Bacillus thuringiensis.
                                          (MYCO ) MYCOGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1998-506734/43
                                                                                                                                                                                                                                                                                                                                                                                                                                            410
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8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TPRGNSNYYPGY 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPAGSSNYVYGY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0040512P
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                                                                         97US-0040512P
                                                                                                     98WO-US005081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muller-Cohn
                                                                                                                                                                                                                                                                                                                                                                      633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB Pred. No. 83; 1; Mismatches
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Best Local S
Matches 8
       capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
                                                                                       The
                                                                                                                                                       genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New insecticidal Bacillus thuringiensis toxins - useful for controlling lepidopteran pests, especially Ostrinia nubilalis, Heliothis virescens and Helicoverpa zea.
                                                                                                             Disclosure; SEQ ID NO 39843; 21pp + Sequence Listing; English
                                                                                                                                                     New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                       Venter
                                                                                                                                                                                                                                                                                                       23-MAR-2000;
                                                                                                                                                                                                                                                                                                                                 23-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                            27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB71017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB71017 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pesticides, especially for the control of Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The polynucleotide coding sequences are useful for recombinant expression the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 32-34; 50pp; English.
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N-PSDB; AAV52611.
                                                                                                                                          interactions.
                                                                                                                                                                                                                                                                  (PEKE)
                                                                                                                                                                                                                                                                                          11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel genes that encode pesticidal toxins
                                                                                     invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                            2001-656860/75.
)B; ABL15120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanogaster polypeptide
                                                                                                                                                                                                                                                                CORP NY
                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid sequence of a novel Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                         2000US-0191637P.
2000US-00614150.
                                                                                                                                                                                                                                                                                                                                 2001WO-US009231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
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                                                                                                                                                                                                                                    , DWG
                                                                                                                                                   detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB Pred. No. 83; 1; Mismatches
                                                                                                                                                                                                                                     Myers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 39843
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83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ovarian antigen; ovary, covarian cancer; breast cancer; tumour; reproductive syndrom ovarian cancer; breast cancer; tumour; reproductive syndrom prosecution; prosecution; prosecution; prosecution; prosecution; prosecution; inflammatory condition; immune disorder; blood disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; cardiovascular disorder; respiratory disorder; drug screening; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; gene therapy; cytostatic; immunomodulatory; neuroprotective;
recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
                                                                                                                                                        ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                         The invention relates to 2175 novel human ovarian antigens ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), a
                                                                                                                                                                                                                                              Claim 11;
                                                                                                                                                                                                                                                                                               Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ov cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABQ56193.
                                                                                                                                                                                                                                                                               diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-2000; 2000US-0209467P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME
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7; Conserv
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                                                                                                                                                                                                                                              SEQ
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                                                                                                                                                                                                                                                ID NO 4248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCI INC
                                                                                                                                                                                                                                            2922pp; English
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:4248.
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                                                                                                                                                                                                                                                                                                                  ovarian
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shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vagnintis), immune disorders (e.g., congenital and acquired (immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, crespiratory disorders (e.g., anaemia), cardiovascular disorders, crespiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polypeptides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may for identification of individuals and in forensic analysis, and the creativity in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed constitution, but was obtained in electronic format directly from WIPO
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP11310 standard; protein;
                                                                                                                                                                                                                                                                                                       30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
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                                                                                          Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                    06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200192523-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                        Disclosure; SEQ ID NO 22602; 1037pp; English
                                                                                                                                                                        WPI; 2002-106308/14.
N-PSDB; ABN27062.
                                                                                                                                                                                                                                 Shimkets RA,
                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                             29-MAY-2001; 2001WO-US010836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORFX protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorder; rheumatoid gravis.
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                                                                                                                                                                                                                                 Leach
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28;
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent

The invention

s.

19008; 21pp + Sequence

Listing; English

Disclosure; SEQ ID NO

뮍 Š

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RESULT 10
ABB64072
ID ABB64472
AC ABB64
XX ABB64
XX Droso
XW Droso
XW Droso
XW Dharm
OX Droso
XW Droso
XX HO200
XY HO200
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
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11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001
                                                                                                                                                                            New isolated nucleic a
                                                                                                                                                                                                                                                                    N-PSDB; ABL08175.
                                                                                                                                                                                                                                                                                                                                                         Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE
                                                                                                                                                                                                                                                                                                 2001-656860/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLHPXGSSNILY
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                                                                                                                                                                                                                                                                                                                                                            PWD,
                                                                                                                                                                            detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                            Myers EW
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RESULT 11
ABP25558
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Best Local S
Matches 7
The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus progenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and artibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is used to determine whether a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                       New Streptococcus protein for the treatment or disease caused by Streptococcus bacteria, such detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                              Tettelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus
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)B; ABN66189.
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INST GENOMIC RES.
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                                                                                                                                                                                           Page 3184; 4525pp; English.
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2000GB-00028727.
2001GB-00005640.
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3; Mismatches
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1;
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                                                                                                                                                                                                                                  prevention of as meningitis,
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Query Match Best Local S

Similarity
7; Conserv

Conservative

51.9%; 58.3%;

Score 41; DB 4; Pred. No. 4.3e+02;

Length 930;

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HITPAGSSNYVY HVTPRGSGTSVY

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RESULT 12
ABU53195
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Matches
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                         This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
Sequence
                                                                                                                                                                                                             Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus that is prevented or treated may be meningitis. acid encoding (I) may be used to recombinantly produce (I) and used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins
                                                                                                                                                                                   Example III; Page 809; 1095pp; English
                                                                                                                                                                                                                                                                                       Wiemann
                                                                                                                                                                                                                                                                                                                                            18-AUG-1999;
28-SEP-1999;
                                                                                                                                                                                                                                                         WPI; 2001-327840/34
                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene therapy; vaccine; disease treatment; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human nucleic acid management-associated DKFZphtes3_2m18 homologue.
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                                                                                                                                                                                                                                                                                                                                                                                      18-AUG-2000;
                                                                                                                                                                                                                                                                                                                 (GEHU-) GERMAN HUMAN GENOME PROJECT
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ΑĄ,
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99US-0156503P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41;
Pred. No.
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RESULT 14
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL10176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                    Sequence 3508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 20175; 21pp + Sequence Listing; English
vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent
                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                          Human polypeptide
                                                                                                                                                                    AAO06759 standard; protein;
                                                                                                                                                                                                                                                  3159
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                                                                               SEQ ID NO 20651.
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Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to the kines, cell proliferation or cell differentiation or which may induce production of which may induce production of other constitution in which may induce production of other constitutions in which may induce production of other constitutions.
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18-MAY-2000;
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10-DEC-2001; 2001US-0339739P
11-DEC-2001; 2001US-0339453P
14-MAR-2002; 2002US-0365091P
                                                                                                                                                                                                                                                                                                                                                   novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder; contig.
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                                                                                                                   10-DEC-2002; 2002WO-US039555
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2000US-00577409.
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Best Local Similarity 72.
Matches 8; Conservative
                                                                                                                                                                               The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                Sequence 242 AA;
                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 2657; 1177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J; Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z_1 Ma Y, Wang D, Chen R, Xu C, Boyle BJ_1
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12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-0372615P.
22-APR-2002; 2002US-00128588.
24-APR-2002; 2002US-0376045P.
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38 PAGSSGYRAGY 48
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                                     PAGSSNYVYGY 14
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                                                                  Score 40; DB 7; Length 242
Pred. No. 1.4e+02;
0; Mismatches 3; Indels
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Search completed: October Job time : 14.6512 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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## ALIGNMENTS

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ABC Transporter UU
hypothetical prote
bet protein - huma
hypothetical prote
DNA helicase II -
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-759 <AQF>
A;Cross-references: GB:AE000738; NID:92983801; PIDN:AAC07360.1; PID:92983803; GB:AE00065;
A;Experimental source: strain VF5
C;Genetics:
                                                                                                                                    submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid R04A9.
A;Reference number: Z18558
A;Reference number: Z18558
A;Recession: T16679
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-780 <GEI>A;Cross-references: EMBL:U41550; NID:g1118045; PID:g1118049; PIDN:AAA83287.1; CESP:R04A9.
A;Cross-references: EMBL:U41550; NID:g1118045; PID:g1118049; PIDN:AAA83287.1; CESP:R04A9.
                                                            A; Cenetics:
A; Genetics:
A; Gene: CESP:R04A9.5
A; Gene: 36/3; 326/3;
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T16679
RYSothetical protein R04A9.5 - Caenorhabditis elegans
CySpecies: Caenorhabditis elegans
CySpecies: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t
CyAccession: T16679
RyGeisel, C.
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A;Gene: bcsA
C;Superfamily: bcsA protein
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C;Species: Campylob
C;Date: 31-Mar-2000
C;Accession: D81368
C;Accession: AF2881

C;Accession: AF2881

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, R;Wood, G.F.; Chen, Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, N.; Karp, P.; Romero, P.; Zhang, S.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Go:
                                                                                                                                                                                                       RESULT 5
AF2881
                                                                                                                                lipase esterase [imported] - Agrobacterium tumefaciens (strain C58, Dupont) (Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  host range factor 1 - Lymantria dispar nuclear polyhedrosis virus (;Species: Lymantria dispar nuclear polyhedrosis virus, LdMnPV C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000 C;Accession: T30415 R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, Virology 253, 17-34, 1999 A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for LA;Reference number: Z20836; MUID:99124785; PMID:9887315 A;Accession: T30415
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A/Experimental source: serotype (
G/Genetics:
A/Gene: Cj0941c
C/Superfamily: hypothetical prote
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A; Residues: 1-218 < KUZ>
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R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, Nature 403, 665-668, 2000
Nature 403, 665-668, 2000
A;Tittle: The genome sequence of the food-borne pathogen Campylobacter jejuni A;Reference number: A81250; MUID:20150912; PMID:10688204
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A; Residues: 1-401 < PAR >
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Matches 7
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Best Local :
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;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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lobacter jejuni
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Pred. No. 11;
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A; Gene: CESP: T04A8.3
A; Map position: 3
A; Introns: 25/2; 43/
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A;Molecule type: DNA
A;Residues: 1-459 <WIL>
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A.; Liu, F.; Wollam, C.; Al
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A;Accession: T24425
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R;Palmer, S.
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A; Residues: 1-250 < KUR>
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A; Map position:
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A;Cross-references: GB:AE008688; PIDN:AAL43468.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF2881
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;Species: Agrobacterium tumefaciens
;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
;Accession: F97657
Query Match
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Allinger, M.; Doughty, D.; Scott, C.;
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; Lappas, C.;
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Markelz, B.;
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Experimental source: strain H37Rv C;Genetics:
                                                                                                                                                                                                                                                                                      R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thom R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fras eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;

A;Title: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: A87019

A;Status: preliminary

A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytochrome b homolog cytB [similarity] - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Apr-2000
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A; Residues: 1-549 < C
RESULT 10
A84107
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C;Accession: A87019
C;Accession: A87019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable cytochrome B [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
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;Genne: qcrB
;Keywords: heme; iron; metalloprotein
;114,216/Binding site: heme iron (His)
;118,231/Binding site: heme iron (His)
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exences: GB:AL450380; NID:g13092952; PIDN:CAC31260.1;
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                                                                      LEKRFTGDYAHH
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Holroyd,
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T30101
                                                                                                                                 R;Cottage, A. submitted to the EMBL Data Library, submitted to the EMBL Data Library, submitted to the EMBL Data Library,
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T24033
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                  A; Experimental source: C; Genetics:
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                                                       A; Cross-references:
                                                                      A;Molecule type: DNA
A;Residues: 1-195 <WIL>
                                                                                                                      A; Reference number:
A; Accession: T24033
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     CESP:R07E3.7
                                                                                                     preliminary; translated
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                                                       EMBL: Z49207;
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A;Molecule type: DNA
A;Residues: 1-732 <570>
A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07376.1; GSPDB:GN001
A;Experimental source: strain C-125
C;Genetics:
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A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycosyltransferase BH3657 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: A84107
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hypothetical protein R07E3.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct 1999 #sequence_revision 15-Oct 1999 #t.C;Accession: T24033
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A;Experimental source: strain Bristol N2; clone C06G3
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6; Conserv
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8; Conserv
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                  #sequence_revision 15-Oct-1999 #text_change
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57.1%;
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Library, June 1
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Pred. No.
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Pred. No. 31
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clone

R07E3

PIDN: CAA89073.1; GSPDB: GN00028; CESP: R07E3.7

from GB/EMBL/DDBJ

May

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lysozyme (EC 3.2.1.17) - phage phi-29
N;Alternate names: morphogenesis protein 2
C;Species: phage phi-29
A;Note: host Bacillus amyloliquefaciens; Bacillus subtilis
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_cl
                                                                                                  A;Cross-references: GB:X04962; NID:g15676; PIDN:CAA28632.1; PID:g15679
R;Vleek, C.; Paces, V.
Gene 46, 215-225, 1986
A;Title: Nucleotide sequence of the late region of Bacillus phage phi-29 completes the A;Reference number: A25816; MUID:87106857; PMID:3803926
A;Accession: A33078
                                                                                                                                                                                                                                              R;Garvey, K.J.; Saedi, M.S.; Ito, J.

Nucleic Acids Res. 14, 10001-10008, 1986
A;Title: Nucleotide sequence of Bacillus phage phi-29 genes 14
A;Reference number: A24721; MUID:87117505; PMID:3027653
A;Accession: B24721
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C; Function:
                                               A;Cross-references: GB:M14782; NID:g215323; PIDN:AAA32288.1; PID:g215333
                                                                  A; Molecule type: DNA
A; Residues: 1-258 < VI
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A;Tille: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: H70468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / phosphoribosyl-ATP diphosphatase C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Aug-2002 C;Accession: H70468
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A; Introns: 46/1; 81/1; 113/3; 147/1
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Matches 6
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,;Residues: 1-205 <AQF>
,Residues: 1-205 <AQF>
,Cross-references: GB:AE000765; NID:g2984199; PIDN:AAC07730.1;
,Experimental source: strain VF5
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Best Local S
Matches 6
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A;Description: catalyzes hydrolysis of the beta-1,4-glycosidic bond C;Superfamily: phage T4 lysozyme; phage T4 lysozyme homology C;Keywords: glycosidase; host cell lysis; hydrolase; late protein F;15-134/Domain: phage T4 lysozyme homology <T4L>
                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-258 <PAC>
*-^~^a-references: GB:M11813; GB:M13904; GB:M13905; NID:g216046;
                                                                                                                                                                                                                                                                                                                                                                                  C;Species: phage PZA
A;Note: host Bacillus subtilis
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1999
C;Accession: A26215; J24831
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Copyright (c) 1993 - 2004 Compugen Ltd.
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PRT; 218	ALIGNMENTS	YBH8_PSEAE	AAC_ACTUT	TNP3_ECOLI	FRU_DROME	MI10_CAEEL	ORC2_MOUSE	Y322 MYCGE	RKI1 SECCE	YHJ6 YEAST	WRK8_ARATH	PRIS_METTH	PRPK_HUMAN	
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		pseudomonas	actinoplane	escherichia	drosophila	caenorhabdi	mus musculu	mycoplasma	secale cere	saccharomyc	arabidopsis	methanobact	homo sapien	

### 밁 5 Query Match Best Local S Matches 6 Q90165; 01-NOV-1997 (Rel. 01-NOV-1997 (Rel. 15-JUL-1999 (Rel. MEDLINE=98139158; PubMed=9499118; Chen C.J., Quentin M.E., Brennan L.A., Kukel C., Thiem S. "Lymantria dispar nucleopolyhedrovirus hrf-1 expands the range of Autographa californica nucleopolyhedrovirus."; J. Virol. 72:2526-2531(1998). -!- FUNCTION: Facilitates ACMNPV replication in two non-p Lymantria dispar multicapsid nuclear polyhedrosis virus (LdWNPV). Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus. NCBI\_TaxID=10449; EMBL; U38895; AAB07701.1; -. PIR; T30415; T30415. SEQUENCE 218 AA; 25675 MW This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). STRAIN=Hamden; SEQUENCE FROM N.A. Host range factor FUNCTION: Facilitates AcMNPV replication in two non-permissive cell lines, IPLB-Ld652Y and IPLB-LdFB. 37 2 IRKRFTSGYSHY 13 Similarity 50.06; Conservative VRYRYERGYGHY 1 8 5 5 25675 MW; 50.0%; Last sequence update) Last annotation update) Created) 48 2 Score 40; DB 1; Pred. No. 4.7; 5DD2BB0E16802001 CRC64; Mismatches 4; Indels Length 218; 3 larval 0; Gaps host 0

RESULT 2
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QCRB\_MYCTU STANDARD; PRT; 549 AA. Q10388; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Ubiquinol-cytochrome c reductase cytochrome B sub OCRB OR RVZ196 OR MTZ252 OR MTCY190.07 OR MBZ219. Mycobacterium tuberculosis, and

B subunit.

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MEDLINB=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Pryor M., Datkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22206494; PubMed=12218036; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Peterson J., DeBoy R., Dodson R.G., Gwinn M., Salzberg S.L., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Kolonay J.F., Utterback T., Weidman J., Khourn H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                            TRANSMEM
                                                                                                                                                                                                             InterPro; IPR005797; Cytb_b6_N.
Pfam; PF00033; cytochrome_b N; 1.
PROSITE; PS00192; CYTOCHROME_B_HEME;
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SUBUNIT: THE MAIN SUBUNITS OF THE UBIQUINOL:CYTOCHROME C ARE: CYTOCHROME B, THE RIESKE PROTEIN AND A CYTOCHROME C SUBCELLULAR LOCATION: Integral membrane protein (Probable SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY: CORRESPON AMINO END OF MITOCHONDRIAL CYTOCHROME B.
                                                                                                                                                                                                                                                                                                                                                    E70784; E70784.
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                                                                                                                                                                                                                                                                                                                                                                              AE007071; AAK46538.1;
BX248341; CAD97072.1;
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393:537-544(1998).
                                                                                                                                                                                         transport;
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P15878;
01-APR-1990
16-OCT-2001
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                between the Swiss Institute . Ther the European Bioinformatics Institutions as long a use by non-profit institutions as not removed.
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wingall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
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                                                                                                                                                                                                                                                                                                                             "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                      Squares S., S
Barrell B.G.,
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QCRB OR MLA12A OR ML0879.
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                                                                                                             SUBUNIT: THE MAIN SUBUNITS OF THE UBIQUINOL:CYTOCHROME ARE: CYTOCHROME B, THE RIESKE PROTEIN AND A CYTOCHROME SUBCELLULAR LOCATION: Integral membrane protein (Probab SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY. CORRESP AMINO END OF MITOCHONDRIAL CYTOCHROME B.
CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE A 12 KDA
                                                                                                       TO FRAMESHIFT ERRORS.
                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Educopean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
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28-FEB-2003
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Pfam; PF00033; cytochrome_b N; 1.
PROSITE; PS00192; CYTOCHROME_B_HEME; FALSE_NEG
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; T
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Acidic nucleoplasmic DNA-binding protein 1 (And-1) (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
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Best Local S
Matches 6
                                                                                                           AQUAE
HIS2 AQUAE
067780;
15-DEC-1998
15-DEC-1998
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear
REPEAT
REPEAT
Aquifex aeolicus.

Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex NCBI TaxID=63363;

[1]
                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Histidine biosynthesis bifunctional protein hisIE [Includes: Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) (PRA-CH);
Phosphoribosyl-AMP cyclohydrolase (EC 3.6.1.31) (PRA-PH)]
Phosphoribosyl-AMP cyclohydrolase (EC 3.6.1.31) (PRA-PH)]
HISI OR HISIE OR AQ_1968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
REPEAT
REPEAT
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                                                                                                                                                                                                                                           828
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В 5

RESULT

STANDARD;

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"Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
-i- FUNCTION: Binds DNA with high affinity. May also be involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00400; WD40; 4.

Pfam; PF000018; WD40; 1.

PROSITE; PS00678; WD_REPEATS_1; 2.

PROSITE; PS50082; WD_REPEATS_REGION;

PROSITE; PS50294; WD_REPEATS_REGION;

Nuclear protein; DNA-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AK036390; BAC29408 1; -.
EMBL; AK052690; BAC35097 1; -.
EMBL; AK052690; BAC35097 1; -.
MGD; MGI:2443514; D630024B06Rik.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not remove
entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Binds DNA with high affinity. May also be involved protein-protein interactions (By similarity). SUBCELLULAR LOCATION: Nuclear; nucleoplasm (By similarity). ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P59328-2; Sequence=VSP_006757, VSP_006758;
Note=No experimental confirmation available;
SIMILARITY: Contains 7 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P59328-1;
                                                                             Similarity 6; Conser
DFREKLNAGYSH 839
                                DIRKRFTSGYSH 12
                                                                                                                                                       970
970
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350
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52
93
134
184
228
271
                                                                             Conservative
                                                                                                                                                             AA;
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970
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131
173
173
223
267
310
                                                                                                                                                             107632
                                                                                               55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence=Displayed
                                                                                                                                                                                                                                                                                                                      ng; Repeat; WD repeat; Alternative splicing.
WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
TPCYVDSEGCVR -> KIIFFLYIKDIF (in isoform
                                                                                                                                                             Œ,
                                                                                                                                                                                                /FTId=VSP 006757.
/FTId=VSP 006757.
/IN ISOFORM 2).
/FTId=VSP 006758.
G -> V (IN REF. 1; BAC29408).
S -> P (IN REF. 1; BAC29408).
                                                                             Score 40; DB Pred. No. 23; 3; Mismatches
                                                                                                                                                             2B2B577A9A6D2792 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.
; WD repeat; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                    1;
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RESULT
LYCV_BE
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Best Local S
Matches 6
                                                                                                                                                                                                                  01-JUL-1989 (Rel. 11, C: 01-JUL-1989 (Rel. 11, La 16-OCT-2001 (Rel. 40, La 14) Lysozyme (EC 3.2.1.17) (Morphogenesis protein 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000765; AAC07730.1; -.
PIR; H70468; H70468.
HAMAP; MF_01019; -; 1.
InterPro; IPR002496; PRA-CH.
InterPro; IPR008179; PRA-PH.
InterPro; IPR008179; Pra_PH/CH.
                                                                                                                                                                                                                                                                                                                                                               BPPH2
LYCV_I
                                                                                                                                                                                                                                                                                                                  LYCV BPPH2
P11187;
01-JUL-1989
(1)
SEQUENCE FROM N.A.
MEDLING-87117505; PubMed-3027653;
MATVEY K.J., Saedi M.S., Ito J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
SEQUENCE
                                                                                                                                   Bacteriophage phi-29.
Viruses; dsDNA viruses,
phi-29-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 392:353-358(1998).
                                                                                                           NCBI_TaxID=10756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD002610; PRA-CH; 1.
ProDom; PD002611; Pra_PH/CH; 1.
Histidine biosynthesis; Multifunctional enzyme; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01502; PRA-CH; 1.
Pfam; PF01503; PRA-PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphoribosylamino)methylideneamino]imidazole-4-carboxamide. PATHWAY: Histidine biosynthesis; second step. PATHWAY: Histidine biosynthesis; third step. SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: In the N-terminal section; belongs to the PRA-CH SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-ATP + H(2)O = 1-(5-phosphoribosyl)-AMP + diphosphate.

CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-AMP + H(2)O = 1-(5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((5-phosphoribosyl)-5-((
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRKRFTSGYSHY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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23943 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
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                                                                                                                                                                                                                                                                       Last sequence up
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                                                                                                                                                                                                                                (Lysis
                                                                                                                                                           no
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Pred. No. 6.7;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORIBOSYL-AMP CYCLOHYDROLASE.
PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE;
8DB5DAA3261A2197 CRC64;
                                                                                                                                                                                                                                                 protein)
                                                                                                                                                           stage;
                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                  258
                                                                                                                                                                                                                                                    update)
) (Muramidase)
                                                                                                                                                           Caudovirales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 205
                                                                                                                                                             Podoviridae,
                                                                                                                                                                                                                                                    (Endolysin)
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RESULT
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DT 01
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Matches 6
                                                                                                                                                                                                                LYCV I
                                                              P07540;
01-APR-1988 (R
01-APR-1988 (R
16-OCT-2001 (R
Lysozyme (EC 3
(Late protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X04962; CAA28632.1; -. EMBL; M14782; AAA32288.1; -. EMBL; M14431; AAA88347.1; -. EMBL; B24721; WMBBP9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell wall by breaking down the peptidoglycan.

capalytic Activity: Hydrolysis of the 1,4-beta-linkages between acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan heteropolymers of the prokaryotes cell walls.

--- DOMAIN: LysM repeats are thought to be involved in peptidoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete sequence of Bacillus phage phi 29 required for the genome encapsidation reaction." Gene 40:311-316(1985)
Bacteriophage PZA.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Late protein;
ACT_SITE :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the homologous sequence Gene 46:215-225(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Nucleotide sequence of the late completes the 19,285-bp sequence the homologous sequence of phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87106857;
Vlcek C., Paces V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of Bacillus phage phi 29 genes homology of gene 15 with other phage lysozymes."; Nucleic Acids Res. 14:10001-10008(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to family 24 of glycosyl hydrolases
-!- SIMILARITY: Contains 2 LysM repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 116-258 FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86165873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding
                                                                                                                                                                                                             BPPZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF01476; LysM; 2.
PF00959; Phage_lysozyme; 1.
; SM00257; LysM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P00720;
                                                                                                                                                                                                                                                                                                                             29 KHYTIGYGHY 38
                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                          KRFTSGYSHY
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IPR002482; LysM._
'1476; LysM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163
214
258 AA;
                                                                (Rel. 07, C
(Rel. 07, I
(Rel. 40, I
C 3.2.1.17)
in gp15).
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Hydrolase; Glycosidase; Bacteriolytic enzyme;
15 15 PROTON DONOR (BY SIMILARITY).
163 207 LYSM 1.
214 258 LYSM 2.
58 AA; 28054 MW; 26AEOC1D927B42D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103L
                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=3879485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               60.0%;
                                                                                                               Last sequence update)
Last annotation updat
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                                                                                         (Lysis protein)
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Pred. No. 8.
                                                                                                                                                                                                             PRT;
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e of phi
e PZA.";
                                                                                                                                                                                                             258 AA.
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                                                                                           (Muramidase)
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RNA stage; Caudovirales; Podoviridae;

SEQUENCE FROM N.A. phi-29-like viruses. NCBI\_TaxID=10757;

PubMed=3095188;

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Matches
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REPEAT
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SEQUENCE FROM N.A.
STRAIN-ATCC 12228;
PubMed=12950922;
PubMed=12950922;
Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
Zhang Y.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
"Genome-based analysis of virulence genes in a non-biofilm-forming
Staphylococcus epidermidis strain (ATCC 12228).";
Mol. Microbiol. 49:1577-1593(2003).
                                                                                                                                                                                                               TARGC_STAEP STANDARD; PRT; 341 AA. 08CP35; 08CP35; 15-MAR-2004 (Rel. 43, Created) 15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) 15-MAR-2004 (Rel. 43, Last annotation update) N-acetyl-gamma-glutamyl-phosphate reductase (1 acetyl-glutamate semialdehyde dehydrogenase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Late
ACT_S
                                                                                                                                                                      Staphylococcus epidermidis. Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00720; 103L.
InterPro; IPR002196; Glyco_hydro_24.
InterPro; IPR002482; LysM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M11813; AAA88492.1; -.
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Gene 44:107-114(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paces V., Vlcek C., Urbanek P.;
"Nucleotide sequence of the lat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                    NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Helps to release the mature phage particles from the cell wall by breaking down the peptidoglycan.
CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between acetyl-D-glucosamine and N-acetyl-muramic acid in peptidoglycan heteropolymers of the prokaryotes cell walls.
DOMAIN: LysM repeats are thought to be involved in peptidoglycar binding.
SIMILARITY: Belongs to family 24 of glycosyl hydrolases.
SIMILARITY: Contains 2 LysM repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RT; SM00257; LysM; 2.
e protein; Hydrolase; Glycosidase; Bacteriolytic enzyme; Repeat.
SITE 15 PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A26215; WMBP15.
                                                                                                                                                                                                     OR SE1212.
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PF00959; Phage_lysozyme; 1.
; SM00257; LysM; 2.
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214
258 AA;
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28052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; I
Pred. No. 8.
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                                                                                                                                                                      Staphylococcus
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8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of Bacillus subtilis phage
                                                                                                                                                                                                                    (EC 1.2.1.38) (AGPR) (
(NAGSA dehydrogenase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptidoglycan
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Best Local &
Matches &
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HAMAP; MF 00150; -; I.
InterPro; IPR000706; AGPR act_site.
InterPro; IPR000734; Semialdh_dh.
Pfam; PF01118; Semialdhyde_dh; I.
Pfam; PF02774; Semialdhyde_dhc; I.
ProDom; PD03765; AGPR act_site; I.
TIGRFAMs; TIGR01850; aTgC; I.
PROSITE; P$01224; ARGC; I.
ARGC; I.
ARGC; I.
ARGC; I.
BY SIMILARITY.
ACT_SITE 147
BY SIMILARITY.
SEQUENCE 341 AA; 38227 MW; CA4B33D3D12DBCBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                         Rd.";
Science 269:496-512(1995).
-!- FUNCTION: Reduces trimethylamine-N-oxide (TMAO)
-!- FUNCTION: amine: an anaerobic reaction coupled t
                                                                                                                                                                                                                                 Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Wenter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Pasteurellaceae; Haemophil PaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Trimethylamine-N-oxide reductase precursor (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P44798;
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                                                                                                                                                                                                             Whole-genome random sequencing
reactions (By similarity).

CATALYTIC ACTIVITY: Trimethylamine + 2 (ferricytochrome + H(2)O = trimethylamine N-oxide + 2 (ferrocytochrome copactors: Molybdenum (molybdopterin) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + phosphate = N-acetyl-5-glutamyl phosphate + NADPH
PATHWAY: Arginine biosynthesis; third step.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: Belongs to the NAGSA dehydrogenase famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: (
SIMILARITY: Belongs to
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8; Conserv
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72.7%;
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                                                                                                                                                                                                                assembly of Haemophilus influenzae
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                                 (ferrocytochrome c) - subunit.
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Matches 6
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O13046;
28-FEB-2003
28-FEB-2003
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                   23-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Acidic nucleoplasmic DNA-binding protein 1 (And-1).
Acidic nucleoplasmic DNA-binding protein 1 (And-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00384; molybdopterin; 1.
Pfam; PF01568; Molydop binding; 1.
TIGRRAMS; TIGR00509; bisC_fam; 1.
TIGRPAMS; TIGR01409; TAT_signal_seq; 1.
PROSITE; PS00551; MOLYBDOPTERIN PROK_1; FALSE_NEG.
PROSITE; PS00499; MOLYBDOPTERIN_PROK_2; 1.
PROSITE; PS00932; MOLYBDOPTERIN_PROK_3; 1.
CONIDERATE; PS00932; MOLYBDOPTERIN_PROK_3; 1.
CONIDERATE; PS00932; MOLYBDOPTERIN_PROK_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; Q57366; 1EU1.
TIGR; HI0643; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U32747; AAC22303.1; -. PIR; H64083; H64083.
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                                                                                                                                                         TISSUE=Oocyte;
MEDLINE=97318764; PubMed=9175701;
                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR009010; Asp_decarb_fold.
InterPro; IPR006658; BisC.
InterPro; IPR006657; Mol_dinuc_bind.
InterPro; IPR006656; Molybdopterin.
InterPro; IPR006655; Prok_Mboxred.
InterPro; IPR0066311; Tat.
                                                                                                                                   'AND-1,
                                                                                                                                               Coehler A., Schmidt-Zachmann
                                                                                                                                                                                        SEQUENCE FROM N.A., SUBCELLULAR LOCATION, SUBUNIT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Periplasmic (By similarity).
SIMILARITY: Belongs to the prokaryotic molybdopterin-containing oxidoreductase family.
CAUTION: Was originally (Ref.1) assigned to be a biotin sulfoxide reductase hence the original gene designation of bisC.
                                                                                                                                                                                                                                                                                                                                                                                                                                         303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIRKRFTSGYSHY 13
                                                                                                                                 a natural chimeric DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                       DFLKKYTSGYAKF 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       825 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91053 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.2%;
46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39;
Pred. No.
                                                                                                                                                  .
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
TRIMETHYLAMINE-N-OXIDE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4254287D42B45E5B CRC64;
                                                                                                                                               Franke W.W.;
                                                                                                                                                                                                                                                                                                                                                                   1127 AA
                                                                                                                                 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no resumg as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 825
                                                                                                                                    combines an HMG-box
                                                                                                                                                                                           AND DNA BINDING
                                                                                                                                                                                                                                                  Euteleostomi;
; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL
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MBL outstation -
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RESULT 11
HIS3_METKA
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00398; HMG; 1.
SMART; SM00320; WD40; 4.
PROSITE; PS50118; HMG BOX 2; 1
PROSITE; PS501678; WD REPEATS 1
PROSITE; PS50082; WD REPEATS 2
PROSITE; PS50294; WD REPEATS R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA BIND
SEQUENCE
                       Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A.; "The confile te genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens."; Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
-!- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-AMP + H(2)0 = 1-(5-
                                                                                                                         SEQUENCE FROM N.A.
STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE-21927647; PubMed=11930014;
MEDLINE-21927647; PubMed=14930014;
                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-Feb-2003 (Rel. 41, Last annotation update)
Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) (PRA-CH).
HISI OR HISI_2 OR MK1537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                      Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Ste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00505; HMG box; 1.
Pfam; PF00400; WD40; 4.
ProDom; PD000018; WD40; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X98884; CAA6738
PIR; T30334; T30334.
HSSP; Q05783; 1HMA.
                                                                                                                                                                               Methanopyrus.
NCBI_TaxID=2320;
                                                                                                                                                                                                                   Methanopyrus kandleri
                                                                                                                                                                                                                                                                                                     HIS3_METKA
P58836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a detween the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                         Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000910; HMG_12_box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 1 HMG box domain
         phosphoribosyl) -5-[(5-
phosphoribosylamino) methylideneamino] imidazole-4-carboxamide
                                                                                                                                                                                                                                                                                                                                                                                  829 DFRSRLTAGYS 839
                                                                                                                                                                                                                                                                                                                                                                                                          Н
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                          DIRKRFTSGYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52
92
134
184
228
271
821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAA67387.1; -.
                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91
131
173
273
267
310
                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124649
                      1-(5-phosphoribosyl)-AMP + H(2)0 = 1-(5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 5.
WD 7.
ASP/GLU-RICH (ACIDIC).
GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGION; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HMG-BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; WD 1.
                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4F4C4A3FC7422082 CRC64;
                                                                                                                                                                                                                                                                                                                   141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
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ing as its content
wed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Length 1127;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                       L Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration - MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYCV BPB03 STANDAKU;

Q37896;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lysozyme (EC 3.2.1.17) (Lysis protein) (Muramidase) (Endolysin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                        MEDINE-98019084; PubMed-9358052;
Pecenkova T. Benes V. Paces J., Vlcek C., Paces V.;
Pecenkova T. Benes V. Paces J., Vlcek C., Paces V.;
Pecenkova T. Benes V. Paces J., Vlcek C., Paces V.;
Pecenkova T. Benes V. Paces J., Vlcek C., Paces V.;
Gene 199:157-163(1997).
Gene 199:157-163(1997).
-I-FUNCTION: Helps to release the mature phage particles from the cell wall by breaking down the peptidoglycan (By similarity).
-I-CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between 1 acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan heteropolymers of the prokaryotes cell walls.
-I-DOWAIN: LysM repeats are thought to be involved in peptidoglycan
                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses, phi-29-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BPB03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01502; PRA-CH; 1.
ProDom; PD002610; PRA-CH; 1.
Histidine biosynthesis; Hydrolase; Complete proteome.
SEQUENCE 141 AA; 16089 MW; 14E92D9A4DFDAFB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_01021; -; 1
InterPro; IPR002496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE010444; AAM02750.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: Histidine biosynthesis; third step.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the PRA-CH family.
EMBL; X99260; CAA67646.1; -.
HSSP; P00720; 103L.
InterPro; IPR002196; Glyco_hydro_24.
InterPro; IPR002492; LysM.
Pfam; PF01476; LysM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage
                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to family 24 of glycosyl hydrolases.-!- SIMILARITY: Contains 2 LysM repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB
Pred. No. 10;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baswendale J., Bayraktaroglu L., Beasley E.M.,
RA Brandon R.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Glodek A., Gong F., Gorrell J.H., Guz., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Guz., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liux, Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Meinerl B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liux, Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sunth T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p17205; Q9VAD9; Q9VAE0;
01-AUG-1990 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serine proteases 1/2 precursor (EC 3.4.21.-).
(SER99DA OR SER1 OR CG7877) AND (SER99DB OR SER2
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insect.
Neoptera; Endopterygora; Diptera; Brachycera; Muchanis (Prosophila)
Neoptera; Endopterygora; Diptera; Brachycera; Muchanis (Prosophila)
NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00959; Phage_lysozyme; 1.

SMART; SM00257; LysM; 2.

Late protein; Hydrolase; Glycosidase; Bact
ACT_SITE 15 15 PROTON DONOR

REPEAT 165 209 LYSM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yun Y., Davis R.L.; 
"Levels of RNA from a family of putative serine protease genes are reduced in Drosophila melanogaster dunce mutants and are regulated cyclic AMP.", Mol. Cell. Biol. 9:692-700(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SER1
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219
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263 LY
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LYSM 2.
; 5C1A7C8282AlDBCE CRC64;
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Pred. No.
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RESULT 14
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ID KRB2_V
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Best Local S
Matches
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Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin d.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin d.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin d.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin d.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin d.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin d.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin d.M., Venter J.C.,
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A Gibbs R.A., Myers E.W., Rubin d.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin d.M., Nethodall d.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin d.M., Nethodall d.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin d.M., Nethodall d.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin d.M., Nethodall d.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin d.M., Nethodall d.M., Net
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00839; V8PROTEASE.
SMART; SM00020; TRYPS:N DOM; 1.
PROSITE; PS50240; TRYPSIN HIS; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
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EMBL; M24379;
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FlyBase; FBgn0003357; Ser99Db.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR008256; Peptidase_S1B_V8
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PIR; JS0260; JS0260.
HSSP; P00761; 1EPT.
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                                                                                                                                                                          ш
                                                                                                                                                                                                                   Similarity 53.8
7; Conservative
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CHARGE RELAY SYSTEM (B
CHARGE RELAY SYSTEM (B
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CHARGE RELAY SYSTEM (B
SY SIMILARITY.
                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
A -> T (IN REF. 1; 1; 4; 44848C523F03384B)
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Pred. No.
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                          PRT;
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                          283
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CRC64;
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(BY SIMILARITY).
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Matches
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Best Local
                                                                                                                                                          2 VACCV

-KRB2 VACCV

P24362;

01-MAR-1992

01-MAR-1992

16-OCT-2001
SEQUENCE FROM N.A.
MEDLINE=91259063; PubMed=2045793;
Smith G.L., Chan Y.S., Howard S.T.;
"Nucleotide sequence of 42 kbp of vaccinia virus strain the right inverted terminal repeat.";
                                                                                                                                            01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Possible protein kinase Bl2 (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Possible protein kinase B12 (EC 2.7.1.-).
                                                                                 NCBI_TaxID=10254;
                                                                                             Orthopoxvirus
                                                                                                        Vaccinia virus (strain )
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              Transferase; Serine/threonine-protein kinase; ATP-binding
DOMAIN 1 283 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG. PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Appendix to 'The complete Virology 179:517-563 (1990) -:- SIMILARITY: BELONGS TO POXVIRUSES SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete DNA sequence of vaccinia Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goebel S.J., Johnson G.P., Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=91021027; PubMed=2219722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Orthopoxvirus.
NCBI_TaxID=10249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD000001; Prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M35027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paoletti E.;
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InterPro; IPR008271; Ser_thr_pkin_AS
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                                                                                                                                                                                                                                                                                                                              Similarity 6; Conser
                                                                                                                                                                                                                                                                               VRICHTISSFYNY
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viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                   33366 MW;
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50.0%;
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                                                                                                        RNA stage; Poxviridae; Chordopoxvirinae;
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Pred. No.
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E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is produced
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Search completed: October 5, 2004, 08:01:53 Job time: 3.16358 secs
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Best Local Similarity
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MEDLINE=90111697; PubMed=2607336;
HOward S.T., Smith G.L.;
"Two early vaccinia virus genes encode polypeptides related to protein kinases.";
J. Gen. Virol. 70:3187-3201(1989).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. POXYURUSES SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000719; Prot kinase.
InterPro; IPR000871; Ser thr pkin AS.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00108; PROTEIN KINASE ST; FALSE NEG.
PROSITE; PS50011; PROTEIN KINASE DOM; ATP-binding.
Transferase; Serime/threonine-protein kinase; ATP-binding.
DOMAIN
1 283
PROTEIN KINASE
TOTALE TOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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EMBL; D00629; BAA00520.1; -.
PIR; A33610; TVVZBW.
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                                                                                                                                                                                                                                         2 IRKRFTSGYSHY 13
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ص
                                                                                                                                                              VRKNFTSSFYNY 42
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                                                                                                                                                                                                                                                                                                                51.4%; Score 37; DB 1; Length 283; ilarity 50.0%; Pred. No. 22; Conservative 3; Mismatches 3; Indels
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
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5: sp_invertebrate:*
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5: sp_mammal:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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SUMMARIES
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9848a2 Clostridium		Salmo	Q9y3s2 homo sapien	17	Q922h9 mus musculu	rea	Q881h7 pseudomonas	Q97g02 clostridium	8t2al dictyosteli		Q9sa04 arabidopsis	Q8s0p3 oryza sativ	lasmoc	Q9uy62 pyrococcus			9kjc5 staphylococ	Q8nyw2 staphylococ	Q8nyx1 staphylococ	×	staphylo	н	94ml9 bacillus am	Q83vm7 streptococc	Q83vn0 streptococc	83vn3 streptococc	21813 ca	86pj4 caenorhabdi

# ALIGNMENTS

RESULT 1

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RESULT 3
Q21694
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Best Local S
Matches 7
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PIR; D70422; D70422.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016760; F:cellulose synthesis; IEA.

GO; GO:0016760; F:cellulose biosynthesis; IEA.

GO; GO:0030244; P:cellulose metabolism; IEA.

GO; GO:0030214; P:cellulose synth.

InterPro; IPR005159; Cellulose synth.

InterPro; IPR00319; Cellulose synth.

InterPro; IPR00319; Cellulose synth.

InterPro; IPR001173; Glyco trans 2.

Pfam; PF00552; Cellulose synth.

Pfam; PF005535; Cellulose synth.

PFAm; PF005535; Cellulose synth.

PRINTS; PR01439; CELLSNTHASEA.
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Aquifex aeolicus.
Bacteria; Aquificae; Aquificales; Aq NCBI_TaxID=63363;
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Best Local :
                                                                 Q21694;
Q21694;
Q1-NOV-1996
Q1-OCT-2001
Q1-OCT-2003
         Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                  Caenorhabditis elegans.
Finkarvota; Metazoa; Nematoda;
                                                        Hypothetical
                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 759 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=VF5;
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(TrEMBLrel.)
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                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                  89561 MW;
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70.0%;
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                                                                  18,
25,
           Caenorhabditis.
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Pred. No. 51;
1; Mismatches
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Last annotation updat
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                    Chromadorea;
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Pred. No.
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                                                                 annotation update)
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                                                                                                               879 AA
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29;
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                      Rhabditida;
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                      Rhabditoidea;
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RESULT 4
Q9PNZ2
ID Q9PNZ2
PRELIMINARY; PRT; 401 AA.
AC Q9PNZ2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation up
DE Putative integral membrane protein.
GN CJ0941C.
OS Campylobacter jejuni.
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Matches 8
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SMART; SM00220; S TKC; 1.

SMART; SM00123; S TKC; 1.

SMART; SM00133; S TKC; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.

PROSITE; PS500107; PROTEIN KINASE DOW; 1.

PROSITE; PS50011; PROTEIN KINASE DOW; 1.

PROSITE; PS500108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

Serine/threonine-protein kinase; Transferase.

Serine/threonine-protein kinase; Transferase.
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G0; G0:000554; C:nucleus; IEA.
G0; G0:0005524; F:RATP binding; IEA.
G0; G0:0005524; F:RATP binding; IEA.
G0; G0:0004674; F:protein serine/threonine kinase activity; IEA.
G0; G0:0003700; F:transcription factor activity; IEA.
G0; G0:0016740; F:transferase activity; IEA.
G0; G0:0016740; F:transferase activity; IEA.
G0; G0:0006468; P:protein amino acid phosphorylation; IEA.
G0; G0:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00433; pkinase C; 1.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000001; Prot_kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001356; Homeobox.
InterPro; IPR000961; Pkinase.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkin As.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U41550; AAA83287.2; PIR; T16679; T16679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P05132; 1CTP.
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STRAIN=Bristol N2;
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PF00069; pkinase; 1
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Pred. No. 59;
0; Mismatches
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EMBL/GenBank/DDBJ databases.
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elegans Sequencing Consortium.";
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RESULT 6
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STRAIN-NCTC 11168;
MEDLINE=20150912; PubMed=10688204;
MEDLINE=20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R. M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Mculle S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
Wh
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EMBL, AL139076; CAB73198.1; -.
PIR; D81368; D81368.
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Campylobacteraceae; Campylobacter.
NCBI_TaxID=197;
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Hypothetical protein.
Dictyostelium discoideum (Slime mold).
Dictyostelium discoideum (Slime mold).
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gloeckner G., Bichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A., "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
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   Q88AW5
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 453 AA; 51421 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baumgart C.;
Submitted (MAR-2003) to the
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Pred. No.
                                                                                                                                                                                                                                                                                                      Score 42; DB Pred. No. 44; 1; Mismatches
       PRT;
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39;
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AC Q8D4

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Matches 7
                                                                                                                                                      "Complete genome sequence of Vibrio vulnificus CI submitted (DEC-2002) to the EMBL/GenBank/DDBJ dat EMBL; AB016812; AA008065.1; -- GO; GO:0005622; C:intracellular; IEA. GO; GO:0004871; F:signal transducer activity; IE. GO; GO:0006935; P:chemctaxie; IEA. GO; GO:0006935; P:chemctaxie; IEA. GO; GO:0007165; P:signal transduction; IEA. InterPro; IER002545; Chew. 1. Pfam; PF01584; Chew; 1. SMART; SM02260; Chew; 1.
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01-JUN-2003
01-JUN-2003
01-OCT-2003
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003
01-MAR-2003
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                                                     Complete
SEQUENCE
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Q8D4X1;
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0005810; P:transport; IEA.

GO; GO:0006810; P:transport; IEA.
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Vibrionaceae; Vibrio.
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(TrEMBLrel. 24, Last sequence up
(TrEMBLrel. 25, Last annotation
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(TrEMBLrel.
(TrEMBLrel.
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                                                            18776 MW;
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urkin A., Kolonay J., Madupu R., Daugherty S.,
Haft D., Selengut J., Nelson W., Davidsen T.,
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24,
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Pred. No. 1.4e+02;
2; Mismatches 3
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                                                                9AA813E8891B7B61 CRC64;
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40;
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DB
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16;
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Length 168;
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nn M.,
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Query Match

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            Q89PJ3;
Q89PJ3;
01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                   Complete
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L. Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., W. Z., Romero P., Gordo Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                          EMBL; AE009195; AAL43468.1; -. EMBL; AE008161; AAK88215.1; -.
                                                                                                                                                                                                                                                                                                                "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipase esterase.
ATU2481 OR AGR_C 4503.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=21608550; PubMed=11743193;
Wood D.W., Setubal J.C., Kaul R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=21608551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nester E.W.;
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01-OCT-2003
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F97657; F97657.
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          (TrEMBLrel. 24, (TrEMBLrel. 24,
                                                                                                                                                                 Conservative
                                                 PRELIMINARY;
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2; Mismatches
                                                 PRT;
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          sequence update)
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on update)
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ida N.F. Jr., Woo L.,
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Dolan M.,
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Best Local S
Matches 8
Query Match
Best Local
                                                                 GG; GG:0003677; F:DNA binding; IEA.
GG; GG:0008168; F:methyltransferase activity; IEA.
GG; GG:0008326; F:site-specific DNA-methyltransferase (cytosi.
GG; GG:0008326; F:stransferase activity; IEA.
GG; GG:0006306; F:DNA methylation; IEA.
InterPro; IPR001255; GS_DNA-meth.
Pfam; PF00145; DNA-methylase; 1.
PROSITE; PS00095; GS_MTASE_2; 1.
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Marel S., Phouanenavong S.,
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                                          Methyltransferase; SEQUENCE 331 AA;
                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE PAMILY EMBL, AY118475; AAM49844.1; -. FlyBase; FBgn0028707; Mt2.
                                                                                                                                                                                                                             Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA C: ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE
                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa; Arthropoda, Hazapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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01-OCT-2002 (TrEMBLrel. 22, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last anno
GM14972p (EC 2.1.1.73) (Modification
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                            methyltransferase).
MT2 OR CG10692.
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STRAIR=USDA 110;
MEDLINE=22484998; PubMed=12597275;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchium Kaneko T., Nakamura Y., Sato S., Minamisawa K., Iriguchi M., Kaw Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005947; BAC48752.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
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 Similarity
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8; Conserv
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37900 MW;
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55.6%;
75.0%;
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Last sequence update)

Last annotation updat
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Pred. No.
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DB
73;
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67;
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M., Kawashima K.,
, Wada T., Yamada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Cytosine-specific
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RX MEDLINES PROWN N.A.

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., RA Ballew R.M., Basu A., Barker B.G., Helt G., Nelson C.R., Gabor G.L., RA Ballew R.M., Basch A., An H.J., Andrews-Pfannkoch C., Baldwin D., RA Beeson K.Y., Benos P.V., Berman B.P., Bandata D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Dewise P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davise P., RA Durbin K.J., Evangelista C.C., Ferrier S., Freischmann W., RA Glodek A., Gong F., Gorg N.S., Gelbart W.M., Glasser K., RA Hostin N.J., Houston K.A., Howland T.J., Hernandez J.R., Houck J., RA Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris M., Maltei B., McIntosh T.C., Kravitz S., Kulp D., Lai Z., Laing Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lin X., Martin M., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosheefi A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosheefi A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosheefi A., RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Mang Z.Y., Massarman D.A., Weinstock G
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01-MAR-2003
01-MAR-2003
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Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
                                                                                                                                                    SEQUENCE
Celniker
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MEDLINE=20196006;
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.A., Gocayne J
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Best Local S
Matches 6
       SEQUENCE FROM N.A.

RESTRAIN-Berkeley;

XX MEDILINE20196006; PubMed=10731132;

XX Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

XA Adams N.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

XA Adams N.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

XA Adams N.D., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

XA Beronge R.A., Lewis S.E., Richards S., Ashburner M., Ffeiffer B.D.,

XA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

XA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

XA Baradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

XA Baradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Baldwin D.,

XA Barlova C., Bayayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

XA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

XA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

XA Borkova D., Botchan M.R., Bouck J., Brökstein P., Brottier P.,

XA Bartos G.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2002) to the EMBL/Geni
EMBL; AE003635; AAN10803.1; -...
FlyBase; FBgn0028707; Mt2.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA methylation; I.
InterPro; IPR001525; C5_DNA meth.
Pfam; PF00145; DNA methylase; 1.
PROSITE; PS00095; C5_MTASE_2; 1.
SEQUENCE 331 AA; 37870 MW; 6F4BC
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Q9VKB3;
Q1-MAY-2000
01-MAY-2000
01-OCT-2003
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Submitted
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Eukaryota; Metazoa; Arthropoda; Hexagoda;
Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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(TIEMBLICE1. 13, Last sequence update)
(TIEMBLICE1. 25, Last annotation updat
(EC 2.1.1.73) (Modification methylase
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era; Muscomorpha;
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g G.L.G.,

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SEQUENCE FROM N.A.

Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbel Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris Kronmiller B., Marshall B., Milburn G., Richter J., Ruseo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Shourner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanoglaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                   Gibbs R.A., Rubin (
e EMBL/GenBank/DDBJ
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                                                                      1.
6F4BCA669C905FAA CRC64;
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databases.
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkev B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.R.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Mushrefi A.,

RA Melson D.R., Nelson K.A., Nixon K., Musskern D.R., Pacleb JM.,

RA Melson D.R., Nelson K.A., Nixon K., Musskern D.R., Pacleb JM.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinscock G.M., Weissenbach J.,

RA Yeb J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang S., Yao Q.A.,

RA Yen g. X.H., Zhong F.M., Rubin G.M., Venter J.C.;

RA Zheng X.H., Zhong F.M., Rubin G.M., Venter J.C.;

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RA MENDOSYL-L-HOMCYSTEINE + DNA 5-METHYLTXANSFERASE FAMILY.

DR HSSP; Old+717; 1655.

DR HSSP; Old+717; 1655.

DR HSSP; Old+717; MG3.1; M.Z.

DR HSSP; Old+717; MG3.1; M.Z.
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Matches
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                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilldae; Drosophila.
                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel 13, Created)
01-MAY-2000 (TrEMBLrel 13, Last sequence update)
01-OCT-2003 (TrEMBLrel 25, Last annotation update)
DNA (5-cytosine) methyltransferase homolog (EC 2.1.1.73) (Modification
             SEQUENCE FROM N.A.
MEDLINE=99449787; PubMed=10518555;
Hung M.S., Karthikeyan N., Huang B., Koo H.-C.,
"Drosophila proteins related to vertebrate DNA"
                                                                                                        Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                      methylase) (Cytosine-specific methyltransferase). MT2 OR DNMT2 OR CG10692.
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PROSITE; PS00095; C5 MTASE 2; 1.
Methyltransferase; Transferase,
SEQUENCE 345 AA; 39334 MW; 11
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GO:0008168; F:methyltransferas activity; IEA.
GO:000826; F:site-specific DNA-methyltransferase (cytosi.
GO:0016740; F:transferase activity; IEA.
GO:0006306; P:DNA methylation; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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75.0%;
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                   Kiger J., 8
(5-cytosine)
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kov B.C., Dunn
, Fleischmann
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Q22136
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L PROC. Natl. Acad. Sci. U.S.A. 96:11940-11945(1999).

L PROC. NATLYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA CYTOSINE = S-10: ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.

C -1- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.

EMBL, AF188647; AAF03835.1; -.

R HSSP; 014717; 1G55.

R REBASE; 4245; M.DmeORFAP.

R FLYBase; FB9n028707; Mt2.

R G0; G0:0003677; F:DNA binding; IEA.

G0; G0:0008168; F:smethyltransferase activity; IEA.

G0; G0:0008369; F:stransferase activity; IEA.

G0; G0:0008369; F:transferase activity; IEA.

G0; G0:0016740; F:transferase activity; IEA.

G0; G0:0016306; P:DNA methylation; IEA.

G0; G0:0016306; P:DNA methylation; IEA.
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Q22136;
01-NOV-1996
                                                                                                                                                                                                                                                                                     Pfam; PF00059; lectin c; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

SEQUENCE 459 AA; 53253 MW; BD173368D31732A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WormPep; T04A8.3; CE01072.
GO; GO:0005529; F:sugar binding;
InterPro; IRR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 282:2012-2018(1998).
EMBL; Z35663; CAA84726.1; -.
PIR; T24425; T24425.
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01-OCT-2003
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MEDLINE=99069613;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biol
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352
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Pred. No. 1e+02;
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RESULT

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ID QSK6S0
ID QSK6S0
ID QSK6S0;
AC QSC172000 (TTEMBLrel. 15, Created)
AC QSK6S0;
AC QSC172000 (TTEMBLrel. 15, Last sequence update)
BE G1/COSyltransferase.
AC QSC172000 (TTEMBLrel. 15, Last sequence update)
BE G1/COSyltransferase.
AC QSC172000 (TTEMBLrel. 15, Last sequence update)
BE G1/COSyltransferase.
AC QSC172000 (TTEMBLrel. 15, Last sequence update)
BE G1/COSyltransferase.
AC QSC172000 (TTEMBLrel. 15, Last sequence of Bacillus.
AC QSC172000 (TTEMBLrel. 124, Last sunctation update)
BE SEQUENCE FROM N.A.
BE SEQUENCE FROM N.A.
BE SEQUENCE FROM N.A.
BE SEQUENCE OF TAKAKI Y., Maeno G., Sasaki R., Masui N., R. WEDLINEE 25; DLWAGHALINA Y., Ogasaswara N., Kuhara S.,
BA Fuyi F., Hirama C., Makamura Y., Ogasaswara N., Kuhara S.,
BA Fuyi F., Hirama C., Makamura Y., Ogasaswara N., Kuhara S.,
BA Fuyi F., Hirama C., Makamura Y., Ogasaswara N., Kuhara S.,
BA Fuyi F., Hirama C., Makamura Y., Ogasaswara N., Kuhara S.,
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BA Fuyi F., Hirama C., Makamura Y., Ogasaswara N., Kuhara S.,
BA Fuyi F., Hirama C., Makamura Y., Ogasasw
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Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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1: geneseqp1980s:*
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geneseqp2004s:*
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### SUMMARIES

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51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	52.1	52.8	52.8	52.8	52.8	52.8
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# ALIGNMENTS

RESULT 1
AMBIOSOL
ID AMBIOSOL
ID AMBIOSOL
ID AMBIOSOL
ID AMBIOSOL
ACCOMMENTATION
ACCOMMENTATION Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3. 10-DEC-2001 AAE10550; AAE10550 standard; peptide; 13 EP1134231-A1 Lama sp. Llama 14-MAR-2000; 2000EP-00200930 20-FEB-2001; 2001EP-00200703. 19-SEP-2001. (UNIL ) UNILEVER NV. species (first entry) antibody VHH CDR3 #19. A

Bezemer S, Van De Burg ž De Haard JJW, Tareilus E;

WPI; 2001-572718/65.

New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.

Claim 4; Page 29; 37pp; English.

The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of liama species (camelid) antibody VHH region

X &

Sequence

13

AA,

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RESULT 2
ABU26547
ID MASC2
XX ABU2
XX ADU2
XX ADU2
XX ADU2
XX ADU1
I9-J
DE Prot
XX ADU2
XX ADU2
XX ADU1
XX ADU2
XX ADU2
XX ADU1
XX ADU2
XX ADU
               cc the 6213 antisense sequences given in the specification where expression confirmation of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense cmucleic acid; (2) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the antisense cmucleic acid; (4) an antibody capable of specifically binding containing the vector; (5) an isolated CC polypeptide; (5) producing the polypeptide; (6) inhibited by the continuous containing the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of cuprired for proliferation, or that has an activity against a biological pathway crequired for proliferation or the biological pathway in which a proliferation required gene or its gene product lies cor a gene on which the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of confirming the catent than the compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisense nucleic acids, useful for identifying proteins or screening homologous nucleic acids required for cellular proliferation to late candidate molecules for rational drug discovery programs.
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DB; ACA30417.
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 54471; 1766pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prokaryotic essential
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Xu HH;
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                                                                        devoid of light chains specific for inhibiting human dietary enzymes or food for inhibiting the activity of one or more human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is a complementarity determining region 3 (CDR3) of llama species (camelid) antibody VHH region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprisheavy chain variable domain derived from immunoglobulin naturally described to the control of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Llama antibody; camelid; anorectic; heavy chain variable domain; VHH; human dietary enzyme inhibitor; medicament; human panoreatic lipase; HPL; food; human gastric lipase; HGL; cosmetic control; body weight; complementarity determining region 3; CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                               The patent
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                                                                                                                                                                                                                                                                                                                                                                                  atent discloses antibodies or their fragments comprising variable domain (VHH) derived from an immunoglobulin nat
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                                                                                The patent discloses antibodies or their fragments comprising a heavy chain variable domain (VHH) derived from an immunoglobulin naturally devoid of light chains specific for inhibiting human dietary enzymes. The antibodies of the invention are useful for the preparation of medicaments or food for inhibiting the activity of one or more human dietary enzymes especially human pancreatic lipase (HPL) or human gastric lipase (HGL) which are useful for the cosmetic control of body weight of human beings. The present peptide sequence is HPL inhibiting VHH fragment, HPL #18 from
                                                                                                                                                                                                                   New antibody or its fragments for inhibiting human dietary enzymes, useful for cosmetic control of body weight of human beings, comprises heavy chain variable domain derived from immunoglobulin naturally devoid of light chains.
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human dietary enzyme inhibitor; medicament; human pancreatic lipase; HPL;
food; human gastric lipase; HGL; cosmetic control; body weight.
                                                                                                                                                                                              Example 2;
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                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2000; 2000EP-00200930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lama sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE10556 standard;
                                                                     present peptide sequence
na (camelid) species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
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 Similarity
7; Conserv
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UNILEVER PLC.
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                                                  130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRRKFTSEYNEY 13
                                                                                                                                                                                              Page 10; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                         Van De Burg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide;
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              56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complementarity determining
                                                                                                                                                                                                                                                                                                         ź
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                                                                                                                                                                                                                                                                                                         De Haard JJW,
  Score 41; DB Pred. No. 38; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPL #18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from llama species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       determining
                         4;
                                                                                                                                                                                                                                                                                                          Tareilus
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                        Length 130;
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Conservative

2

Indels

0

Gaps

0

17-JAN-2001

(first entry)

RESULT 6
AAB27255
ID AAB2
XX
AC AAB2
XX
AC AAB2
XX
AC 17-J

AAB27255;

AAB27255

standard;

protein;

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30

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RESULT 5
AAP01953
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                          Query Match
Best Local S
Matches
                                                                                                    The invention describes a novel isolated polymucleotide comprising a nucleotide sequence encoding one of 17 specific cyclin dependent kinase inhibitor (CDKI) polypeptides, cell cycle regulators involved in control of cell division, growth and death. The nucleotide sequences can be used in a vector to transform a host cell to produce the CDKI polypeptide. They can also be used in methods for selecting and obtaining a nucleic acid sequence that encodes CDKI or affects the level of CDKI expression. The encoded protein can be used in a method for evaluating a compound for its ability to inhibit the activity of a CDKI. The inhibitors can be used as herbicides. They can also be used to inhibit plant growth. The polymucleotide sequences can be used in gene mapping and as genetic markers. The sequence is the soybean CDKI clone s12.pk0117.h4 as described in the method of the invention
                                                                                                                                                                                                                                                                                                                       Cyclin dependent kinase inhibitor sequences, useful herbicides and plant growth inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyclin dependent kinase plant growth inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2001
                                                                               Sequence
                                                                                                                                                                                                                                                                                             Claim 10; Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-679375/66
                                                                                                                                                                                                                                                                                                                                                                                                       Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2000; 2000WO-US009106
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                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRKRFTSGYSHY
 DIRKRFTSGYSH 12
                                                                               60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PONT DE
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0128192P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kinase inhibitor (CDKI) clone s12.pk0117.h4.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                       Cahoon RE;
                                       58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                            Score 40; DB Pred. No. 26; 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDKI; herbicide; cell cycle;
                                                     ω,
                                                     Length 60;
                             Indels
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RESULT 7
AAW24387
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the soybean cyclin-dependent kinase inhibitor (CDKI): Its coding sequence was isolated by searching a soybean seedling cDNA library for sequences similar to those encoding the CDKI from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI is involved in the cell cycle, and may promote or inhibit cell division and growth. The protein and its coding sequence are useful in the production of transgenic plants which produce increased or decreased amounts of the CDKI protein, in the identification of herbicides, in genetic and physical mapping and in the isolation of the CDKI gene in
                   06-APR-1995;
                                        06-APR-1995;
                                                                                       US5639454-A
                                                                                                              Lymantria dispar
                                                                                                                                      insect
                                                                                                                                                Gypsy moth; nuclear
                                                                                                                                                                        Lymantria dispar nuclear polyhedrosis virus 25.7 kDa protein
                                                                                                                                                                                                 26-SEP-1997
                                                                                                                                                                                                                         AAW24387;
                                                                                                                                                                                                                                              AAW24387 standard; protein; 218 AA
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-679375/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soybean; cyclin-dependent kinase CDKI; cell growth; herbicide.
                                                                17-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                            other organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2000; 2000WO-US009106.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soybean cyclin-dependent kinase inhibitor #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200060087-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DUPO ) DU PONT DE NEMOURS & CO
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                                                                                                                                                                                                                                                                                                           ω
                                                                                                                                     pest;
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                                                                                                                                                                                                                                                                                                                                DIRKRFTSGYSH 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weng
                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                  nuclear polyhedrosis virus; LdMNPV; insecticide; pesticide; baculovirus; broad host range; virulence; increase.
                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0128192P
                   95US-00417822
                                         95US-00417822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58pp;
                                                                                                                                                                                                                                                                                                                                                                 55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
                                                                                                                                                                                                                                                                                                                                                      Score 40; DB
Pred. No. 26;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                         ω
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RESULT 8
ABB65205
ID ABB6
XX ABB6
XX ABB6
XX Dros
XX PD W02(
XX Dros
XX PD W02(
XX WD1.
XX PI Veni
XX New
PT Inti
XX New
PT gen
PX New
PT gen
XX Dis
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a protein of 25.7 kDa encoded by the p25.7 gene from Lymantria dispar nuclear polyhedrosis virus (LdMNPV). The LdMNPV p25.7 gene enables recombinant baculoviruses to replicate in cells, tissue or insect species in which the natural baculovirus isolate cannot replicate. In addition to extending host range of certain baculoviruses, the p25.7 gene can also increase virulence against the usual host of the unaltered virus. For example, insertion of this sequence into Autographa californica nuclear polyhedrosis virus (AMMPV) resulted in a significant reduction in LD50 required to control insects that are susceptible to infection by unaltered ACMNPV
                                                               New isolated nucleic a genes from Drosophila interactions.
                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 22407
                                                                                                                           N-PSDB; ABL09308
                                                                                                                                                                    Venter
                                                                                                                                                                                                                        23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                              27-SEP-2001
                                                                                                                                                                                                                                                                                                                         WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB65205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB65205 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 218 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lymantria dispar nuclear polyhedrosis virus p25.7 g
insecticidal nuclear polyhedrosis baculovirus with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-332002/30.
N-PSDB; AAT77280.
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                                                                                                                                                                                              (PEKE ) PE CORP NY.
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                                                                                                                                        2001-656860/75
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                                                                                                                                                                   JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IRKRFTSGYSHY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Similarity 6; Conserv
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                                                                                                                                                                   Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                 acid
a and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48
                                                                                                                                                                   片
                                                                                                                                                                   PWD,
                                                                              detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                            biology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB
Pred. No. 94;
2; Mismatches
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22
                                                                                                                                                                   Myers
                                                                                                                                                                                                                                                                                                                                                                                            cell
                                                                                                                                                                    Σ
                                                                                                                                                                                                                                                                                                                                                                                          signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene - used to produce
h increased host range.
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The invention relates to an isolated nucleic capable of detecting 1000 or more genes from

or more genes

acid detection reagent Drosophila. The invent

invention

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Disclosure; SEQ ID NO

22407; 21pp + Sequence

Listing; English

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RESULT 9
AAM17463
ID
AXX
AAM17463
AAM17463
AXX
AAM17463
AXX
AAM17A
AXX
AAM17A
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Best Local Similarity
Matches 6; Conserv:
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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                                                                                                                  The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US000670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cervical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #3897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID NO 22289; 487pp; English.
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; microarray; gene expression; cervical epithelial cell; al cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
                                                                 the printed specification, but y from WIPO at ftp.wipo.int/pub/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTSGYSHY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; protein; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTKGYTHY 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel
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2000US-00608408.
2000US-00632366.
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2000US-0236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 4;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                  was
                                                                                              obtained in
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                                                                                              electronic
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Sequence

40 AA

RESULT 11
ABB31275
ID ABB31
XX
AC ABB31

ABB31275 standard; peptide; 40

A

ABB31275;

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RESULT 10
ABB36483
ID ABB36
XX ABB36
XX ABB36
XX ABB36
XX ABB36
XX Pept
XX Huma
XX Huma
XX Homc
XX PD 09-
XX PD 09-
XX PR 26-
PR 26-
PR 27
PR 27
PR 21
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                                                                    Query Match
Best Local Similarity
Thes 7; Conserv
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Best Local S
Matches 7
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30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                   The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #3989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB36483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                         Sequence 40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome-derived single exon nucleic acid probes useful for expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VRKRFTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 IRKRFTSG
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7; Conserv
                                       2 IRKRFTSG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULAR DYNAMICS
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VRKRFTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 29118; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0207456P.
2000US-0068408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000US-0236359P.
2000US-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     liver; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoded by human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.2%;
                                                                                                                   54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression; single exon nucleic acid probe.
                                                                                           ۲,
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Pred. No. 25;
1; Mismatches
                                                                                                                   Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       foetal liver single exon probe.
                                                                                              Mismatches
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                                                                                                                   DB
25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
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                                                                                                                                          Length 40
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                                                                                              Gaps
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RESULT 12
ABB21825
ID ABB21
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AC ABB21
XX
DT 23-JF
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Best Local S
Matches 7
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-03236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                          from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic NNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
        23-JAN-2002
                                         ABB21825;
                                                                    ABB21825
                                                                                                                                                                                                                                                                                   Sequence 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New spatially-addressable set of single exon nucleic for measuring gene expression in sample derived from comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-496933/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157271-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #3926 encoded by breast cell single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                     -
                                                                                                                                                                                  N
                                                                                                                                                                                                                 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULAR DYNAMICS INC
                                                                                                                                                   VRKRFTSG
                                                                                                                                                                                  IRKRFTSG 9
                                                                    standard; protein; 40 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 14243; 327pp + Sequence Listing;
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                                                                                                                                                                                                                                                                                   <u>A</u>
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
     (first entry)
                                                                                                                                                     ω
                                                                                                                                                                                                                                 54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                 Score 39; DB
Pred. No. 25;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR
                                                                                                                                                                                                                                                DB 4; Length 40;
                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid probes, useful human breast,
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                                                                                                                                                                                                                 Gaps
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RESULT 13
AAM69647
ID AAM69
XX AAM69
AC AAM69
XX 06-NC
XX Human
XX Human
XX Micro
XX Homo
XX Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00608208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21335-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, stagling, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease.
                                                               Human; bone marrow expressed exon; gene expression analysis; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                     Human bone marrow expressed probe encoded protein SEQ ID NO:
                        Homo sapiens
                                                                                                                                                                                    06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                             AAM69647;
                                                                                                                                                                                                                                                                           AAM69647 standard; protein; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001; 2001WO-US000666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   congenital heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein #3824 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157274-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           IRKRFTSG
                                                                                                                                                                                                                                                                                                                                                                                             VRKRFTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 23595; 530pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease
                                                                                                                                                                                                                                                                                                                                                                                                                                            φ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB
Pred. No. 25;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                          probe;
                                                                                                                                          29953.
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Best Local S
Matches 7
                     04 FEB-2000; 2000US-0180312P.
26 MAY-2000; 2000US-0207456P.
30 JUN-2000; 2000US-00608408.
03 AUG-2000; 2000US-00632366.
21 SEP-2000; 2000US-0234687P.
27 SEP-2000; 2000US-02345359P.
04 - CCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure expression in bone marrow samples, which may enable the improved diagnosis and treatment of cances such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000; 2000US-00632366.
203-SEP-2000; 2000US-0234687F.
27-SEP-2000; 2000US-0236359F.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0608408.
                                                                                                            30-JAN-2001; 2001WO-US000667
                                                                                                                                                      WO200157275-A2
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                Human; brain
Alzheimer's o
                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                       05-NOV-2001
                                                                                                                                                                                                                                                                                                   AAM57247 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-488900/53.
                                                                                                                                                                                                                                 brain expressed single
                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
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  MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                            IRKRFTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 29953; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                n expressed exon; gene expression analysis; probe; microarray; disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001WO-US000668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DK,
                                                                                                                                                                                                                                                                                                                                                        œ
                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                             54.2%;
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                                                                                                                                                                                                                                                                                                   40
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Pred.
                                                                                                                                                                                                                                 exon
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                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                 probe encoded protein SEQ
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No.
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25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probes useful
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for analyzing
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NO
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RESULT 19
ABG51329
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Best Local S
Matches 7
                                                                                                                                                  04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40
                                                                                                                                                                                                                 30-JAN-2001;
                                                                                                                                                                                                                                                                                        hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                 Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                     25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                         ABG51329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example
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                                                                                                                         (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SG,
                                                          genome-derived single exon nucleic expression in human adult liver.
                                                                                      2001-488898/53.
                                                                                                                                                                                                                                                                                                                   liver peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
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                                                                                                                         MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                      IRKRFTSG
                                                                                                                                                                                                                                                                                                                                                                                                                      VRKRFTSG
                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                  2000US-0180312P.
2000US-0207456P.
2000US-00608408.
2000US-00632366
2000US-0234687P.
2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                  2001WO-US000664
                                                                                                        DK,
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                                                                                                                                                                                                                                                                                                                                                                         peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29352; 650pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                    SEQ ID No
                                                                                                       Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probes
                                                                                                         Σ
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                                                                                                                                                                                                                                                                                                                                                                         40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                    29977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       red. No. 25;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for analyzing gene
                                                                                                         DR;
                                                                     acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
                                                                     probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression
                                                                      useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
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The invention relates to a single exon nucleic acid probe (SENP) (I) measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in specification (or complements/ fragments). The probe hybridises at his

for

ID NO 29977;

658pp;

English

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CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC involved in genetic liver diseases such as cirrhosis,
CC involved in genetic liver diseases such as cirrhosis,
CC associated with coronary heart disease. ABG47348-ABG5930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent dosease. ABG47348-ABG5930 represent human
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX
XX
XX
XX
Sequence 40 AA;
Cuery Match
Best Local Similarity 87.5%; Prod. No. 25;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps
CQ
2 IRKRFTSG 8
Search completed: October 5, 2004, 08:00:07
Job time: 13.8904 secs
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